

	CTGCTGATGCCTGGCTGTGCGAAGCACTTCATCCAGGCTATCTGCTTCTATGAGTGCTCC CCAAACCTGGGGCCCTGGATCCAGCCAGTGGCCCCGAGTGGGCAGGGAGAGCGAGTTGTG AATGTGCCGCTGTGCCAGGAGGACTGTGAGGAGTGGTGGGAAGACTGTCGCATGTCTTAC ACATGCAAATCCAACCTGGCGTGGTGGCTGGGACTGGAGTCAGGGGAAGAACCGCTGCCCC AAAGGGGCCCAGTGCCTCCCTTTCTCCCATTAATCTCCCAACCCAGCTGACCTGTGTGAG AAGACTTGGAGCAATTCTTTCAAAGCCAGCCCTGAGCGACGGAACAGTGGGCGGTGTCTC CAGAAGTGGTTTGAGCCTGCTCAGGGCAACCCCAATGTGGCCGTGGCCCGCCTCTTCGCC AGCTCTGCCCCATCCTGGGAACTGTCTTACACCATCATGGTCTGCTCCCTGTTCTTGCCG TTCCTTCTCTGAGAGCCCTTCTTCTCCCACTCACATTCCTGCATGTCCACCAACTGTGGG TCA		
	ORF Start: ATG at 61		ORF Stop: TGA at 790
	SEQ ID NO: 48	243 aa	MW at 27942.7kD
NOV14a, CG138573-01 Protein Sequence	MACWWPLLELWTVMPWAGDELLNICMNAKHHKRVSPEDKLYEECI PWKDNACCTLTT SWEAHLDVSPLYNFSLFHCGLLMPGCRKHFIQAICFYECSPNLGPWIQPVAPSGQGERVV NVPLCQEDCEEWWEDCRMSYTKSNWRGGWDWSQGNRCPKGAQCLPFSHYFPTPADLCE KTWSNSFKASPERRNSGRCLQKWFEPAGNPVAVARLFASSAPSWELSYTIMVCSLFLP FLS		

Further analysis of the NOV14a protein yielded the following properties shown in Table 14B.

Table 14B. Protein Sequence Properties NOV14a	
PSort analysis:	0.7480 probability located in microbody (peroxisome); 0.4420 probability located in mitochondrial matrix space; 0.1282 probability located in mitochondrial inner membrane; 0.1282 probability located in mitochondrial intermembrane space
SignalP analysis:	Cleavage site between residues 20 and 21

A search of the NOV14a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several
5 homologous proteins shown in Table 14C.

Table 14C. Geneseq Results for NOV14a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE09454	Human sbg72825FOLATEa protein - <i>Homo sapiens</i> , 250 aa. [WO200160850-A1, 23-AUG-2001]	1..243 1..250	243/250 (97%) 243/250 (97%)	e-156
AAB50286	Human folate receptor II protein SEQ ID NO: 6 - <i>Homo sapiens</i> , 255 aa. [WO200071754-A1, 30-NOV-2000]	4..222 5..226	130/222 (58%) 158/222 (70%)	8e-82

ABG19167	Novel human diagnostic protein #19158 - <i>Homo sapiens</i> , 248 aa. [WO200175067-A2, 11-OCT-2001]	19..222 29..235	120/207 (57%) 144/207 (68%)	7e-70
ABG04155	Novel human diagnostic protein #4146 - <i>Homo sapiens</i> , 206 aa. [WO200175067-A2, 11-OCT-2001]	46..242 1..204	101/205 (49%) 128/205 (62%)	5e-54
ABG19166	Novel human diagnostic protein #19157 - <i>Homo sapiens</i> , 187 aa. [WO200175067-A2, 11-OCT-2001]	19..153 27..176	66/151 (43%) 81/151 (52%)	9e-30

In a BLAST search of public sequence databases, the NOV14a protein was found to have homology to the proteins shown in the BLASTP data in Table 14D.

Table 14D. Public BLASTP Results for NOV14a				
Protein Accession Number	Protein/Organism/Length	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9EQF4	Folate receptor 3 (Folate receptor 4) (Delta) - <i>Mus musculus</i> (Mouse), 244 aa.	1..241 1..242	166/242 (68%) 191/242 (78%)	e-104
P15328	Folate receptor alpha precursor (FR-alpha) (Folate receptor 1) (Folate receptor, adult) (Adult folate-binding protein) (FBP) (Ovarian tumor-associated antigen MOv18) (KB cells FBP) - <i>Homo sapiens</i> (Human), 257 aa.	7..242 10..255	140/246 (56%) 169/246 (67%)	1e-84
Q9XSH1	Membrane-bound folate binding protein - <i>Sus scrofa</i> (Pig), 249 aa.	7..239 8..247	138/240 (57%) 167/240 (69%)	4e-84
P41439	Folate receptor gamma precursor (FR-gamma) (Folate receptor 3) - <i>Homo sapiens</i> (Human), 243 aa.	19..222 27..230	129/204 (63%) 152/204 (74%)	5e-82

P35846	Folate receptor alpha precursor (FR-alpha) (Folate receptor 1) (Folate-binding protein 1) - <i>Mus musculus</i> (Mouse), 255 aa.	7..242 10..251	135/242 (55%) 168/242 (68%)	7e-82
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PFam analysis predicts that the NOV14a protein contains the domains shown in Table 14E.

Table 14E. Domain Analysis of NOV14a			
Pfam Domain	NOV14a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Folate_rec	4..238	133/243 (55%) 181/243 (74%)	4e-110

Example 15.

- 5 The NOV15 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 15A.

Table 15A. NOV15 Sequence Analysis	
	SEQ ID NO: 49 1885 bp
NOV15a, CG138606-01 DNA Sequence	TCCTCAAATACAATGCTTCAAAAAACGCTGCTGATCTTGATCTCTTTTTCAGTAGTAACC TGGATGATTTTATAATTTCTCAGAAGCTTCAAAAGCTTGGTCTGCTCTAAACTTATCC ATCTCTGTCCATTACTGGAACAACCTCCGCAAAGTCCTTATTCCTAAAACATCACTGATA CCATTAAAGCCACTAACAGAGACTGAACTCAGAATAAAGGAAATCATAGAGAAACTAGAT CAGCAGATCCCACCCAGACCTTTCACCCATGTGAACACCACCACAGTGCCACACACAGC ACAGCCACCATCCTCAACCCTCGAGATACATACTGCAGGGGAGACCAGCTGGACATCCTA CTGGAGGTGAGGGACCACTTGGGACAGAGGAAGCAATATGGTGGGGATTTCCTGAGGGCC AGGATGTCTCCCCAGCACTGACGGCAGGTGCTTCAGGAAAGGTGATGGACTTCAACAAT GGCACCTACCTGGTCAGCTTCACTCTGTTCTGGGAGGGCCAGGTCTCCCTGCTCTGCTG CTCATCCACCCAGTGAAGGGGCGTCGGCTCTCTGGAGGGCAAGGAACCAAGGCTATGAT AAAATTATTTTCAAAGGCAAATTTGTTAATGGCACCTCTCATGTCTTCACTGAATGTGGC CTGACCCCTAAACTCAAATGCTGAAGCTCTGTGAATATCTGGATGACAGAGACCAAGAAGCC TTCTATTGTATGAAGCCTCAACACATGCCCTGTGAGGCTCTGACCTACATGACCACCCGG AATAGAGAGGTATCTTATCTTACAGACAAGGAAAACAGCCTTTTCCACAGGTCCAAAGTG GGAGTTGAAATGATGAAGGATCGTAAACACATTGATGTCACTAATTGTAACAAGAGAGAA AAAATAGAAGAGACATGCCAAGTTGGAATGAAGCCTCCTGTCCCTGGTGGTTATACTTTA CAAGGAAAATGGATAACAACATTTTGCAACCAGGTTCAAGTTAGACACAATTAAGATAAAT GGCTGTTTGAAGGCAAACTCATTTACCTCCTGGGAGACTCTACACTACGTCACTGAGTATC TACTACTTCCCCAAAGTTGTAAAAACACTGAAGTTTTTTGATCTTCTATGAAACTGGAATC TTAAAGAAACATTTGCTTCTGGATGCAGAAAGACACACTCAGATTCAATGGAAAAACAT AGCTATCCCTTCGTCACTTTCCAGCTCTACTCTCTGATAGATCATGATTATATCCCTCGG GAAATTGACCGGTATCAGGTGACAAAAACAGCCATCGTCATCACCTTTGGCCAGCAC TTTAGACCATTTCCTATTGACATTTTATTTCGAGGGCCATCGGTGTTCAAAGGCTATT GAAAGACTGTTCTTAAGAAGCCAGCCACTAAAGTGATTATTAAGACAGAAAACATCAGG GAGATGCACATAGAGACAGAGAGGTTTGGAGACTTCCATGGTTATATTCACTATCTTATC ATGAAGGATATTTTCAAAGACCTCAACGTGGGCATCATTGATGCCTGGGACATGACCATT GCATATGGCACTGACACTATCCACCCACCTGATCATGTGATTGGAAATCAGATTAAACATG

	TTCTTAAACTACATTTCGCTAAGGGATAAATACTATACAAAATCACTAGGAACCAATCTCT GCACATAATCCACATGTATTGTAAAGTAAAGTTTACTCATTTTAGGAACCAAGGAAAAT AAATTTAAAAGAATCTGTTTGGGGAGGAAGGCTATGTAAGGACAATGACAACTGATAAGG GATGCAAAACCAAGAGAATCATTCATGAAGAATGACTATACCATGCCTGGTTCTGATGCT CGTTTAAATATTAAAAAAGTTTTT		
	ORF Start: ATG at 13		ORF Stop: TAA at 1639
	SEQ ID NO: 50	542 aa	MW at 62656.8kD
NOV15a, CG138606-01 Protein Sequence	MLQKTLILISFSVVTWMIFIISQNF TKLWSALNLSISVHYWNNSAKSLFPKTS LIPLKP LTETELRIKEIIEKLDQQIPPRPFTHVNTTTSATHSTATILNPRDTYCRGDQLDILLEVR DHLGQRKQYGGDFLRARMSSPALTAGASGKVMDFNNGTYLVSFTLFWEGQVLSLLLIHP SEGASALWRARNQGYDKIIFKGKFNVTSHVFTECGLTLNSNAELCEYLDDRDQEAFCM KPQHMPCEALTYMTTRNREVSYLTDKENS LFHRSKVGVEMMKDRKHIDVTNCNKREKIEE TCQVGMKPPVPGGYTLQGWITTFPCNQVQLDTIKINGCLKGKLIYLLGDSTLRQWIYYFP KVVKTLKFFDLHETGIFKKHLLLD AERHTQIQWKKHSYPFVTFQLYSLIDHDYIPREIDR LSGDKNTAIVITFGQHFRRPFIIDIFIRRAIGVQKATERLFLRSPATKVIIKTENIREMHI ETERFGDFHGYIHYLIMKDIKFDLNVGIIDAWDMTIAYGTDTHPPDHVIGNQINMFLNY IC		

Further analysis of the NOV15a protein yielded the following properties shown in Table 15B.

Table 15B. Protein Sequence Properties NOV15a	
PSort analysis:	0.6850 probability located in plasma membrane; 0.6400 probability located in endoplasmic reticulum (membrane); 0.3700 probability located in Golgi body; 0.2923 probability located in microbody (peroxisome)
SignalP analysis:	Cleavage site between residues 19 and 20

- A search of the NOV15a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 15C.

Table 15C. Geneseq Results for NOV15a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU96185	Human secreted protein, SEQ ID No 87 - <i>Homo sapiens</i> , 547 aa. [WO200224721-A1, 28-MAR-2002]	1..542 6..547	542/542 (100%) 542/542 (100%)	0.0
ABG27904	Novel human diagnostic protein #27895 - <i>Homo sapiens</i> , 590 aa. [WO200175067-A2, 11-OCT-2001]	26..542 74..590	515/517 (99%) 515/517 (99%)	0.0

AAU83597	Human PRO protein, Seq ID No 12 - <i>Homo sapiens</i> , 544 aa. [WO200208288-A2, 31-JAN-2002]	4..542 9..544	372/540 (68%) 441/540 (80%)	0.0
AAU96219	Human secreted protein, SEQ ID No 121 - <i>Homo sapiens</i> , 303 aa. [WO200224721-A1, 28-MAR-2002]	1..298 6..303	291/298 (97%) 291/298 (97%)	e-170
AAB74709	Human membrane associated protein MEMAP-15 - <i>Homo sapiens</i> , 277 aa. [WO200112662-A2, 22-FEB-2001]	4..273 9..277	220/270 (81%) 245/270 (90%)	e-129

In a BLAST search of public sequence databases, the NOV15a protein was found to have homology to the proteins shown in the BLASTP data in Table 15D.

Table 15D. Public BLASTP Results for NOV15a				
Protein Accession Number	Protein/Organism/Length	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q05004	Brush border 61.9 kDa protein precursor - <i>Oryctolagus cuniculus</i> (Rabbit), 540 aa.	1..542 1..540	427/542 (78%) 486/542 (88%)	0.0
AAH29049	Hypothetical 46.9 kDa protein - <i>Homo sapiens</i> (Human), 405 aa.	138..542 1..405	404/405 (99%) 404/405 (99%)	0.0
Q9CX72	4432416J03Rik protein - <i>Mus musculus</i> (Mouse), 558 aa.	6..542 24..558	339/539 (62%) 416/539 (76%)	0.0
Q96DL1	CDNA FLJ25224 fis, clone STM00905 - <i>Homo sapiens</i> (Human), 365 aa.	2..292 18..308	205/291 (70%) 239/291 (81%)	e-116
Q969Y0	CDNA FLJ30102 fis, clone BNGH41000137, weakly similar to brush border 61.9 kDa protein precursor (Unknown) (Protein for MGC:15606) - <i>Homo sapiens</i> (Human), 559 aa.	18..542 19..555	168/543 (30%) 287/543 (51%)	3e-69

PFam analysis predicts that the NOV15a protein contains the domains shown in

5 Table 15E.

Table 15E. Domain Analysis of NOV15a			
Pfam Domain	NOV15a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 16.

The NOV16 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 16A.

Table 16A. NOV16 Sequence Analysis			
	SEQ ID NO: 51	1638 bp	
NOV16a, CG138751-01 DNA Sequence	ACACGCGCCAGCTCTGTAGCCTCCTCCGTCGACTCAGCCTTAGGTACCGGTCAGGCAAA ATGCGGTCTCTCCCTGGCTCCGGAGTCTGGTTCTTCCGGGCCTTCTCCAGGGACAGCTGG TTCCGAGGCCTCATCCTGTGCTGACCTTCCTAATTTACGCCTGCTATCACATGTCCAGG AAGCCTATCAGTATCGTCAAGAGCCGTCTGCACCAGAACTGCTCGGAGCAGATCAAACCC ATCAATGATACTCAGTCTCAATGACACCATGTGGTGCAGCTGGGCCCCATTTGACAAG GACAACTATAAGGAGTTACTAGGGGGCGTGGACAACGCCTTCCTCATCGCCTATGCCATC GGCATGTTTCATCAGTGGGGTTTTTGGGGAGCGGCTTCCGCTCCGTACTACCTCTCAGCT GGAATGCTGCTCAGTGGCCTTTTCACTCGCTCTTTGGCCTGGGATATTTCTGGAACATC CACGAGCTCTGGTACTTTGTGGTCATCCAGGTCTGTAATGGACTCGTCCAGACCACAGGC TGGCCCTCTGTGGTGACCTGTGTTGGCAACTGGTTCGGGAAGGGGAAGCGGGGTTTCATC ATGGGCATCTGGAATTCCACACATCTGTGGGCAACATCCTGGGCTCCCTGATCGCCGGC ATCTGGGTGAACGGGCAGTGGGGCTGTGTTTCATCGTGCCTGGCATCATTACTGCCGTC ATGGGCGTCATCACCTTCCTCTCTCATCGAACACCCAGAAGATGTGGACTGCGCCCCCT CCTCAGCACCACGGTGAGCCAGCTGAGAACCAGGACAACCCTGAGGACCCTGGGAACAGT CCCTGCTCTATCAGGGAGAGCGGCCTTGAGACTGTGGCCAAATGCTCCAAGGGGCCATGC GAAGAGCCTGCTGCCATCAGCTTCTTTGGGGCGCTCCGGATCCAGGCGTGGTTCGAGTTC TCTCTGTGCTGCTGTTTGCCAAGCTGGTCAGTTACACCTTCCTCTACTGGCTGCCCTC TACATCGCCAATGTGGCTCACTTTAGTGCCAAGGAGGCTGGGGACCTGTCTACACTCTTC GATGTTGGTGGCATCATAGGCGGCATCGTGGCAGGGCTCGTCTCTGACTACACCAATGGC AGGGCCACCACTTGCTGTGTATGCTCATCTTGGCTGCCCCATGATGTTCTGTGATAAC TACATTGGCCAGGACGGGATTGCCAGCTCCATAGGTGAGGTCCCAGTGATGCTGATCATC TGTGGGGGCTGGTCAATGGCCCATACGCGCTCATCACTGCTGCTCTGCTGATCTG GGGACTCACAAGAGCCTGAAGGGCAGGCAAGCCCTGTCCACGGTCACGGCCATCATT GACGGCACCGGCTCCATAGGTGCGGCTCTGGGGCCTCTGCTGGCTGGGCTCATCTCCCC ACGGGCTGGAACAATGTCTTCTACATGCTCATCTCTGCCGACGTCCTAGCCTGCTGGTC CTTTGCCGTTAGTATACAAAGAGATCTTGGCCTGGAAGGTGTCCCTGAGCAGAGGCAGC GGGTGAGTCCGGGAGCTGAAGCTGCCCTCTACCAACCTCATTCTCGTGGGAATCAGC CCAGCGCTCAGTTTCTCC		
	ORF Start: ATG at 61		ORF Stop: TGA at 1564
	SEQ ID NO: 52	501 aa	MW at 54257.6kD
NOV16a, CG138751-01 Protein Sequence	MRSSLAPGVWFFRAFSRDSWFRGLILLTFLIYACYHMSRKPISIVKSRHLQNCSEQIKP INDTHSLNDTMWCSWAPFDKDYKELLGGVDNAFLIAYAIGMFISGVFGERLPLRYLSA GMLLSGLFTSLFGLGYFVNIHELWYFVVIQVNCGLVQTTGWPSVVTVCVGNWFGKGRGFI MGIWNSHTSVGNILGSLIAGIWNQWGLSFIVPGIITAVMGVITFLFIEHPEDVDCAP PQHHGEPAENQDNPEDPGNSPCSIRESGLETVAKCSKGPCEEPAAISFFGALRIPGVVEF SLCLLFAKLVSYTFYWLPLYIANVAHFAKEAGDLSTLFDVGGIIGGIVAGLVSDYTNG RATTCVMLILAAPMMFLYNYIGQDGIASSIGEVPVMLIICGGLVNGFYALITTAVSADL GTHKSLKGTAKALSTVTAIIDTGSIGAAALGPLLAGLISPTGWNVVFYMLISADVLA CLV LCRLVYKEILAWKVSLSRGS		

	SEQ ID NO: 53	1573 bp	
NOV16b, CG138751-02 DNA Sequence	GACTCAGCCTTAGGTACCGGT CAGGCAAAATGCGGTCTCCCTGGCTCCGGGAGTCTGGT TCTTCCGGGCCTTCTCCAGGGACAGCTGGTTCCGAGGCCTCATCCTGCTGCTGACCTTCC TAATTTACGCCTGCTATCACATGTCCAGGAAGCCTATCAGTATCGTCAAGAGCCGTCTGC ACCAGAACTGCTCGGAGCAGATCAAACCCATCAATGATACTCACAGTCTCAATGACACCA TGTGGTGCAGCTGGGCCCCATTTGACAAGGACAATAAAGGAGTTACTAGGGGGCGTGG ACAACGCCTTCTCATCGCTATGCCATCGGCATGTTTCATCAGTGGGGTTTTTGGGGAGC GGCTTCCGCTCCGTTACTACCTCTCAGCTGGAATGCTGCTCAGTGGCCTTTTCACCTCGC TCTTTGGCCTGGGATATTTCTGGAACATCCACGAGCTCTGGTACTTTGTGGTTCATCCAGG TCTGTAATGGACTCGTCCAGACCACAGGCTGGCCCTCTGTGGTGACCTGTGTGGCAACT GGTTCCGGGAAGGGGAAGCGGGGGTTCATCATGGGCATCTGGAATTCCCACACATCTGTGG GCAACATCTGGGCTCCCTGATCGCCGGCATCTGGGTGAACGGGCAGTGGGGCTGTCTGT TCATCGTGCCTGGCATCATTACTGCCGTTCATGGGCGTCATCACCTTCTCTTCTCATCG AACACCCAGAAGATGTGGACTGCGCCCTCTCAGCACCACGGTGAGCCAGCTGAGAACC AGGACAACCCTGAGGACCCTGGGAACAGTCCCTGCTCTATCAGGGAGAGCGGCCTTGAGA CTGTGGCCAAATGCTCCAAGGGGCCATGCGAAGAGCCTGCTGCCATCAGCTTCTTTGGGG CGCTCCGGATCCCAGGCGTGGTTCGAGTTCTCTGTGTCTGCTGTTTGGCAAGCTGTCGA GTTACACCTTCTCTACTGGCTGCCCTCTACATCGCCAATGTGGCTCACTTTAGTGCCA AGGAGGCTGGGGACCTGTCTACACTCTTCGATGTTGGTGGCATCATAGGCGGCATCGTGG CAGGGCTCGTCTCTGACTACCAATGGCAGGGCCACCATTGCTGTGTCTGCTCATCTCT TGGCTGCCCCCATGATGTTCTGTACAACTACATTGGCCAGGACGGGATTGCCAGCTCCA TAGTGATGCTGATCATCTGTGGGGCCCTGGTCAATGGCCCATACGCGCTCATCACTCTG CTGTCTCTGCTGATCTGGGGACTCACAAGAGCCTGAAGGGCAACGCCAAAGCCCTGTCCA CGGTCACGGCCATCATTGACGGCACCGGCTCCATAGGTGCGGCTCTGGGGCCTCTGCTGG CTGGGCTCATCTCCCCACGGGCTGGAACAATGTCTTCTACATGCTCATCTCTGCCGACG TCCTAGCCTGCTTGCTCCTTTGCCGGTTAGTATACAAAGAGATCTTGGCCTGGAAGGTGT CCCTGAGCAGAGGACGGGTGAGTCCGGGGAGCTGAAGCTGCCCTCTACCAACCTCAT TTCTCGTGGGAAT		
	ORF Start: ATG at 30		ORF Stop: TGA at 1521
	SEQ ID NO: 54	497 aa	MW at 53902.2kD
NOV16b, CG138751-02 Protein Sequence	MRSSLAPGVWFFRAPSRDSWFRGLILLTFLIYACYHMSRKPI SIVKSRHLHQCSEQIKP INDTHSLNDTMWCSWAPFDKDYKELLGGVDNAFLIAYAIGMFISGVFGERLPLRYLISA GMLLSGLFTSLFGLGYFWNHIELWYFVVIQVCNGLVQTTGWPSVVTVCVGNWFGKGRGFI MGIWNSHTSVGNILGSLIAGIWNQWGLSFIVPGIITAVMGVITFLFLIEHPEDVDCAP PQHHGEPAENQDNPEDPGNSPCSIRESGLETVAKCSKGPCEEPAAISFFGALRIPGVVEF SLCLLFAKLVSYTFLYWLPLYIANVAHFSAKEAGDLSTLFDVGGIIGGIVAGLVSDYTNG RATTCVVMLILAAPMMFLYNYIGQDGIASSIVMLIICGGLVNGPYALITTAVSADLGTHK SLKGNALSTVTAIIDGTSGI AALGPLLAGLISPTGWNNVFYMLISADVLACLLLCRL VYKEILAWKVSLSRGSG		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 16B.

Table 16B. Comparison of NOV16a against NOV16b.		
Protein Sequence	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV16b	1..501 1..497	450/501 (89%) 451/501 (89%)

Two polymorphic variants of NOV16a have been identified and are shown in Table 41D. Further analysis of the NOV16a protein yielded the following properties shown in

5 Table 16C.

Table 16C. Protein Sequence Properties NOV16a	
PSort analysis:	0.6318 probability located in mitochondrial inner membrane; 0.6000 probability located in plasma membrane; 0.4778 probability located in mitochondrial intermembrane space; 0.4262 probability located in mitochondrial matrix space
SignalP analysis:	Cleavage site between residues 37 and 38

A search of the NOV16a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 16D.

Table 16D. Geneseq Results for NOV16a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM00776	Human bone marrow protein, SEQ ID NO: 139 - <i>Homo sapiens</i> , 211 aa. [WO200153453-A2, 26-JUL-2001]	181..391 1..211	205/211 (97%) 206/211 (97%)	e-118
AAM00889	Human bone marrow protein, SEQ ID NO: 365 - <i>Homo sapiens</i> , 201 aa. [WO200153453-A2, 26-JUL-2001]	170..368 3..201	193/199 (96%) 195/199 (97%)	e-113
AAG31980	<i>Arabidopsis thaliana</i> protein fragment SEQ ID NO: 38498 - <i>Arabidopsis thaliana</i> , 476 aa. [EP1033405-A2, 06-SEP-2000]	24..489 31..462	220/470 (46%) 296/470 (62%)	e-110
AAB42327	Human ORFX ORF2091 polypeptide sequence SEQ ID NO:4182 - <i>Homo sapiens</i> , 192 aa. [WO200058473-A2, 05-OCT-2000]	295..489 2..192	185/195 (94%) 187/195 (95%)	e-100
ABB64855	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 21357 - <i>Drosophila melanogaster</i> , 432 aa. [WO200171042-A2, 27-SEP-2001]	145..491 80..421	192/352 (54%) 232/352 (65%)	4e-98

In a BLAST search of public sequence databases, the NOV16a protein was found to have homology to the proteins shown in the BLASTP data in Table 16E.

Table 16E. Public BLASTP Results for NOV16a				
Protein Accession Number	Protein/Organism/Length	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q8TED4	CDNA FLJ23627 fis, clone ADSU02391, highly similar to <i>Mus musculus</i> cAMP inducible 2 protein (Ci2) mRNA - <i>Homo sapiens</i> (Human), 501 aa.	1..501 1..497	494/501 (98%) 495/501 (98%)	0.0
Q9WU81	cAMP inducible 2 protein - <i>Mus musculus</i> (Mouse), 501 aa.	1..501 1..497	435/501 (86%) 461/501 (91%)	0.0
Q8TEM2	FLJ00171 protein - <i>Homo sapiens</i> (Human), 396 aa (fragment).	1..346 12..357	346/346 (100%) 346/346 (100%)	0.0
Q8R070	Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1 - <i>Mus musculus</i> (Mouse), 531 aa.	5..489 4..515	308/516 (59%) 377/516 (72%)	e-173
AAF46705	CG10069-PA - <i>Drosophila melanogaster</i> (Fruit fly), 516 aa.	17..491 30..505	257/489 (52%) 320/489 (64%)	e-136

PFam analysis predicts that the NOV16a protein contains the domains shown in

5 Table 16F.

Table 16F. Domain Analysis of NOV16a			
Pfam Domain	NOV16a Match Region	Identities/ Similarities for the Matched Region	Expect Value
sugar_tr	9..494	66/553 (12%) 308/553 (56%)	0.28

Example 17.

The NOV17 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 17A.

Table 17A. NOV17 Sequence Analysis

NOV17a, CG139062-01 DNA Sequence	SEQ ID NO: 55	5590 bp
	CTGCGGCCGCGCGGAGCTAGGCTGGGTTTTTTTTTTCTCCCCTCCCTCCCCCTTTT TCCATGCAGCTGATCTAAAAGGGAATAAAAGGCTGCGCATAATCATATAATAAAGAAG GGGAGCGCGAGAGAAGGAAAGAACCGGGAGGTGGAAGAGGAGGGGAGCGTCTCAAAG AAGCGATCAGAATAATAAAAGGAGCGCGGCTCTTGCCTTCTGGAACGGGCCGCTCTTG AAAGGGCTTTTGAAAAGTGGTGTGTTTTCCAGTCGTGCATGCTCCAATCGGCGGAGTAT ATTAGAGCCGGGACGCGGCGGCGCAGGGGCGAGCGGCGACGGCAGCACCGGCGGCGAGCAC CAGCGCGAACAGCAGCGGCGGCGTCCCGAGTGCCCGCGGCGCGCGGCGCAGCGATGCGTT CCCCACGGACGCGCGGCGGTCGCGGCGCCCCCTAAGCCTCCTGCTCGCCCTGCTCTGTG CCCTGCGAGCCAAGGTGTGTGGGCTCGGGTCAGTTCGAGTTGGAGATCCTGTCCATGC AGAACGTGAACGGGGAGCTGCAGAACGGGAAGTCTGCGGCGGCGCCCGAACCCGGGAG ACCGCAAGTGACCCGCGACGAGTGTGACACATACTTCAAAGTGTGCTCAAGGAGTATC AGTCCCGCTCACGGCCGGGGCCCTGCAGCTTCGGCTCAGGCTCCAGCCTGTGCATCG GGGGCAACACCTTCAACCTCAAGGCCAGCCGCGCAACGACCGCAACGATCGTGCTGC CTTTCAGTTTCGCTGGCCGAGGTCTATACGTTGCTTGTGGAGGCGTGGGATTCAGTA ATGACACCGTTCAACCTGACAGTATTATTGAAAAGGCTTCTCACTCGGGCATGATCAACC CCAGCCGGCAGTGGCAGACGCTGAAGCAGAACACGGGCGTTGCCCACTTTGAGTATCAGA TCCGCGTGACCTGTGATGACTACTACTATGGCTTTGGCTGCAATAAGTCTGCGGCCCCA GAGATGACTTCTTTGGACACTATGCTGTGACCAGAATGGCAACAACTTGCATGGAAG GCTGGATGGGCCCCGAATGTAACAGAGCTATTTGCCGACAAGGCTGCAGTCTTAAGCATG GGTCTTGCAAACCTCCAGGTGACTGCAGGTGCCAGTATGGCTGGCAAGGCCTGTACTGTG ATAAGTGCATCCACACCCGGGATGCGTCCACGGCATCTGTAATGAGCCCTGGCAGTGCC TCTGTGAGACCAACTGGGGCGGCCAGCTCTGTGACAAAGATCTCAATTACTGTGGGACTC ATCAGCCGTGTCTCAACGGGGGAACCTGTAGCAACACAGGCCCTGACAAATATCAGTGT CCTGCCCTGAGGGGTATTTCAGGACCCAACCTGTGAAATGCTGAGCAGCCCTGCCTCTCTG ATCCCTGTCAACAGAGGCAGCTGTAAGGAGACCTCCCTGGGCTTTGAGTGTGAGTGT CCCCAGGCTGGACCGGCCCCACATGCTCTACAAACATTGATGACTGTTCTCTTAATAACT GTTCCCACGGGGGCACCTGCCAGGACCTGGTTAACGGATTAAAGTGTGTGCCCCCAC AGTGGACTGGGAAAACGTGCCAGTTAGATGCAAATGAATGTGAGGCCAAACCTTGTGTAA ACGCCAAATCCTGTAAGAATCTCATTGCCAGCTACTACTGCGACTGTCTTCCCGCTGGA TGGGTGAGAATTGTGACATAAATATTAATGACTGCCTTGGCCAGTGTGAGAATGACGCCCT CCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGCAGGCGATC ACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGTCACTGTC AGAATGAAATCAACAGATTCCAGTGTCTGTGTCCCACTGGTTTCTTGGAAACCTGTGTC AGCTGGACATCGATTATTGTGAGCCTAATCCCTGCCAGAACGGTGCCAGTGCTACAACC GTGCCAGTGACTATTTCTGCAAGTGCCCCGAGGACTATGAGGGCAAGAACTGCTCACACC TGAAAGACCACTGCCGCACGACCCCTGTGAAGTGATTGACAGCTGCACAGTGGCCATGG CTTCCAACGACACACCTGAAGGGGTGCGGTATATTTCTCCAACGTCTGTGGTCTCACG GGAAGTGCAAGAGTCAGTCGGGAGGCAAAATCACCTGTGACTGTAACAAAGGCTTACGG GAACATACTGCCATGAAAATATTAATGACTGTGAGAGCAACCCCTGTAGAAACGTTGGCA CTTGCATCGATGGTGTCAACTCTACAAGTGCATCTGTAGTGACGGCTGGGAGGGGGCT ACTGTGAAACCAATATTAATGACTGCAGCCAGAACCCTGCCACAATGGGGGCACGTGTC GCGACCTGGTCAATGACTTCTACTGTGACTGTAAAAATGGGTGGAAAGGAAAGACCTGCC ACTCACGTGACAGTCAGTGTGATGAGGCCACGTGCAACAACGGTGGCACCTGCTATGATG AGGGGGATGCTTTTAAAGTGATGTGTCTTGGCGGCTGGGAAGGAACAACCTGTAACATAG CCCGAAACAGTAGCTGCCTGCCCAACCCCTGCCATAATGGGGGCACATGTGTGGTCAACG GCGAGTCCTTTACGTGCGTCTGCAAGGAAGGCTGGGAGGGGCCCCTGTGTCTCAGAATA CCAATGACTGCAGCCCTCATCCCTGTTACAACAGCGGCACCTGTGTGGATGGAGACAAC GGTACCGGTGCGAATGTGCCCCGGGTTTTGCTGGGCCGACTGCAGAATAAACATCAATG AATGCCAGTCTTACCTTGTGCTTTGGAGCGACCTGTGTGGATGAGATCAATGGCTACC GGTGTGTCTGCCCTCCAGGGCAGTGGTGCCCAAGTGCCAGGAAGTTTCAGGGAGACCTT GCATCACCATGGGGAGTGTGATACCAGATGGGGCCAAATGGGATGATGACTGTAATACCT GCCAGTGCTGAATGGACGGATGCGCTGCTCAAAGGTCTGGTGTGGCCCTCGACCTTGCC TGCTCCACAAAGGGCAGCGAGTGCCCGAGCGGCGAGCTGCATCCCCATCCTGGACG ACCAGTGCTTCGTCCACCCCTGCACTGGTGTGGGCGAGTGTGGTCTTCCAGTCTCCAGC CGGTGAAGACAAAGTGACACCTTGACTCTATTACCAGGATAACTGTGCGAACATCACAT TTACCTTTAACAAGGAGATGATGTACCAGGTCTTACTACGAGCACATTTGCAGTGAAT TGAGGAATTTGAATATTTTGAAGAATGTTCCGCTGAATATTCAATCTACATCGTTGCG	

	AGCCTTCCCCTTCAGCGAACAAATGAAATACATGTGGCCATTTCTGTGAAGATATACGGG ATGATGGGAACCCGATCAAGGAAATCACTGACAAAATAATCGATCTTGTTAGTAAACGTG ATGGAAACAGCTCGCTGATTGCTGCCGTTGCAGAAGTAAGAGTTTCAGAGGCGGCTCTGA AGAACAGAACAGATTTCTTGTTCCCTTGCTGAGCTCTGTCTTAACTGTGGCTTGATCT GTTGCTTGGTGACGGCCTTCTACTGGTGCCCTGCGGAAGCGGCGGAAGCCGGGCAGCCACA CACACTCAGCCTCTGAGGACAACACCACCAACAACGTGCGGGAGCAGCTGAACCAGATCA AAAACCCCATTTAGAAAACATGGGGCCAACACGGTCCCCATCAAGGATTACGAGAACAAGA ACTCCAAAATGTCTAAAATAAGGACACACAATTCTGAAGTAGAAGAGGACGACATGGACA AACACCAGCAGAAAGCCCGGTTTGCCAAGCAGCCGGCTATACGCTGGTAGACAGAGAAG AGAAGCCCCCAACGGCAGCCGACAAAACACCCAACTGGACAAAACAAACAGGACAACA GAGACTTGGAAAGTGCCAGAGCTTAAACCGAATGGAGTACATCGTATAGCAGACCGCGG GCACTGCCGCGCTAGGTAGAGTCTGAGGGCTTGTAGTTCTTTAACTGTCTGTCTATAC TCGAGTCTGAGGCCGTTGCTGACTTAGAATCCCTGTGTAAATTTAAGTTTGTGACAAGCTG GCTTACACTGGCAATGGTAGTTTCTGTGGTTGGCTGGGAAATCGAGTGCCGCATCTCACA GCTATGCAAAAAGCTAGTCAACAGTACCCTGGTTGTGTGTGCCCTTGCAGCCGACACGGT CTCGGATCAGGCTCCAGGAGCTGCCAGCCCCCTGGTCTTTGAGCTCCCACCTCTCGCC AGATGTCCTAATGGTGATGCAGTCTTAGATCATAGTTTATTATATTTATTGACTCTTG AGTTGTTTTTGTATATTGGTTTTATGATGACGTACAAGTAGTTCTGTATTTGAAAGTGCC TTTGACGCTCAGAACCACAGCAACGATCACAATGACTTTATTATTATTTTTTTAATTG TATTTTTGTGTTGGGGGAGGGGAGACTTTGATGTCAGCAGTTGCTGGTAAATGAAGAA TTTAAAGAAAAAATGTCAAAAGTAGAAGTTGTATAGTTATGTAAATAATCTTTTTTA TTAATCACTGTGTATATTGATTATTAACCTAATAATCAAGAGCCTTAAACATCATTCT CTTTTTATTTATATGTATGTGTTTGAATTTGAAGGTTTTTGATAGCATTGTAAGCGTATG GCTTTATTTTTTTGAAGCTCTTCTATTACTTGTGCTTATAAGCCAAAATTAAGGTGTTT GAAAATAGTTTATTTTAAACAATAGGATGGGCTTCTGTGCCCAGAATACTGATGGAATT TTTTTGTACGACGTCAGATGTTTAAAACACCTTCTATAGCATCACTTAAACACGTTTTT AAGGACTGACTGAGGAGTTTGAGGATTAGTTTGAACAGGTTTTTTGTTTTGTTGTTTT TTTGTTTTCTGCTTTAGACTTGAAAAGAGACAGGCAGGTGATCTGCTGCAGAGCAGTAA GGGAACAAGTTGAGCTATGACTTAACATAGCCAAAATGTGAGTGGTTGAATATGATTAA AATATCAAATTAATTGTGTGAAGTTGGAAGCACACCAATCTGACTTTGTAAATCTGATT TCTTTTACCATTCTGTACATAATACTGAACCACTTGTAGATTTGATTTTTTTTTTAATCT ACTGCATTTAGGGAGTATTCTAATAAGCTAGTTGAATACTTGAACCATAAATGTCCAGT AAGATCACTGTTTAGATTGGCCATAGAGTACACTGCCTGCCTTAAGTGAGGAATCAAAG TGCTATTACGAAGTTCAAGATCAAAAAGGCTTATAAACAGAGTAATCTTGTGTGTTTAC CATTGAGACCGTGAAGATACTTTGTATTGTCTATTAGTGTATATGAACATACAAATGC ATCTTTGATGTGTTGTTCTTGGCAATAAATTTTGAAGTAATATTTATTAATTTTTTTT GTATGAAAC		
	ORF Start: ATG at 414		ORF Stop: TAG at 4068
	SEQ ID NO: 56	1218 aa	MW at 133797.1kD
NOV17a, CG139062-01 Protein Sequence	MRSPTTRGRSGRPLSLLALLCALRAKVCASGQFELEILSMQNVNGELQNGNCCGGARN PGDRKCTRDECDTYFKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKASRGNDNRRI VLPFSFAWPRSYYTLLEAWDSSNDTVQPDIIIEKASHSGMINPSRQWTLKQNTGVAFHE YQIRVTCDDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP KHGSKLPGDCRCQYGWQGLYCDKCIHPGCVHIGICNEPWQCLCETNWWGQLCDKDLNYC GTHQPCLNNGGTCSTNGPDKYQCSCEGYSGPNCEIAEHAACSDPCHNRGSKETSLSGFEC ECSPGWTGPTCSTNIDDCSPNNCSHGGTCQDLVNGFKVCVPPQWTGKTCQLDANECEAKP CVNAKSCKNLIASYYCDCLPGWMGQNCNDININDCLGQCONDASCRDLVNGYRCICPPGYA GDHCERDIDECASNPLNGGHQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQNGAQ YNRASDYFCKCPEDYEGKNCSHLKDHCRTPCEVIDSCTVAMASNDTPEGVRYISSNVCG PHGKCKSQSGGKFTCDCKNGFTGTCHENINDCESNPRNGGTCIDGVNSYKICICSDGWE GAYCETNINDCSQNPCHNGGTCRDLVNDYFCDCKNGWKGTCHSRDSQCDEATCNGGTC YDEGDAFKCMCPGGWEGTTCNIARNSSCLPNPCHNGGTCVNVGESFTVCCKEGWEGPICA QNTNDCSPHPCYNSGTCDVDGDNWYRCECAPGFAGPDCRININECQSSPCAFGATCVDEIN GYRCVCPPGHSGAKCQEVSGRPCITMGSVIPDGAKWDDDCNTCQLNNGRIACSKVWCGPR PCLLHKHGHSECPGQSCIPILDDQCFVHPCTGVGECRSSSLQPVKTCTSDSYQDNCAN ITFTFNKEMMSPGLTTEHICSELRLNLILKNVSAEYSIYIACEPSPSANNEIHVAISAED IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAAVEVRVQRRPLKNRTDFLVPPLSSVLTVA WICCLVTAFYWLKRRRKPGSHTHSASEDNTNNVREQLNQIKNP1EKHGANTVPIKDYE		

	NKNSKMSKIRTHNSEVEEDMDKHQQKARFAKQPAYTLVDRBEKPPNGTPTKHPNWTNKO DNRDLESAQSLNRMEYIV
	SEQ ID NO: 57 4333 bp
NOV17b, CG139062-02 DNA Sequence	CTGCGGCCGCGCCGCGAGCTAGGCTGGGTTTTTTTTTCTCCCTCCCTCCCCCTTTT TCCATGCAGCTGATCTAAAAGGGAATAAAAGGCTGCGCATAATCATAATAATAAAGAAG GGGAGCGCGAGAGAAGGAAAGAAAGCCGGAGGTGGAAGAGGAGGGGAGCGTCTCAAAG AAGCGATCAGAATAATAAAAGGAGGCCGGGCTCTTGCCCTCTGGAACGGGCGGCTCTTG AAAGGGCTTTTGAAAAGTGGTGTGTTTCCAGTCGTGCATGCTCCAATCGGCGGAGTAT ATTAGAGCCGGGACGCGCGCGCCGACGGGGCAGCGCGACGGCAGCACCGGCGGCAGCAC CAGCGCGAACAGCAGCGCGCGGCTCCGAGTGCCGCGGCGCGCGGCGCAGCGATGCGTT CCCCACGGACGCGCGCGCCGGTCCGGGCGCCCCCTAAGCCTCTGCTCGCCCTGCTCTGTG CCCTGCGAGCCAAGGTGTGTGGGGCCTCGGGTCAGTTCGAGTTGGAGATCCTGTCCATGC AGAACGTGAACGGGAGCTGCAGAACGGGAACCTGCTGCGGCGCGCCCGGAACCCGGGAG ACCGCAAGTGCACCCGCGACGAGTGTGACACATACTTCAAAGTGTGCCTCAAGGAGTATC AGTCCCGCTCACGGCCGGGGGCCCTGCAGCTTCGGCTCAGGGTCCACGCTGTCTATCG GGGCAACACCTTCAACCTCAAGGCCAGCCGCGCAACGACCGCAACCGCATCGTGCTGC CTTTCAGTTTCGCCTGGCCGAGGTCTATACGTTGCTTGTGGAGGCGTGGGATTCCAGTA ATGACACCGTTCAACCTGACAGTATTATTGAAAAGGCTTCTACTCGGGCATGATCAACC CCAGCCGGCAGTGGCAGACGCTGAAGCAGAACACGGGCGTTGCCACTTTGAGTATCAGA TCCGCGTGACCTGTGATGACTACTACTATGGCTTTGGCTGCAATAAGTTCTGCCGCCCA GAGATGACTTCTTTGGACACTATGCCTGTGACCAGAATGGCAACAAACTTGCATGGAAG GCTGGATGGGCCCCGAATGTAACAGAGCTATTTGCCGACAAGGCTGCAGTCTAAGCATG GGTCTTGCAACTCCCAGGTGACTGCAGGTGCCAGTATGGCTGGCAAGGCTGTACTGTG ATAAGTGCATCCACACCCGGGATGCGTCCACGGCATCTGTAATGAGCCCTGGCAGTGCC TCTGTGAGACCAACTGGGGCGGCCAGCTCTGTGACAAAGATCTCAATTACTGTGGGACTC ATCAGCCGTGTCTCAACGGGGGAACCTGTAGCAACACAGGCCCTGACAAATATCAGTGTT CCTGCCCTGAGGGGTATTCAAGGACCCAACTGTGAAATTGCTGAGCACGCCTGCCTCTCTG ATCCCTGTCAACAAGAGGCGAGCTGTAAAGGAGACCTCCCTGGGCTTTGAGTGTGAGTGT CCCCAGGCTGGACCGGCCCCACATGCTCTACAAACATTGATGACTGTTCTCCTAATAACT GTTCCACGGGGGCACCTGCCAGGACCTGGTTAACGGATTTAAGTGTGTGTGCCCCCAC AGTGGACTGGGAAAACGTGCCAGTTAGATGCAATGAATGTGAGGCCAAACCTTGTGTAA ACGCCAAATCCTGTAAGAATCTCATTGCCAGCTACTACTGCGACTGTCTTCCCGGCTGGA TGGGTGCAATTTGTGACATAAATATTATGACTGCCTTGGCCAGTGTGAGATGACGCCCT CCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGACGGCGATC ACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGTCACTGTC AGAATGAAATCAACAGATTCCAGTGTCTGTGTCCACTGGTTTCTCTGAAACCTCTGTC AGCTGGACATCGATTATTGTGAGCCTAATCCCTGCCAGAACGGTGCCAGTGTACAACC GTGCCAGTGACTATTTCTGCAAGTGCCCGGAGGACTATGAGGGCAAGAAGTGTCAACACC TGAAAGACCACTGCCGACGACCCCTGTGAAGTGATTGACAGCTGCACAGTGGCCATGG CTTCCAACGACACACCTGAAGGGGTGCGGTATATTCTCCTCAACGTCTGTGGTCTCTACG GGAAGTGCAAGAGTCAGTCGGGAGGCAAAATCACCTGTGACTGTAAACAAAGGCTTACGG GAACATACTGCCATGAAAATATTAATGACTGTGAGAGCAACCCCTGTAGAAACGGTGGCA CTTGATCGATGGTGTCAACTCTACAAGTGCATCTGTAGTGACGGCTGGGAGGGGGCT ACTGTGAAACCAATATTAATGACTGCAGCCAGAACCCTGCCACAATGGGGGCACGTGTC GCGACCTGGTCAATGACTTCTACTGTGGCTGTAAAATGGGTGGAAAGGAAAGACCTGCC ACTCACGTGACAGTCAGTGTGATGAGGCCAACACGGTCCCCATCAAGGATTACGAGAACA AGAACTCCAAAATGTCTAAAATAAGGACACACAATTCTGAAGTAGAAGAGGACGACATGG ACAAACACCAGCAGAAAGCCCGTTTGCCAAGCAGCCGGCTACACGCTGGTAGACAGAG AAGAGAAGCCCCCAACGGCACGCGGACAAAACACCCAACTGGACAAACAACAGGACA ACAGAGACTTGGAAGTGCACAGCTTAAACCGAATGGAGTACATCGTATAGCAGACCG CGGGCACTGCCCGCTAGGTAGAGTCTGAGGGCTTGTAGTTCTTTAACTGTGCTGTCA TACTCGAGTCTGAGGCCGTTGCTGACTTAGAATCCCTGTGTTAATTAAAGTTTGACAAG CTGGCTTACACTGGCAATGGTAGTTTCTGTGGTTGGCTGGGAAATCGAGTGCCGCATCTC ACAGCTATGCAAAAAGCTAGTCAACAGTACCCTGGTGTGTGTCTCCCTTGCAGCCGACAC GGTCTCGGATCAGGCTCCAGGAGCCTGCCAGCCCTGGTCTTTGAGCTCCCACTTCT GCCAGATGCTCTAATGGTGTGAGTCTGAGTCTAGATCATAGTTTTATTATTATTGACTC TTGAGTTGTTTTGTATATTGGTTTTATGATGACGTACAAGTAGTTCTGTATTTGAAAGT GCCTTTGCAGCTCAGAACCACAGCAACGATCACAATGACTTTATTATTATTTTTTAA TTGTATTTTTGTTGTTGGGGGAGGGGAGACTTTGATGTCAGCAGTTGCTGGTAAAATGAA

	GAATTTAAAGAAAAAATGTCAAAAGTAGAAGCTTTGTATAGTTATGTAAATAATTCTTTT TTATTAATCACTGTGTATATTTGATTTATTAACCTTAATAATCAAGAGCCTTAAAAACATCA TTCCTTTTATTTATATGTATGTGTTTAGAATTGAAGGTTTTTGATAGCATTGTAAGCGT ATGGCTTTATTTTTTTGAACTCTTCTCATTACTTGTGCTTATAAGCCAAAATTAAGGTG TTTGAAAATAGTTTATTTTAAACAATAGGATGGGCTTCTGTGCCCAGAATACTGATGGA ATTTTTTTTGTACGACGTCAGATGTTTAAACACCTTCTATAGCATCACTTAAAAACGCT TTTAAGGACTGACTGAGGCAGTTTGAGGATTAGTTTAGAACAGGTTTTTTTGTGTTGTTG TTTTTGTGTTTTCTGCTTTAGACTTGAAGAGACAGGCAGGTGATCTGCTGCAGAGCAG TAAGGGAACAAGTTGAGCTATGACTTAACATAGCCAAAATGTGAGTGGTTGAATATGATT AAAAATATCAAATTAATTGTGTGAAGCTTGAAGCACACCAATCTGACTTTGTAAATTCTG ATTTCTTTTACCATTTCGTACATAATACTGAACCACTTGTAGATTTGATTTTTTTTTTAA TCTACTGCTTATAGGGAGTATTCTAATAAGCTAGTTGAATACTTGAACCATAAAATGTCTC AGTAAGATCACTGTTTAGATTGCCATAGAGTACACTGCCTGCCTTAAGTGAGGAAATCA AAGTGCTATTACGAAGTTCAAGATCAAAAAGGCTTATAAACAGAGTAATCTTGTGGTT CACCATTGAGACCGTGAAGATACTTTGTATTGTCTATTAGTGTATATGAACATACAAA TGCATCTTTGATGTGTTGTTCTTGGCAATAAATTTTGAAGTAATATTTATTAATTTT TTTGTATGAAAAAC		
	ORF Start: ATG at 414	ORF Stop: TAG at 2811	
	SEQ ID NO: 58	799 aa	MW at 88212.4kD
NOV17b, CG139062-02 Protein Sequence	MRSPTTRGRSGRPLSLLLALLCALRAKVCASGQFELEILSMQNVNDELQNGNCCGGARN PGDRKCTRDECDTYFKVCLKEYQSRVTAGGPCSFGSGSTPVIIGNTFNLKASRGNDNRRI VLFFSFAWPRSYLLVEAWDSSNDTVQPDSEIEKASHSGMINPSRQWQTLKQNTGVAHFE YQIRVTCDDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP KHGSKLPGDCRCQYGWQGLYCDKCIHPHGCVHVICNEPWQCLCETNWWGQCLCDKDLNYC GTHQPCLNNGGTCSTNGPDKYQCSCPEGYSGPNCIEIAEHACLSDPCHNRGSKETSLSGFEC ECSPGWTGPTCSTNIDDCSPNNCSHGCTQDLVNGFKVCPPQWTGKTCQLDANECEAKP CVNAKSKNLIASYYCDCLPGWMQNCININDCLGQCQNDASCRDLVNGYRCICPPGYA GDHCERDIDECASNPLNGGHCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQNGAQC YNRASDYFKCPCPEYEGKNCSHLKDHCRTPCEVIDSCTVAMASNDTPEGVRYISSNVCG PHGKCKSQSGGKFTCDCKNGFTGTYPHENINDCESNPCRNNGTCTIDGVNSYKICSDGWE GAYCETNINDCSQNPCHNGGTCRDLVNDFYCGCKNGWKGTCHSRDSQCDEANTVPIKDY ENKNSKMSKIRTHNSEVEEDMDKHQQKARFAKQPAYTLVDREKPPNGTPTKHPNWTNK QDNRDLESAQSLNRMEYIV		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 17B.

Table 17B. Comparison of NOV17a against NOV17b.		
Protein Sequence	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV17b	27..712	685/686 (99%)
	27..712	685/686 (99%)

Five polymorphic variants of NOV17b have been identified and are shown in Table 41E.

5 Further analysis of the NOV17a protein yielded the following properties shown in Table 17C.

Table 17C. Protein Sequence Properties NOV17a

PSort analysis:	0.4600 probability located in plasma membrane; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Cleavage site between residues 34 and 35

A search of the NOV17a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 17D.

Table 17D. Geneseq Results for NOV17a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB07822	Human notch agonist ligand - <i>Homo sapiens</i> , 1218 aa. [WO200218544-A2, 07-MAR-2002]	1..1218 1..1218	1218/1218 (100%) 1218/1218 (100%)	0.0
AAW87894	Human JAGGED1 protein - <i>Homo sapiens</i> , 1218 aa. [WO9858958-A2, 30-DEC-1998]	1..1218 1..1218	1218/1218 (100%) 1218/1218 (100%)	0.0
AAW44301	Human serrate 1 - <i>Homo sapiens</i> , 1218 aa. [WO9802458-A1, 22-JAN-1998]	1..1218 1..1218	1218/1218 (100%) 1218/1218 (100%)	0.0
AAU84344	Protein JAG1 differentially expressed in breast cancer tissue - <i>Homo sapiens</i> , 1218 aa. [WO200210436-A2, 07-FEB-2002]	1..1218 1..1218	1217/1218 (99%) 1217/1218 (99%)	0.0
AA Y59597	Human Serrate protein sequence - <i>Homo sapiens</i> , 1218 aa. [US6004924-A, 21-DEC-1999]	1..1218 1..1218	1215/1218 (99%) 1216/1218 (99%)	0.0

5 In a BLAST search of public sequence databases, the NOV17a protein was found to have homology to the proteins shown in the BLASTP data in Table 17E.

Table 17E. Public BLASTP Results for NOV17a

Protein Accession Number	Protein/Organism/Length	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P78504	Jagged 1 precursor (Jagged1) (hJ1) - <i>Homo sapiens</i> (Human), 1218 aa.	1..1218 1..1218	1218/1218 (100%) 1218/1218 (100%)	0.0
Q9QXX0	Jagged 1 precursor (Jagged1) - <i>Mus musculus</i> (Mouse), 1218 aa.	1..1218 1..1218	1176/1218 (96%) 1194/1218 (97%)	0.0
Q63722	Jagged 1 precursor (Jagged1) - <i>Rattus norvegicus</i> (Rat), 1219 aa.	1..1218 1..1219	1175/1219 (96%) 1191/1219 (97%)	0.0
A56136	jagged protein precursor - rat, 1220 aa.	1..1218 1..1220	1168/1223 (95%) 1184/1223 (96%)	0.0
Q90819	C-Serate-1 protein - <i>Gallus gallus</i> (Chicken), 1193 aa (fragment).	27..1218 1..1193	1047/1193 (87%) 1111/1193 (92%)	0.0

PFam analysis predicts that the NOV17a protein contains the domains shown in Table 17F.

Table 17F. Domain Analysis of NOV17a			
Pfam Domain	NOV17a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DSL	167..229	42/67 (63%) 63/67 (94%)	3.9e-40
EGF	300..333	18/47 (38%) 28/47 (60%)	1e-06
EGF	340..371	16/47 (34%) 26/47 (55%)	3.3e-08
EGF	378..409	18/47 (38%) 30/47 (64%)	2.9e-09
EGF	416..447	13/47 (28%) 19/47 (40%)	0.003
EGF	454..484	14/47 (30%) 26/47 (55%)	4.6e-07
EGF	491..522	16/47 (34%) 24/47 (51%)	1.7e-07
EGF	529..560	17/47 (36%) 26/47 (55%)	2.5e-08

EGF	595..626	13/47 (28%) 24/47 (51%)	0.19
EGF	633..664	15/47 (32%) 25/47 (53%)	1.3e-08
EGF	671..702	15/47 (32%) 30/47 (64%)	1.1e-09
EGF	709..740	13/47 (28%) 23/47 (49%)	0.00072
EGF	748..779	17/47 (36%) 27/47 (57%)	3.1e-09
EGF	786..817	17/47 (36%) 28/47 (60%)	3.5e-07
EGF	824..855	16/47 (34%) 25/47 (53%)	1.7e-05
vwc	863..917	18/84 (21%) 33/84 (39%)	0.055

Example 18.

The NOV18 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 18A.

Table 18A. NOV18 Sequence Analysis			
	SEQ ID NO: 59	587 bp	
NOV18a, CG139363-01 DNA Sequence	GGAGCTTGCTGACCATCCCTGGGAGCTTTAATGTTTACTTCTATCTTGCAGAGTTTTTCA CTGAACTTCACCCTGCCGCGGAACACAGTAAGTACAGCAGCCCCATTGACACATCTGGT AAGGGCGACTGTGGGCCCTCTCTGGATTAGCGGCGGCATACCATTGCTGGTGGCCACA GCCCTGCTGGTGGCTTTACTATTACTTTGATTACCCGAAGAAGAAGCAGCATTGAGGCC ATGGAGGTGATTAGTCCATCTTGTATGAAAGAATTCTCTGCTGTAGTTTTTAAAAACCT ATTTGTTTCCTTAAGAATCCTAGGAGATCACCCACACATGAGAAGAATACGATGGGAGCA CAAGAGGCCACATATATGTGAAGACTGTAGCAGGAAGCGAGGAACCTGTGCATGACCGT TACCGTCTACTATAGAAATGGAAAGAAGGAGGGGATTGTGGTGGCTTGTGCCCAGACTG AGCCTGGAATTGATGCAGCTCAGTCAAGGAGCAGCAGACCTGGCACTGGAACAGGGTTGA AAACCCAGGGTTTTGTACTTGGAGAGGAAAGATGCCAAGCTGCTTCT		
	ORF Start: ATG at 31		ORF Stop: TGA at 538
	SEQ ID NO: 60	169 aa	MW at 18578.4kD
NOV18a, CG139363-01 Protein Sequence	MFTSILQSFSLNFTLPANTVSTAAPIQTSGKDCGPSLGLAAGIPLLVATALLVALLFTL IHRRRSSIEAMEVISPSCKEFSAVVFKKPICFLKNPRRSPTHEKNTMGAQEAHIYVKTV AGSEEPVHDIRYRPTIEMERRRGLWLVPRLSLELMQLSQGAADLALEQG		
	SEQ ID NO: 61	528 bp	
NOV18b, CG139363-02 DNA Sequence	GGGAGCTTTAATGTTTACTTCTATCTTGCAGAGTTTTTCACTGAACCTCACCCCTGCCGGC GAACACAACGTCTCTCTCTGTACAGGTGGGAAAGAAACGGAAGTGTGGGCCCTCTCTTGG ATTAGCGGCGGGCATAACCATTGCTGGTGGCCACAGCCCTGCTGGTGGCTTTACTATTAC TTGATTACCGAAGAAGAAGCAGCATTGAGGCCATGGAGGAAAGTGACAGACCATGTGA AATTTAGAAATTGATGACAATCCCAAGATATCTGAGAATCCTAGGAGATCACCCACACA TGAGAAGAATACGATGGGAGCACAAGAGGCCACATATATGTGAAGACTGTAGCAGGAAG CGAGGAACCTGTGCATGACCGTTACCGTCTCTACTATAGAAATGGAAAGAAGGAGGGGATT GTGGTGGCTTGTGCCCAGACTGAGCCTGGAATGATGCAGCTCAGTCAAGGAGCAGCAGAC		

	CTGGCACTGGAACAGGGTTGAAAACCCAGGGTTTGTACTTGGAGAGG		
	ORF Start: ATG at 11		ORF Stop: TGA at 452
	SEQ ID NO: 62	147 aa	MW at 16372.4kD
NOV18b, CG139363-02 Protein Sequence	MFTSILQSFSLNFTLPANTTSSPVTGGKETDCGPSLGLAAGIPLLVATALLVALLFTLIH RRRSSIEAMEESDRPCEISEIDDPKISENPRRSPTHEKNTMGAQEAHIYVKTAVGSEEP VHDYRPTIEMERRRGLWWLVPRLSLE		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 18B.

Table 18B. Comparison of NOV18a against NOV18b.		
Protein Sequence	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV18b	1..153	108/153 (70%)
	1..147	114/153 (73%)

Further analysis of the NOV18a protein yielded the following properties shown in Table 18C.

Table 18C. Protein Sequence Properties NOV18a	
PSort analysis:	0.8569 probability located in mitochondrial inner membrane; 0.4456 probability located in mitochondrial intermembrane space; 0.2847 probability located in mitochondrial matrix space; 0.2847 probability located in mitochondrial outer membrane
SignalP analysis:	Cleavage site between residues 64 and 65

- 5 A search of the NOV18a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 18D.

Table 18D. Geneseq Results for NOV18a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABG23422	Novel human diagnostic protein #23413 - <i>Homo sapiens</i> , 163 aa. [WO200175067-A2, 11-OCT-2001]	8..153 15..163	123/153 (80%) 127/153 (82%)	3e-58
AAM79058	Human protein SEQ ID NO 1720 - <i>Homo sapiens</i> , 141 aa. [WO200157190-A2, 09-AUG-2001]	8..153 2..141	116/146 (79%) 122/146 (83%)	1e-56

AA Y94922	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50 - <i>Homo sapiens</i> , 141 aa. [WO200009552-A1, 24-FEB-2000]	8..153 2..141	115/146 (78%) 121/146 (82%)	1e-55
ABG23423	Novel human diagnostic protein #23414 - <i>Homo sapiens</i> , 209 aa. [WO200175067-A2, 11-OCT-2001]	8..158 35..179	115/151 (76%) 122/151 (80%)	2e-55
AAM80042	Human protein SEQ ID NO 3688 - <i>Homo sapiens</i> , 133 aa. [WO200157190-A2, 09-AUG-2001]	8..141 11..133	104/134 (77%) 109/134 (80%)	3e-47

In a BLAST search of public sequence databases, the NOV18a protein was found to have homology to the proteins shown in the BLASTP data in Table 18E.

Table 18E. Public BLASTP Results for NOV18a				
Protein Accession Number	Protein/Organism/Length	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96PE5	Transmembrane protein HTMP10 - <i>Homo sapiens</i> (Human), 141 aa.	8..153 2..141	116/146 (79%) 122/146 (83%)	4e-56
Q29102	Transmembrane protein sp83.5 - <i>Sus scrofa</i> (Pig), 142 aa.	8..153 2..142	104/147 (70%) 117/147 (78%)	5e-50
P54423	Cell wall-associated protease precursor (EC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52] - <i>Bacillus subtilis</i> , 894 aa.	91..167 662..737	22/77 (28%) 39/77 (50%)	2.7
Q9A7Z7	Hypothetical protein CC1570 - <i>Caulobacter crescentus</i> , 311 aa.	108..151 184..227	14/44 (31%) 23/44 (51%)	3.5
Q8S9L6	AT4g21410/T6K22_140 - <i>Arabidopsis thaliana</i> (Mouse-ear cress), 679 aa.	16..77 265..326	19/62 (30%) 32/62 (50%)	3.5

PFam analysis predicts that the NOV18a protein contains the domains shown in

5 Table 18F.

Table 18F. Domain Analysis of NOV18a			
Pfam Domain	NOV18a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 19.

The NOV19 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 19A.

Table 19A. NOV19 Sequence Analysis			
	SEQ ID NO: 63	471 bp	
NOV19a, CG140188-01 DNA Sequence	CCACCCTTGCTGCCACTAACATGGAGACTTGTACCGTGTCCCATCTTAGTGCTCGAAT GTCCCAACCTGAAGCTGAAGAAGCCGCCCTGGCTGCAAGTGCTGTCGGCCATGATTGTGT ATGCTCTGATGGTGGTGTCTTACTTCCTCGTCACTGGAGGAATAATTTATGATGTTATTG TTGAACCTCCAAGCATTGGCTCTATGACTGATGAACACGGGCATCAGAGGCCAGTAGCTT TCTTGGCCTACAGAGTAAATGAACAATGTATTATGGAAGGACTTGCATCCAGCTTCCTGT TTACAATAGGAGGTTTAGGTTTCATATTCCTGGACCGATGGAATGCACCAATATCCCAA AACTCAATAGATTCTTCTTCTATTTCATTGGATTTCGTTGTGTCTATTGAGCTTTTTC TGGCTAGAGTATTCATGAGAATGAAACTGCCGGGCTATCTGATGGGTTAGA		
	ORF Start: ATG at 21		ORF Stop: TAG at 468
	SEQ ID NO: 64	149 aa	MW at 16975.3kD
NOV19a, CG140188-01 Protein Sequence	METLYRVPFLVLECPNLKLLKPPWLQVLSAMIVYALMVSYFLVTGGIIYDVIVEPPSIG SMTDEHGHQRPVAFLAYRVNEQCIMEGLASSFLFTIGGLGFIFLDRWNAPNIPKLNRFLL LFIFGVCVLLSFFMARVFMRMKLPGYLMG		

Further analysis of the NOV19a protein yielded the following properties shown in
 5 Table 19B.

Table 19B. Protein Sequence Properties NOV19a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Cleavage site between residues 48 and 49

A search of the NOV19a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 19C.

Table 19C. Geneseq Results for NOV19a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY53631	A bone marrow secreted protein designated BMS155 - <i>Homo sapiens</i> , 149 aa. [WO9933979-A2, 08-JUL-1999]	1..149 1..149	137/149 (91%) 142/149 (94%)	1e-75
AAY53042	Human secreted protein clone pu282_10 protein sequence SEQ ID NO:90 - <i>Homo sapiens</i> , 149 aa. [WO9957132-A1, 11-NOV-1999]	1..149 1..149	137/149 (91%) 142/149 (94%)	1e-75
AAB12143	Hydrophobic domain protein isolated from WERI-RB cells - <i>Homo sapiens</i> , 149 aa. [WO200029448-A2, 25-MAY-2000]	1..149 1..149	137/149 (91%) 142/149 (94%)	1e-75
AAY59670	Secreted protein 108-005-5-0-F6-FL - <i>Homo sapiens</i> , 149 aa. [WO9940189-A2, 12-AUG-1999]	1..149 1..149	137/149 (91%) 142/149 (94%)	1e-75
AAY60146	Human endometrium tumour EST encoded protein 206 - <i>Homo sapiens</i> , 171 aa. [DE19817948-A1, 21-OCT-1999]	1..149 23..171	137/149 (91%) 142/149 (94%)	1e-75

In a BLAST search of public sequence databases, the NOV19a protein was found to have homology to the proteins shown in the BLASTP data in Table 19D.

Table 19D. Public BLASTP Results for NOV19a				
Protein Accession Number	Protein/Organism/Length	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9NRP0	DC2 (Hydrophobic protein HSF-28) (Hypothetical 16.8 kDa protein) - <i>Homo sapiens</i> (Human), 149 aa.	1..149 1..149	137/149 (91%) 142/149 (94%)	4e-75
Q9P075	HSPC307 - <i>Homo sapiens</i> (Human), 167 aa (fragment).	1..149 19..167	137/149 (91%) 142/149 (94%)	4e-75

Q9CPZ2	2310008M10Rik protein (RIKEN cDNA 2310008M10 gene) - <i>Mus musculus</i> (Mouse), 149 aa.	1..149 1..149	136/149 (91%) 142/149 (95%)	9e-75
Q9P1R4	HDCMD45P - <i>Homo sapiens</i> (Human), 160 aa (fragment).	1..149 12..160	136/149 (91%) 141/149 (94%)	3e-74
Q8TBU1	Similar to DC2 protein - <i>Homo sapiens</i> (Human), 119 aa.	31..149 1..119	118/119 (99%) 118/119 (99%)	4e-63

PFam analysis predicts that the NOV19a protein contains the domains shown in Table 19E.

Table 19E. Domain Analysis of NOV19a			
Pfam Domain	NOV19a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 20.

The NOV20 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 20A.

Table 20A. NOV20 Sequence Analysis			
	SEQ ID NO: 65	755 bp	
NOV20a, CG140305-01 DNA Sequence	GGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGG CAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCTCCCTTTTGCCTGTGTCAAGAT GAATACATGGAGTCTCCACAAACCGGAGGACTACCCCGAGACTGCAGTAAGTGTGTGCAT GGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGCCACCGGCCCTCCTGGCATT CCAGGAAACCATGGAAACAATGGCAACAATGGAGGCCACTGGTCATGAAGGAGCCAAAGGT GAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTATGGCTTCTCTGGCA ACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTGAGACCAACATTGGA AACTTCTTTGATGTCATGACTGGTAGATTGGGGCCCCAGTATCAGGTGTGTATTCTTC ACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAAT GGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGC AATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGC GCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTCAGGATTCTGCTCTTTGAAACT AAGTAAATATATGACTAGAAATAGCTCCACTTTGGG		
	ORF Start: ATG at 49		ORF Stop: TAA at 724
	SEQ ID NO: 66	225 aa	MW at 24836.9kD
NOV20a, CG140305-01 Protein Sequence	MLWRQLIYWQLLALFFLPFLCQDEYMESPQTGGLPPDCSKCHGDYSFRGYQPPGPPG PPGIPGNHGNNGNNGATGHEGAKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVE TNIGNFFDVTGRFGAPVSGVYFFTFSMMKHEDVEEVVYLMHNGNTVFSMYSYEMKGKS DTSSNHAVLKLAKGDEVWLRMGNALHGDHQRFFSTFAGFLFETK		
	SEQ ID NO: 67	842 bp	
NOV20b, CG140305-02	GGAGCTCTGCTGTCTTCTCAGGTAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGG CAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCTCCCTTTTGCCTGTGTCAAGAT		

DNA Sequence	GAATACATGGAGTCTCCACAAACCGAGGACTACCCCAGACTGCAGTAAGTGTGTGCAT GGAGACTACAGCTTTTCGAGGCTACCAAGGCCCTGGGCCACCGGGCCCTCCTGGCATT CCAGGAAACCATGGAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGT GAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGCGAGCATGGCCCCAAA GGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTTCATGGCTTCTCTG GCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATT GGAAACTTCTTTGATGTCTGACTGGTAGATTGGGGCCCCAGTATCAGGTGTGTATTTC TTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCAC AATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCC AGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTGGCTGCGAATGGGCAAT GGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCTGCTCTTTGAA ACTAAGTAAATATATGACTAGATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT AA		
	ORF Start: ATG at 49	ORF Stop: TAA at 787	
	SEQ ID NO: 68	246 aa	MW at 26994.2kD
NOV20b, CG140305-02 Protein Sequence	MLWRQLIYWQLLALFFLPFLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG PPGIPGNHGNNGNNGATGHEGAKGEKGDGDLGPRGERGQHGPKEGKYPGIPPELQIAF MASLATHFSNQNSGIIFFSSVETNIGNFFDVMTGFRGAPVSGVYFFTFSMMKHEDVEEVYV YLMHNGNTVFSMYSYEMKGKSDTSSNHAFLKLAGDEVWLRMGNGALHGDHQRFFSTFAGF LLFETK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 20B.

Table 20B. Comparison of NOV20a against NOV20b.		
Protein Sequence	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV20b	1..225	188/246 (76%)
	1..246	188/246 (76%)

Two polymorphic variants of NOV20a have been identified and are shown in Table 41F. Further analysis of the NOV20a protein yielded the following properties shown in

5 Table 20C.

Table 20C. Protein Sequence Properties NOV20a	
PSort analysis:	0.7666 probability located in outside; 0.2383 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 23 and 24

A search of the NOV20a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 20D.

Table 20D. Geneseq Results for NOV20a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU84371	Novel human secreted or membrane-associated protein #10 - <i>Homo sapiens</i> , 246 aa. [WO200204600-A2, 17-JAN-2002]	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134
AAB88447	Human membrane or secretory protein clone PSEC0232 - <i>Homo sapiens</i> , 246 aa. [EP1067182-A2, 10-JAN-2001]	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134
AAB18909	A novel polypeptide designated PRO1484 - <i>Homo sapiens</i> , 246 aa. [WO200056889-A2, 28-SEP-2000]	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134
AAB29580	Human adipocyte complement related protein homolog zacrp3, SEQ ID NO:2 - <i>Homo sapiens</i> , 246 aa. [WO200063377-A1, 26-OCT-2000]	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134
AAB15548	Human immune system molecule from Incyte clone 1890540 - <i>Homo sapiens</i> , 246 aa. [WO200060080-A2, 12-OCT-2000]	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134

In a BLAST search of public sequence databases, the NOV20a protein was found to have homology to the proteins shown in the BLASTP data in Table 20E.

Table 20E. Public BLASTP Results for NOV20a				
Protein Accession Number	Protein/Organism/Length	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXJ4	Complement-clq tumor necrosis factor-related protein 3 precursor (Secretory protein CORS26) - <i>Homo sapiens</i> (Human), 246 aa.	1..225 1..246	225/246 (91%) 225/246 (91%)	e-134

Q9ES30	Collagenous repeat-containing sequence of 26kDa protein - <i>Mus musculus</i> (Mouse), 246 aa.	1..225 1..246	215/246 (87%) 217/246 (87%)	e-127
CAC51163	Sequence 59 from Patent WO0149728 - <i>Homo sapiens</i> (Human), 223 aa.	28..126 101..220	98/120 (81%) 99/120 (81%)	2e-53
Q9ESN4	Gliacolin precursor - <i>Mus musculus</i> (Mouse), 255 aa.	45..222 64..253	66/194 (34%) 97/194 (49%)	1e-22
Q8TE71	EEG1L - <i>Homo sapiens</i> (Human), 1077 aa.	88..223 940..1076	51/138 (36%) 87/138 (62%)	3e-22

PFam analysis predicts that the NOV20a protein contains the domains shown in Table 20F.

Table 20F. Domain Analysis of NOV20a			
Pfam Domain	NOV20a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Collagen	37..95	23/60 (38%) 37/60 (62%)	0.00032
Clq	98..221	45/137 (33%) 76/137 (55%)	2.3e-17

Example 21.

The NOV21 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 21A.

Table 21A. NOV21 Sequence Analysis			
	SEQ ID NO: 69	1725 bp	
NOV21a, CG140639-01 DNA Sequence	CGGCCGCGCTGCAGACCCGCTGCTGTTGTCCGGGTCTGTGCGGTCCCGAGGGCCCTCCG TGCCGCCGCGCCATGGGCAATTGCCACACGGTGGGGCCCAACGAGGCGCTGGTGGTTTC AGGGGGCTGTTGTGGTCCGACTATAAACAGTACGTGTTGGCGGTGGGCCCTGGCCCTG GTGGTGTATCTCCGACACTCAGAGGATTTCCCTAGAGATTATGACGTTGCAGCCCCGCTG CGAGGACGTAGAGACGGCCGAGGGGTAGCTTTAACTGTGACGGGTGTCGCCAGGTGAA GATCATGACGAGAGAAGGAACCTCGGCCGTGGCTTGTGAGCAGTTTCTGGGTAAGAATGT GCAGGACATCAAAAACGTCGTCCTGCAGACCCTGGAGGGACATCTGCGCTCCATCCTCGG GACCCTGACAGTGGAGCAGATTATCAGGACCGGGACAGTTTGCCAAGCTGGTGCGGGA GGTGGCAGCCCCGTGATGTTGGCCGATGGGCATTGAGATCCTCAGCTTCACCATCAAGGA CGTGTATGACAAAGTGGACTATCTGAGCTCCCTGGGCAAGACGCAGACTGCCGTGGTGCA GAGAGATGCTGACATTGGCGTGGCCGAGGCTGAACGGGACGCAGGCATCCGGGAAGCTGA GTGCAAGAAGGAGATGCTGGATGTGAAGTTCATGGCAGACACCAAGATTGCTGACTCTAA GCGAGCCTTCGAGCTGCAAAAGTCAGCCTTCAGTGAGGAGGTTAATCATCAAGACAGCTGA GGCCCAGTTGGCCTATGAGCTGCAGGGGGCCCGTGAACAGCAGAGAAGATCCGGCAGGAAGA GATTGAGATTGAGGTTGTGCAGCGCAAGAAACAGATTGCCGTGGAGGCACAGGAGATCCT GCGTACGGACAAGGAGCTCATCGCTACAGTGCGCCGGCTGCCGAGGCCGAGGCCACCG CATCCAGCAGATTGCCGAGGTTGAAAAGGTGAAGCAGTCTCTTGGCACAGGCAGAGGC TGAGAAGATCCGCAAAATCGGGGAGGCGGAAGCGGCAGTCATCGAGGCGATGGGCAAGGC		

	AGAGGCTGAGCGGATGAAGCTCAAGGCAGAAGCCTACCAGAAATACGGGGATGCAGCCAA GATGGCCTTGGTGCTAGAGGCCCTGCCCCAGATTGCTGCCAAAATCGTGCCCCACTTAC CAAGGTCGATGAGATTGTGGTCCTCAGTGGAGACAACAGTAAGGTCACATCAGAAGTGAA CCGACTGCTGGCCGAGCTGCCTGCCTCTGTGCATGCCCTCACAGGCGTGGACCTGTCTAA GATACCCCTGATCAAGAAGGCCACTGGTGTGCAGGTGTGAGGCTCCTGCAGGCCCACTCT CTTCAGCAGCCACCCGGCCCTCCCTCCAGCACCCGTTTTAATCCACAGAACACCGGAA CGTTACTGACTCTGGTGCCTTATCTCGAAGGGACCAGAAGTGTGCGTGTTCAGGCCATC TCTGGCTGTCTTCTGTCTCTCCTGTCTGTCCACCTCCTCCTCTTCTCTCTCTTACCCC ACTTTCAGTGCCACTTTCATCAGGTTTGTGTCTCATCTCCCTGCGTGTCTTTCTTTGT CTGTCTTTTCTTTCCCCATGCACATCATGTAGATTAAAGCTGAAGATGTTTATTACAAT CACTCTCTGTGGGGGGTGGCCCTGCTGCTCCTCAGAATCCTGGTG		
	ORF Start: ATG at 74		ORF Stop: TGA at 1358
	SEQ ID NO: 70	428 aa	MW at 47063.7kD
NOV21a, CG140639-01 Protein Sequence	MGNCHTVGPNEALVVS GGCCGSDYKQYVFGGWAWAWWCISDTQRISLEIMTLQPRCEDVE TAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKNVQDIKNVVLQTLLEGHLRSILGTLTV EQIYQDRDQFAKLREVAAPDVGRMGIEILSFTIKDVIDKVDYLSLGLKTQTAVVQRDAD IGVAEAEERDAGIREAECKKEMLDVKFMADTKIADSKRAFELQKSAFSEEVNIKTAEAQLA YELQGAREQQKIRQEEIEIEVVQRKKQIAVEAQEILRTDKELIATVRRPAEAEAHRIQQI AEGEKVKQVLLAQAEAEKIRKIGEAEEAVIEAMGKAEARMKLAEEAYQKYGDAAKMALV LEALPQIAAKIAAPLTKVDEIVVLSGDN SKVTSEVNRLLAELPASVHALTGVDLSKIPLI KKATGVQV		
	SEQ ID NO: 71	1389 bp	
NOV21b, CG140639-02 DNA Sequence	CTGCTGTGTCCGGGTCTGTGCGGTCCCGAGGGCCCTCCGTGCCGCCGGCGCCATGGGCA ATTGCCACACGGTGGGGCCCAACGAGGCGCTGGTGGTTTCAGGGGGCTGTTGTGGTTCGG ACTATAACAGTACGTGTTTGGCGGCTGGGCTGGGCTGGTGGTGTATCTCCGACACTC AGAGGATTTCCTAGAGATTATGACGTTGACGCCCCGCTGCGAGGACGTAGAGACGGCCG AGGGGGTAGCTTTAACTGTGACGGGTGTCGCCAGGTGAAGATCATGACGGAGAAGGAAC TCCTGGCCGTGGCTTGTGAGCAGTTTCTGGTAAGAATGTGCAGGACATCAAAAACGTGCG TCCTGCAGACCCTGGAGGGACATCTGCGCTCCATCCTCGGGACCCCTGACAGTGGAGCAGA TTTATCAGGACCGGGACCACTTTGCCAAGCTGGTGGGGAGGTGGCAGCCCTGATGTTG GCCGCATGGGCATTGAGATCCTCAGCTTCAACCATCAAGGACGTGTATGACAAAAGTGGACT ATCTGAGCTCCCTGGGCAAGACGACAGCTGCCGTGGTGCAGAGAGATGCTGACATTGGCG TGGCCGAGGCTGAACGGGACGACGAGCATCCGGGAAGCTGAGTGCAAGAAGGAGATGCTGG ATGTGAAGTTTATGGCAGACACCAAGATTGCTGACTCTAAGCGAGCCTTCGAGCTGCAAA AGTCAGCCTTCACTGAGGAGGTTAATCAAGACAGCTGAGGCCCACTTGGCCTATGAGC TGCAGGGGGCCCGTGAACAGCAGAAGATCCGGCAGGAAGAGATTGAGATTGAGTTGTGC AGCGCAAGAAACAGATTGCCGTGGAGGCACAGGAGATCCTGCGTACGGACAAGGAGCTCA TCGTACAGTGCGCCGGCTGCCGAGGCCGAGGCCACCGCATCCAGCAGATTGCCGAGG GTGAAAAGGTGAAGCAGGTCTCTTGGCACAGGCAGAGGCTGAGAAGATCCGCAAAATCG GGGAGGCGGAAGCGGCAGTCATCGAGGCGATGGGCAAGGCAGAGGCTGAGCGGATGAAGC TCAAGGCAGAAGCCTACCAGAAATACGGGGATGCAGCCAAGATGGCCTTGGTGTAGAGG CCCTGCCCCAGATTGCTGCCAAAATCGCTGCCCACTTACCAAGGTCGATGAGATTGTGG TCCTCAGTGGAGACAACAGTAAGGTACATCAGAAGTGAACCGACTGCTGGCCGAGCTGC CTGCCTCTGTGCATGCCCCACAGGCGTGGACCTGTCTAAGATACCCCTGATCAAGAAGG CCACTGGTGTGAGGTGTGAGGCTCCTGCAGGCCCACTCTCTTACGAGCCACCCGGCCC TCCCTCCAG		
	ORF Start: ATG at 54		ORF Stop: TGA at 1338
	SEQ ID NO: 72	428 aa	MW at 47047.6kD
NOV21b, CG140639-02 Protein Sequence	MGNCHTVGPNEALVVS GGCCGSDYKQYVFGGWAWAWWCISDTQRISLEIMTLQPRCEDVE TAEGVALTVTGVAQVKIMTEKELLAVACEQFLGKNVQDIKNVVLQTLLEGHLRSILGTLTV EQIYQDRDQFAKLREVAAPDVGRMGIEILSFTIKDVIDKVDYLSLGLKTQTAVVQRDAD IGVAEAEERDAGIREAECKKEMLDVKFMADTKIADSKRAFELQKSAFSEEVNIKTAEAQLA YELQGAREQQKIRQEEIEIEVVQRKKQIAVEAQEILRTDKELIATVRRPAEAEAHRIQQI AEGEKVKQVLLAQAEAEKIRKIGEAEEAVIEAMGKAEARMKLAEEAYQKYGDAAKMALV LEALPQIAAKIAAPLTKVDEIVVLSGDN SKVTSEVNRLLAELPASVHAPTGVDSLKIPLI KKATGVQV		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 21B.

Table 21B. Comparison of NOV21a against NOV21b.		
Protein Sequence	NOV21a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV21b	1..428	407/428 (95%)
	1..428	407/428 (95%)

Further analysis of the NOV21a protein yielded the following properties shown in Table 21C.

Table 21C. Protein Sequence Properties NOV21a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV21a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 21D.

Table 21D. Geneseq Results for NOV21a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV21a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW38288	Epidermal surface antigen - <i>Homo sapiens</i> , 379 aa. [US5691460-A, 25-NOV- 1997]	50..428 1..379	377/379 (99%) 377/379 (99%)	0.0
AAR51108	Human epidermal surface antigen - <i>Homo sapiens</i> , 291 aa. [WO9407906-A, 14- APR-1994]	50..326 1..277	276/277 (99%) 276/277 (99%)	e-148
ABB69326	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 34770 - <i>Drosophila</i> <i>melanogaster</i> , 378 aa. [WO200171042-A2, 27-SEP- 2001]	50..417 1..369	243/370 (65%) 307/370 (82%)	e-134

ABB62956	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 15660 - <i>Drosophila melanogaster</i> , 426 aa. [WO200171042-A2, 27-SEP-2001]	6..416 7..421	202/417 (48%) 301/417 (71%)	e-104
ABB65943	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 24621 - <i>Drosophila melanogaster</i> , 430 aa. [WO200171042-A2, 27-SEP-2001]	6..416 7..425	202/421 (47%) 301/421 (70%)	e-102

In a BLAST search of public sequence databases, the NOV21a protein was found to have homology to the proteins shown in the BLASTP data in Table 21E.

Table 21E. Public BLASTP Results for NOV21a				
Protein Accession Number	Protein/Organism/Length	NOV21a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z2S9	Flotillin-2 (Reggie-1) (REG-1) - <i>Rattus norvegicus</i> (Rat), 428 aa.	1..428 1..428	425/428 (99%) 426/428 (99%)	0.0
Q9DC36	Adult male lung cDNA, RIKEN full-length enriched library, clone:1200003P16, full insert sequence - <i>Mus musculus</i> (Mouse), 428 aa.	1..428 1..428	424/428 (99%) 425/428 (99%)	0.0
Q9BT16	Similar to flotillin 2 - <i>Homo sapiens</i> (Human), 385 aa.	1..375 1..375	374/375 (99%) 374/375 (99%)	0.0
Q14254	Flotillin-2 (Epidermal surface antigen) (ESA) - <i>Homo sapiens</i> (Human), 379 aa.	50..428 1..379	379/379 (100%) 379/379 (100%)	0.0
Q60634	Flotillin-2 (Epidermal surface antigen) (ESA) - <i>Mus musculus</i> (Mouse), 379 aa.	50..428 1..379	376/379 (99%) 377/379 (99%)	0.0

PFam analysis predicts that the NOV21a protein contains the domains shown in

5 Table 21F.

Table 21F. Domain Analysis of NOV21a			
Pfam Domain	NOV21a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Band_7	12..190	37/215 (17%) 99/215 (46%)	0.28
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Example 22.

The NOV22 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 22A.

Table 22A. NOV22 Sequence Analysis			
	SEQ ID NO: 73	1201 bp	
NOV22a, CG140843-01 DNA Sequence	CCGCGGAGTGCAGCGACCGCGCCGCGCTGAGGGAGGCGCCCCACCATGCCGCGGGCCCC GGCGCCGCTGTACGCCTGCCTCCTGGGGCTCTGCGCGCTCCTGCCCGGCTCGCAGGTCT CAACATATGCACTAGTGGAAGTGCCACCTCATGTGAAGAATGTCTGCTAATCCACCCAAA ATGTGCCTGGTGCTCCAAAGAGGACTTCGGAAGCCCACGGTCCATCACCTCTCGGTGTGA TCTGAGGGCAAACCTTGTCAAAAATGGCTGTGGAGGTGAGATAGAGAGCCAGCCAGCAG CTTCCATGTCTGAGGAGCCTGCCCTCAGCAGCAAGGGTTCGGGCTCTGCAGGCTGGGA CGTCATTCAGATGACACCACAGGAGATTGCCGTGAACCTCCGGCCCGGTGACAAGACCAC CTTCCAGCTACAGGTTCCGCCAGGTGGAGGACTATCCTGTGGACCTGTACTACCTGATGGA CCTCTCCCTGTCCATGAAGGATGACTTGGACAATATCCGGAGCCTGGGCACCAAACCTCGC GGAGGAGATGAGGAAGCTCACCAGCAACTTCCGGTTGGGATTTGGGTCTTTTGTGTGATAA GGACATCTCTCCTTCTCCTACACGGCACCGAGGTACCAGACCAATCCGTGCATTGGTTA CAAGTTGTTTCCAAATTGCGTCCCTCCTTGGGGTTCGCCCATCTGCTGCCTCTCACAGA CAGAGTGACAGCTTCAATGAGGAAGTTCGGAACAGAGGGTGTCCCGGAACCGAGATGC CCCTGAGGGGGGCTTTGATGCAGTACTCCAGGCAGCCGTCTGCAAGGTAACCTTCCTTTC TGGTCTGTCCCTGCATGGGGAGGTCAAGGTAGAGAGCGTCAGTGGGTGTTGGTACTTCC TGCAGGAGTCTTTGAGTGCCCCAGCATGTGGCTCCTGACCACTCTGAAGTCAGAGGGTGA GCTCAGTGGAACCTCTGGGAAATCTACAGCAGTCAAATCAGCCGGAGCTCGGGAATGGAT TGGGCTGGTCTGTGTCTCTGTGTGTCAGGGTGTGGTTGTGTGCAATGGAGTACTGTCTGCTA GAAGACAGCTGTCTGCATTTATACATTGGCTTTTGGTTTATTTTCAGGGGAAAAAAGTA AAGGTCAAGTCATAGGCATAGAAGCTTGTAGAGCTTTCTGGACCAATTTGGCAAACCTT A		
	ORF Start: ATG at 47		ORF Stop: TAG at 1079
	SEQ ID NO: 74	344 aa	MW at 37466.6kD
NOV22a, CG140843-01 Protein Sequence	MPRAPAPLYACLLGLCALLPRLAGLNICTSGSATSCEBCLLIHPKCAWCSKEDFGSPRSI TSRCDLRANLVKNGCGGEIESPASSFHVLRSLPLSSKSGSAGWDVIQMTPEIAVNLRP GDKTTFQLQVRQVEDYPVDLYLMDLSLSMKDDLDNIRSLGTLAEEMRKLTSNFRLLGFG SFVDKDISPFSTAPRYQTNPCIGYKLFPCVPSFGFRHLLPLTDRVDSFNEEVRKQRV RNRDAPEGGFDAVLQAAVCKVTLFSGPVPWAGGQGRERQWVLLVLPAGVFECPSMWLLTTL KSEGELSGTSGKSTAVKSAGAREWIGLVSVSGCGCVQWSTVC		

One polymorphic variant of NOV22a has been identified and is shown in Table

- 5 41G. Further analysis of the NOV22a protein yielded the following properties shown in Table 22B.

Table 22B. Protein Sequence Properties NOV22a	
PSort analysis:	0.4849 probability located in outside; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Cleavage site between residues 25 and 26

A search of the NOV22a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 22C.

Table 22C. Geneseq Results for NOV22a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV22a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU76337	Human anti-dual integrin protein #3 - <i>Homo sapiens</i> , 799 aa. [WO200212501-A2, 14-FEB-2002]	1..260 1..260	260/260 (100%) 260/260 (100%)	e-153
AAW02194	Human integrin beta subunit protein, beta-5 - <i>Homo sapiens</i> , 799 aa. [US5527679-A, 18-JUN-1996]	1..260 1..260	260/260 (100%) 260/260 (100%)	e-153
AAW13573	Mouse beta-3 integrin - Mus sp, 787 aa. [WO9708316-A1, 06-MAR-1997]	5..259 6..257	149/260 (57%) 186/260 (71%)	5e-77
AAW13574	Mouse beta-3 integrin (truncated) - Mus sp, 720 aa. [WO9708316-A1, 06-MAR-1997]	5..259 6..257	149/260 (57%) 186/260 (71%)	5e-77
AAU76336	Human anti-dual integrin protein #2 - <i>Homo sapiens</i> , 788 aa. [WO200212501-A2, 14-FEB-2002]	5..259 7..258	149/260 (57%) 184/260 (70%)	1e-76

5 In a BLAST search of public sequence databases, the NOV22a protein was found to have homology to the proteins shown in the BLASTP data in Table 22D.

Table 22D. Public BLASTP Results for NOV22a				
Protein Accession Number	Protein/Organism/Length	NOV22a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
A38308	integrin beta-5 chain precursor - human, 799 aa.	1..260 1..260	260/260 (100%) 260/260 (100%)	e-153

P18084	Integrin beta-5 precursor - <i>Homo sapiens</i> (Human), 799 aa.	1..260 1..260	260/260 (100%) 260/260 (100%)	e-153
O70309	Integrin beta-5 precursor - <i>Mus musculus</i> (Mouse), 798 aa.	1..260 1..260	241/260 (92%) 252/260 (96%)	e-141
Q8SQB9	Integrin beta 5 subunit precursor protein - <i>Bos taurus</i> (Bovine), 800 aa.	1..260 1..260	235/260 (90%) 246/260 (94%)	e-137
Q9GK49	Integrin beta-5 subunit - <i>Bos taurus</i> (Bovine), 791 aa (fragment).	11..260 2..251	225/250 (90%) 235/250 (94%)	e-131

Pfam analysis predicts that the NOV22a protein contains the domains shown in Table 22E.

Table 22E. Domain Analysis of NOV22a			
Pfam Domain	NOV22a Match Region	Identities/ Similarities for the Matched Region	Expect Value
integrin_B	35..260	142/230 (62%) 225/230 (98%)	1.4e-185

Example 23.

The NOV23 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 23A.

Table 23A. NOV23 Sequence Analysis			
	SEQ ID NO: 75	1272 bp	
NOV23a, CG141540-01 DNA Sequence	CCTAGGCCACGTGCTGCTGGGTCTCAGTCCTCCACTTCCCGTGTCTCTGGAAGTTGTCA GGAGCAATGTTGCGCTTGACGTGTTGGTAATGGGAGTTTCTGCCTCCACCCTTCAGCCT GCGGCACACACAGGGGCTGCCAGAAGCTGCCGTTTCGTGGGAGGCATTACAAGCGGGAG TTCAGGCTGGAAGGGGAGCCTGTAGCCCTGAGGTGCCCCAGGTGCCCTACTGGTTGTGG GCCTCTGTGAGCCCCCGCATCAACCTGACATGGCATAAAAAATGACTCTGCTAGGACGGTC CCAGGAGAAGAAGAGACCGGATGTGGGCCCCAGGACGGTGCTCTGTGGCTTCTGCCAGCC TTGCAGGAGGACTCTGGCACCTACGTCTGCACTACTAGAAATGCTTCTTACTGTGACAAA ATGTCCATTGAGCTCAGAGTTTTTGAGAATACAGATGCTTTCCTGCCGTTTCATCTCATAC CCGCAAATTTTAACCTTGTCAACCTCTGGGGTATTAGTATGCCCTGACCTGAGTGAATTC ACCCGTGACAAAATGACGTGAAGATTCAATGGTACAAGGATTCTCTTCTTTGGATAAA GACAATGAGAAATTTCTAAGTGTGAGGGGGACCACTCACTTACTCGTACACGATGTGGCC CTGGAAGATGCTGGCTATTACCGCTGTGTCTGACATTTGCCCATGAAGGCCAGCAATAC AACATCACTAGGAGTATTGAGCTACGCATCAAGAGGTCAAGACTGAQAATCCCGTGTAAAG GTGTTTCTGGGAACCGGCACACCCTTAACCACCATGCTGTGGTGGACGCCAATGACACC CACATAGAGAGCGCCTACCCGGGAGGCCGCGTGACCGAGGGGCCACGCCAGGAATATTCA GAAAATAATGAGAACTACATTGAAGTGCCATTGATTTTTGATCCTGTCACAAGAGAGGAT TTGCACATGGATTTTAAATGTGTTGTCCATAATACCCTGAGTTTTTCAGACACTACGCACC ACAGTCAAGGAAGCCTCCTCCACGTTCTCCTGGGGCATTGTGCTGGCCCCACTTTCACTG GCCTTCTTGGTTTTTGGGGGAATATGGATGCACAGACGGTGCAAACACAGAAGTGGAAAA GCAGATGGTCTGACTGTGCTATGGCCTCATCATCAAGACTTTCAATCCTATCCCAGTGA		

	AATAAATGGAATGAAATAATTCAAACACAAACTCCGTACGTCTTCTCTTATGGAAGTGGC TGTGTCTTTTG		
	ORF Start: ATG at 67		ORF Stop: TGA at 1198
	SEQ ID NO: 76	377 aa	MW at 43181.9kD
NOV23a, CG141540-01 Protein Sequence	MLRLYLVMGVSASTLQPAHTGAARSCRFRGRHYKREFRLEGEPPVALRCPQVPYWLWAS VSPRINLTWHKNDASRTVPGEETRMWAQDGLWLLPALQEDSGTYVCTTRNASYCDKMS IELRVFENTDAFLPFISYPQILTLSTSGVLVCPDLSEFTRDKTDVKIQWKDSLLLDKDN EKFLSVRGTTLLVHDVALEDAGYYRCVLTFAHEGQQYNITRSIELRIKRSRLTIPCKVF LGTGTPLTTLMLWWTANDTHIESAYPGRVTEGPRQEYSENNENYIEVPLIFDPVTREDLH MDFKCVVHNTLSFQTLRTTVKEASSTFSWGIVLAPLSLAFVLVGGIWMHRRCKHRTGKAD GLTVLWPHHQDFQSYPK		
	SEQ ID NO: 77	1286 bp	
NOV23b, CG141540-02 DNA Sequence	GCCACGTGCTGCTGGGTCTCAGTCCCTCCACTTCCCGTGTCTCTGGAAGTTGT CAGGAGC AATGTTGCGCTTGACGTGTTGGTAATGGGAGTTTCTGCCTTCACCCTTCAGCCTGCGGC ACACACAGGGGCTGCCAGAAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGGAGTT CAG GCTGGAAGGGGAGCCTGTAGCCCTGAGGTGCCCCAGGTGCCCTACTGGTTGTGGGCCCTC TGTCAGCCCCCGCATCAACCTGACATGGCATAAAATGACTCTGCTAGGACGGTCCCAGG AGAAGAAGAGACACGGATGTGGGCCAGGACGGTGCTCTGTGGCTTCTGCCAGCCTTGCA GGAGGACTCTGGCACCTACGTCTGCACTACTAGAAATGCTTCTTACTGTGACAAAATGTC CATTGAGCTCAGAGTTTTTGAGAATACAGATGCTTTCCTGCCGTTTCATCTCATACCCGCA AATTTTAACCTTGTCAACCTCTGGGGTATTAGTATGCCCTGACCTGAGTGAATTCACCG TGACAAAACCTGACGTGAAGATTCAATGGTACAAGGATTCTCTCTTTGGATAAAGACAA TGAGAAATTTCTAAGTGTGAGGGGACCACTCACTTACTCGTACACGATGTGGCCCTGGA AGATGCTGGCTATTACCGCTGTGTCCTGACATTTGCCCATGAAGGCCAGCAATACAACAT CACTAGGAGTATTGAGCTACGCATCAAGAAAAAAGAAGAGACCATTCTCTGTGATCAT TTCCCCCTCAAGACCATATCAGCTTCTCTGGGGTCAAGACTGACAATCCCGTGTAAGGT GTTTCTGGGAACCGGCACACCCTTAACCACCATGCTGTGGTGGACGGCCAATGACACCA CATAGAGAGCGCTACCCGGGAGGCCGCGTGACCGAGGGGCCACGCCAGGAATATT CAGA AAATAATGAGAACTACATTGAAGTGCCATTGATTTTTGATCTGTGCACAAGAGAGGATTT GCACATGGATTTTAAATGTGTTGTCCATAATACCCTGAGTTTT CAGACACTACGCACCAC AGTCAAGGAAGCCTCCTCCAGTTCTCTGGGGCATGTGTCTGGCCCCACTTTCACTGGC CTTCTTGTTTTTGGGGGAATATGGATGCACAGACGGTGCAACACAGAACTGGAAAAGC AGATGGCTGACTGTGCTATGGCCTCATCATCAAGACTTTCAATCCTATCCCAAGTGAAA TAAATGGAATGAAATAATTCAAACAC		
	ORF Start: ATG at 62		ORF Stop: TGA at 1256
	SEQ ID NO: 78	398 aa	MW at 45420.6kD
NOV23b, CG141540-02 Protein Sequence	MLRLYLVMGVSAFTLQPAHTGAARSCRFRGRHYKREFRLEGEPPVALRCPQVPYWLWAS VSPRINLTWHKNDASRTVPGEETRMWAQDGLWLLPALQEDSGTYVCTTRNASYCDKMS IELRVFENTDAFLPFISYPQILTLSTSGVLVCPDLSEFTRDKTDVKIQWKDSLLLDKDN EKFLSVRGTTLLVHDVALEDAGYYRCVLTFAHEGQQYNITRSIELRIKKKKEBTIPVII SPLKTISASLSRLTIPCKVFLGTGTPLTTLMLWWTANDTHIESAYPGRVTEGPRQEYSE NNENYIEVPLIFDPVTREDLHMDFKCVVHNTLSFQTLRTTVKEASSTFSWGIVLAPLSLA FLVLGGIWMHRRCKHRTGKADGLTVLWPHHQDFQSYPK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 23B.

Table 23B. Comparison of NOV23a against NOV23b.		
Protein Sequence	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Region

NOV23b	1..377	375/398 (94%)
	1..398	376/398 (94%)

Six polymorphic variants of NOV23a have been identified and are shown in Table 41H. Further analysis of the NOV23a protein yielded the following properties shown in Table 23C.

Table 23C. Protein Sequence Properties NOV23a	
PSort analysis:	0.4600 probability located in plasma membrane; 0.2676 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 14 and 15

- A search of the NOV23a protein against the Geneseq database, a proprietary
- 5 database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 23D.

Table 23D. Geneseq Results for NOV23a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB08207	Human type II Interleukin-1 receptor - <i>Homo sapiens</i> , 398 aa. [WO200187328-A2, 22-NOV-2001]	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0
AAE16581	Human interleukin-1 receptor DNAX designation 2 (IL-1RD2) protein - <i>Homo sapiens</i> , 398 aa. [US6326472-B1, 04-DEC-2001]	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0
AAU78089	Human interleukin 1R2 (IL-1R2) protein sequence - <i>Homo sapiens</i> , 398 aa. [WO200211767-A2, 14-FEB-2002]	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0
AAM24185	Human EST encoded protein SEQ ID NO: 1710 - <i>Homo sapiens</i> , 398 aa. [WO200154477-A2, 02-AUG-2001]	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0

AAB37792	Human interleukin-1 receptor, type II precursor - <i>Homo sapiens</i> , 398 aa. [WO200064479-A1, 02-NOV-2000]	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0
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In a BLAST search of public sequence databases, the NOV23a protein was found to have homology to the proteins shown in the BLASTP data in Table 23E.

Table 23E. Public BLASTP Results for NOV23a				
Protein Accession Number	Protein/Organism/Length	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P27930	Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta) (Antigen CDw121b) - <i>Homo sapiens</i> (Human), 398 aa.	1..377 1..398	375/398 (94%) 376/398 (94%)	0.0
Q29612	Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta) - <i>Cercopithecus aethiops</i> (Green monkey) (Grivet), 393 aa.	1..372 1..393	342/393 (87%) 351/393 (89%)	0.0
AAB05878	Soluble type II interleukin-1 receptor - <i>Homo sapiens</i> (Human), 296 aa.	1..275 1..296	273/296 (92%) 274/296 (92%)	e-159
Q9N2H5	Interleukin-1 receptor type II precursor - <i>Equus caballus</i> (Horse), 403 aa.	4..376 4..396	258/394 (65%) 297/394 (74%)	e-147
P43303	Interleukin-1 receptor, type II precursor (IL-1R-2) - <i>Rattus norvegicus</i> (Rat), 416 aa.	1..376 1..409	232/411 (56%) 282/411 (68%)	e-127

PFam analysis predicts that the NOV23a protein contains the domains shown in

5 Table 23F.

Table 23F. Domain Analysis of NOV23a			
Pfam Domain	NOV23a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ig	43..110	13/70 (19%) 46/70 (66%)	0.00014

ig	165..209	9/47 (19%) 35/47 (74%)	0.0011
ig	230..307	14/78 (18%) 56/78 (72%)	4.3e-05

Example 24.

The NOV24 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 24A.

Table 24A. NOV24 Sequence Analysis			
	SEQ ID NO: 79	4744 bp	
NOV24a, CG141580-01 DNA Sequence	GCTCGGAAC TACACTTCCCGGCAGAACGCGGGCGCGCACGCGCACCGGGGCCTCAGCC ATGGCGACCGTGCTGTCCAGGGCGCTCAAGCTGCCGGGAAGAAGAGCCAGACCTAGGG GAGTATGATCCACTTACCCAGGCTGACAGTGATGAGAGCGAAGACGATCTGGTGCTTAAC CTGCAGAAGAATGGAGGGGTCAAAAATGGGAAGAGTCCTTTGGGAGAAGCGCCAGAACCC GACTCAGATGCTGAGGTTGCAGAGGCTGCAAAGCCACATCTTTCAGAAGTACCCACGGAG GGCTACCCCTCAGAACCCCTTGGGGGCCTGGAACAGAAGGCGGCCTCCTCCCTGGTGTCA TATGTGCGCACGTCTGTCTTCTGCTGACTTTGGGGATCTCGATGATCCTGGTGCTCCTG TGTGCTTTCCTGATCCCCCTGTCTCCAGAGATCTGCACAGCACCTGGAGCCGCCACTTG GGCTCCAGGGAGGTGGGGACCTGTCTCCATTGGAATTGGCTGATGTGAATGGAGATGGC CTGCGTGATGTGCTTCTCTCTTTGTGATGTCAAGGAACGGGAGTGCAGTAGGTGTCTCA AGACCAGCTGCTAATCTTGTATGCCTTTCGGGGATGAATGGCAGCACACTGTGGTCTAGT CTTCTCCCTGAGGAGGCTCGAGATATCACATGTTTGGAGCTGATGCCAGGAAGCTTGGCT GAAACCATCTGCCTTGTGACAGGGACACACAAGATGCTCAGCGCATTCAATGCAACGTCA GGGAAAGCCATTTGGACTTTAAACCCAACTACTTGTCCAACGGTACCTTGGCTGCCCA GTTGTGGTACTGCCAGACTTGGATGAAGACGGTGTTCGAGACCTTGTGGTTCTGGCCATT GGGGAATTGCAGCCAGATCTGTGCTTCTGCTGGTGTCTGGCCGGACCGGAAATCCAGTG GGTCGACCTGTGAAGTACAACATCGTTGGAGTTGGGAATCTGATTGGTCTCTCAGGTTTAC ATCACCAAAATGGGGCTGTCTACATCCTGTTTGGCTTTGGAAATATACAAGCTGTCCGA CTGCGGGACATTTTGTTCAGGCCCAAAATCGAGACAGCTCACCACCTTCTCTGCAGATA GAAGAGCCAGAATGGGAAAAGCGAAGATCCATCAACCTGTCTGAGCTCATTGATGTTTAC AGTGATGGTGTGAACTACTCCAGATGGTGAAGGCACAGATTCCAACCTGCAGCAACCTT CTGATTACAACCAGACAAAGCCTTGTGCTGCTTCGGGGGCAAAATCTGACACCTTACTGG GCATTGAGACTTCAAGGCCTGCGCAGCCAGCCTACTCCTGGATATTTCACTGATGATCAG ACATTAGACTTCCTTCTGCAGATACAGGATGGAGTTGGGATGAAAAGATGATGGTTGTG GATGGTGAATCTGGCTCCATTGTTTGGAGTTACCGTGCTCCGTGTACATGAAAGAAACG CCAGCCACCTCAGCAGTTACTTCAGACCAGAAGTCTGTCTTCTCTTCTGGGCCGAAGGG CTGTCAGCTGCATCTCCCAATTCCGATATCATCTTAGGAAGTGAAGCCGCCAGCCTTAC CACCTTTACCTCCTGCATCCTGCGTTCCCTCCATCCTTCTGGATCTGGCCACACCACC GGCACAGTGACGCTTCAGAGGTTGGAATTAACGACCTCTGGAAGATGCCTTTTATGTT ACCAGGACAACAGGGCCAAGCTCCGAAGGCCATCCAGCAGCCCTGGTGGTCAAGCCTT AGTCTACGGTGGGCACTAATGGAGGGCCAGATGGCTCAGCTACAGGAGTCCACCCCCAAA ATTGGCCGTGGGAGCTGCGAAGATTTCTCTTAGGATAAAGTTTGTGGAAGTCCCTAC GAGATCTAATCTGATGGAATCTTCAGTTGCAGAAGAAGTGAACAGAGTGATACCTCTC TACTCTCCTGTCACTGTAAATCAGTTCTATGGAGAGAAGACTTCTCGCTCTATTAC CACCTCCCTGATGGTTGCAAAGGCTTGGGAAGGCATGTTGGAGTCTTTGACGGCAGCATG ATCTATTTGGCTGGGGCATCTTACCTACCTTTTCAGTCCCTGCATTAATCCCTCTAGGA ACTCTGCGTGGACCGTTTGGAAATGTGAATCTCTTAAGTATTTAATTTTTTGGTATGTC TAATTTATGAAGTCTTGCTGGGAAAGCCAGTGAAGTCTATGACTAGGAAACATTTGTTG TACATTGTGCTGTGTGTGTATATTTTAGTGTTGTGGTGAAGTTATTTTCCAGGTATGT CCTAAGCTTCAGGGATCCAGTTTCTTGTCTTCTGAAATATATCTGGTTTGTGTTGTCAT TTTGAGACTTCCAGATGCCCTACCTCTGATGTTGAGGGCCACTTATTTCTCTCTTATTC		

	TTTCCACCTGTACCTTGGCTACTTCCAAATTGTAGACAGAATGAGAAAGATTATAGTG GAAGACTGAGTTAGCCATCCAAGCATTTTCATCTCTCTTGTTTTATATCCTATTTCCCTTA GATTTTCCATCCATGTCTATTAAAGTGACCACAAGAATAACTATATTCTATCACAAGGGG AGCAAGAGGATGTAGTCTCAGTGACCCATCTCTGACCAAGTCCACATGTTGTGTTATATG TGGCTCTGATGGTCTGCCAGTCATGATCTTTTTCTGTGGCGACATCAGAAGTGATGT TTGCATGCTGTCTTCAACTTAGAGGAGAACTGGAAGTCAGGAGCCTTTGATGTCCTTATC CTGCTGTATGTCTCTCTGCACTCTTTTCTATAGGGCACCTCCTTAGCTCCCCTCACTC TGTTTCTCTTCTATTAGGGATATGTTCTGGACTTTTCTTCTGCTACTTGAGTCCAG GATGCAACCATTTGTCTGCACTCTCTTCTTCTGAGAGCCTTTGAAGCATTGTATTT TGGGAAAATTCTCTGTAAATACTATAACTTTTATAAATGGTTAAGTTATTTAGAATTAT CTCCAGTGCTTACTTCTCCCTTCTTCTGTATAAATCTGCTACTTCAATTAAGTTCTCCTC TAACTTTTAGGTCATTGTTTATATAGCAGAAAATTCAATGTTAGCGGATGGAAAAGTGC TTCTTGAATAACCTTGATAGGTCATCCCTGAGTGCACCTCAGGTCTCTCTTACCTGGG CTTGTATCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTGTGCGCCAG GCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAACCTTCGCCTCCTGGGTTCAAGCGA TTCTCCAGCCTTAGCCTCCCAAGTAGCTGGGACTACAGGTGCCCGCTACCATGCCTGGCT AATTTTTTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCA CGAACTCCTGACCTCAGATAATCCACCTGCTTCTGCCTCCCAAAGTGCTGGGATTACAGG CGTGAGCCACCATGCCCGGCTGGGCTTGATCTTTAGCTTGTGTTAGTAAAGGATTCT AGAAAATTATGAAGTCCAGATTCAAAGGGATCTCTGTTAATTACCACTGACAGGCATTA TGACCTAACAGGAGGTTGGTAGCAGTAGATCCAAGCATGCATGTTGCCTGGCCTGTAGAT TGGCCTTATCAGGTTTCTGGGTGCCTCTGCCTTAAGATCCTGAAGGCAAATTTGTTTCA ACAGTTTGAAGTCATCTGTGGGTCCAGCTTGACTTTGGAGGAATAAGAAGATACTTCTA GAGTATGGGAATGATTCCAGATAATTTCTGGGATTGAATCTACTTGAGTTTAAAGGCGCT GGGACCTAATTTGGTTTAGTATAGAATTTGAAGAATTAATTTATAGGCAGCTGAATACCC AAACTTGGGTGGTGGTCTGTGGTTTGGCTGAGCTGCGGGCATAACCTGGTCTCTGT TTATGTTAAGGCTTCTGGGAAGCCAGCCACTCTGCGCAGGAGTGAAACATGAAGTTGTT TTCTGAGGACCTGTTTGGTGGGATTGTTTGGGCAGAGGACTGTGTTTATGCAGGGCAAA TCCCAGAAAGATAAGAGGAAGCTAGAGAACTTAATGTACCTGAATTCTTCATGGTGTAT TTGCAAACTAACTTAACATAGATTCTTTGACTATGGTAAGTTTGAATCTCTCCTTGCCA AACAACTTATAAGTTTAGTTTCTTCTTCTCTGACCGGTCAGGAAAGGTGTAAGT GGTGGCTGAAAATTGAGGAAGCTTCATCTGACCAATGTGGGTGCTGGTTTCTGTGAAAT GTGTCCCTAAGCCTCCTTCTCCTTGCAGGCAGCCACCCACCCAGGTGTCTAAGATAGGAC ATGCTCCTTTCTTCTCTAATCCATCCTGAGGTTGCCGGCAAAGCCAATATGACCACTA CTGAGAAATAGTAATGACTTCTACAAATGCAAGGGTCTTACCCTCCTTTCCCTTAAAC ACCCTCCCTTTTCTTAGACCCCGTTTTTGGCATCCCCCAAATGTGTGGTATGGTGAAC TAATCCCTGAATGTGAATTGCTATCCTTATTGCCCTATTAAAGAGAGCCAGCTGGTAT ATTGTCAGGAAGCACTATTTAAAATGTGAAGTGTATAGAGTAAATAAATAAATACTCTA CAGG		
	ORF Start: ATG at 61		ORF Stop: TAA at 1927
	SEQ ID NO: 80	622 aa	MW at 67037.7kD
NOV24a, CG141580-01 Protein Sequence	MATVLSRALKLPKKSPDLGEYDPLTQADSEDEDDLVLNLQKNGGVKNGKSPLGEAPEP DSDAEVABAAKPHLSEVTTEGYPSLEPLGLEQKAASSLVSYVRTSVFLLTLGISMILVLL CAFLIPCPRDLHSTWSRHLGSQGGDLSPLELADVNGDGLRDVLLSFVMSRNGSAVGVS RPAANLVCLSGMNGSTLWSSLLPEEARDITCLELMPGSLAETICLVGTGTHKMLSAFNATS GKAIWTLNPNYLSNGTLAAPVVVLPDLDEDGVRLDVVLAIGELQPDLCFLLVSGRTGNPV GRPVKYNIVGVNLIQPVYITNGAVYILFGFGNIQAVALRDFVQAQNRDSSPPSLQI EEPWEKRRSINLSELIDVSDGVVELLMVKAPDSNCSNLLITRQSLVLLRQNLTPYW ALRLQGLRSQPTPGYFTDDQTLDFLLQIQDGVGMKMMVVDGDSGSIVWSYRAPCHMKET PATSAVTSQKSVFLFWAEGLSAASPNSDIILGTEPPSLHHLVLLHPAFPSILLDLANTT GTVTASEVGINDLWKDAFYVTRTITGSPSEGHPAALVVSKLSLRWALMEGQMAQLQESTPK IGRGELRRFLSRIKFVEAPYEI		

Two polymorphic variants of NOV24a have been identified and are shown in Table 41I. Further analysis of the NOV24a protein yielded the following properties shown in Table 24B.

Table 24B. Protein Sequence Properties NOV24a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV24a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 24C.

Table 24C. Geneseq Results for NOV24a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB04610	Human quinoprotein dehydrogenase 33 protein SEQ ID NO:2 - <i>Homo sapiens</i> , 302 aa. [CN1307126-A, 08-AUG-2001]	1..284 1..284	283/284 (99%) 283/284 (99%)	e-160
ABB05665	Human transmembrane protein clone amy2_11d2 #2 - <i>Homo sapiens</i> , 552 aa. [WO200198454-A2, 27-DEC-2001]	61..615 6..548	146/565 (25%) 261/565 (45%)	3e-46
ABB89951	Human polypeptide SEQ ID NO 2327 - <i>Homo sapiens</i> , 552 aa. [WO200190304-A2, 29-NOV-2001]	61..615 6..548	145/565 (25%) 260/565 (45%)	1e-45
ABB89787	Human polypeptide SEQ ID NO 2163 - <i>Homo sapiens</i> , 121 aa. [WO200190304-A2, 29-NOV-2001]	232..324 1..99	83/99 (83%) 87/99 (87%)	3e-39
ABB62154	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 13254 - <i>Drosophila melanogaster</i> , 989 aa. [WO200171042-A2, 27-SEP-2001]	125..465 153..502	86/378 (22%) 145/378 (37%)	5e-14

- 5 In a BLAST search of public sequence databases, the NOV24a protein was found to have homology to the proteins shown in the BLASTP data in Table 24D.

Table 24D. Public BLASTP Results for NOV24a				
Protein Accession Number	Protein/Organism/Length	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9CXB0	8430419L09Rik protein - <i>Mus musculus</i> (Mouse), 624 aa.	1..622 1..624	544/624 (87%) 580/624 (92%)	0.0
Q9P261	KIAA1467 protein - <i>Homo sapiens</i> (Human), 432 aa (fragment).	191..622 1..432	432/432 (100%) 432/432 (100%)	0.0
Q99L10	Similar to RIKEN cDNA 8430419L09 gene - <i>Mus musculus</i> (Mouse), 183 aa (fragment).	440..622 1..183	152/183 (83%) 164/183 (89%)	5e-84
Q96S30	Hypothetical 69.3 kDa protein - <i>Homo sapiens</i> (Human), 636 aa.	61..615 72..605	145/558 (25%) 261/558 (45%)	1e-46
Q9H0X4	Hypothetical 59.7 kDa protein - <i>Homo sapiens</i> (Human), 552 aa.	61..615 6..548	146/565 (25%) 261/565 (45%)	8e-46

PFam analysis predicts that the NOV24a protein contains the domains shown in Table 24E.

Table 24E. Domain Analysis of NOV24a			
Pfam Domain	NOV24a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 25.

- 5 The NOV25 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 25A.

Table 25A. NOV25 Sequence Analysis		
	SEQ ID NO: 81	905 bp
NOV25a, CG141643-01 DNA Sequence	AACAGCGGCCCTGCGGCTGGCGCGGCGGACGGGATGAGGCGCTGCAGTCTCTGCGCTTTC GACGCCGCCCGGGGGCCAGGCGGCTGATGCGTGTGGGCCTCGCGCTGATCTTGGTGGGC CACGTGAACCTGCTGCTGGGGCCGTGCTGCATGGCACCGTCCTGCGGCACGTGGCCAAT CCCCGCGGCGCTGTACGCCGGAGTACACCGTAGCCAATGTCATCTCTGTCGGCTCGGGG CTGCTGGTGAGCGCGGCAGGCGACCCGGGCGGGGCGGGCTCCCGGAGAGCCAGCAGG CCAAAGGCTTTGTGTCTTCCACAGAGCGTTTCCGTGGGACTTGTGGCCCTCTGGCGTCC	

	AGGAACCTTCTTCGCCCTCCACTGCACTGGGTCTGCTGGCACTAGCTCTGGTGAACCTG CTCTTGTCGGTTGCTGCTCCCTGGGCCTCCTTCTGCTGTGTCCTACTGCTGGCCAAC GGTGGCCGCCGCTTATTGCTGACTGCCACCCAGGACTGCTGGATCCTCTGGTACCACTG GATGAGGGGCGGGACATACTGACTGCCCTTTGACCCACAGAATCTATGATACAGCC TTGGCTCTCTGGATCCCTTCTTGTCTCATGTCTGCAGGGGAGGCTGCTCTATCTGGTTAC TGCTGTGTGGCTGCACTCACTCTACGTGGAGTTGGGCCTGCAGGAAGGACGGACTTCAG GGGCAGGTAGTAGCTGGGTGTGACGCAAGAGTGAAACAGAAAGCCTGGCAGCCACGGTTT CCTGGGATTAAAGTCAAAGCATTATGAATATGGCACTAAAGTGACTGAGCTACCAGACCA ATGATCCTGTAAGGCAGCCACAGAATAAAAAACAACAATTATTATTAACTGCTCTGGA TTCTC		
	ORF Start: ATG at 34		ORF Stop: TGA at 805
	SEQ ID NO: 82	257 aa	MW at 26717.2kD
NOV25a, CG141643-01 Protein Sequence	MRRCSLCAFDAARGFRRMLRVGLALILVGHVNLLGAVLHGTVLRHVANPRGAVTPEYTV ANVISVGSGLLVSAAGDPGGGRAPGEPSPKALCLPQSVSVGLVALLASRNLLRPPLHWV LLALALVNLLLSVACSLGLLLAVSLTVANGRRLIADCHPGLDPLVPLDEGPHTDCPF DPTRIYDTALALWIPSLMSAGEAALSGYCCVAALTLRGVGPCKRDGLQGQVVAGCDARV KQKAWQPRFPPIKVKAL		

Further analysis of the NOV25a protein yielded the following properties shown in Table 25B.

Table 25B. Protein Sequence Properties NOV25a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 37 and 38

A search of the NOV25a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several
5 homologous proteins shown in Table 25C.

Table 25C. Geneseq Results for NOV25a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AA Y78805	Hydrophobic domain containing protein clone HP10508 protein sequence - <i>Homo sapiens</i> , 231 aa. [WO200000506-A2, 06-JAN-2000]	1..257 1..231	231/257 (89%) 231/257 (89%)	e-127
ABB90256	Human polypeptide SEQ ID NO 2632 - <i>Homo sapiens</i> , 240 aa. [WO200190304-A2, 29-NOV-2001]	1..232 1..206	205/232 (88%) 206/232 (88%)	e-111

AAU83615	Human PRO protein, Seq ID No 48 - <i>Homo sapiens</i> , 222 aa. [WO200208288-A2, 31-JAN-2002]	19..232 1..188	187/214 (87%) 188/214 (87%)	1e-99
AAG81326	Human AFP protein sequence SEQ ID NO:170 - <i>Homo sapiens</i> , 222 aa. [WO200129221-A2, 26-APR-2001]	19..232 1..188	187/214 (87%) 188/214 (87%)	1e-99
AAB43588	Human cancer associated protein sequence SEQ ID NO:1033 - <i>Homo sapiens</i> , 243 aa. [WO200055350-A1, 21-SEP-2000]	102..232 79..209	127/131 (96%) 129/131 (97%)	9e-70

In a BLAST search of public sequence databases, the NOV25a protein was found to have homology to the proteins shown in the BLASTP data in Table 25D.

Table 25D. Public BLASTP Results for NOV25a				
Protein Accession Number	Protein/Organism/Length	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH27812	Similar to RIKEN cDNA 2010001C09 gene - <i>Mus musculus</i> (Mouse), 249 aa.	1..232 10..215	185/232 (79%) 194/232 (82%)	e-100
CAC38576	Sequence 169 from Patent WO0129221 - <i>Homo sapiens</i> (Human), 222 aa.	19..232 1..188	187/214 (87%) 188/214 (87%)	4e-99
Q9D817	2010001C09Rik protein - <i>Mus musculus</i> (Mouse), 223 aa.	1..232 10..189	163/232 (70%) 171/232 (73%)	3e-82
Q969K7	Hypothetical 23.8 kDa protein (Similar to RIKEN cDNA 1810017F10 gene) (Beta-casein-like protein) - <i>Homo sapiens</i> (Human), 222 aa.	18..210 17..177	66/193 (34%) 104/193 (53%)	6e-26
Q8VCL0	RIKEN cDNA 1810017F10 gene - <i>Mus musculus</i> (Mouse), 219 aa.	18..210 17..177	69/195 (35%) 101/195 (51%)	1e-24

PFam analysis predicts that the NOV25a protein contains the domains shown in

5 Table 25E.

Table 25E. Domain Analysis of NOV25a			
Pfam Domain	NOV25a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 26.

The NOV26 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 26A.

Table 26A. NOV26 Sequence Analysis			
	SEQ ID NO: 83	446 bp	
NOV26a, CG142003-01 DNA Sequence	CTGGGGATAGAGCCTCCTCAAATCCAAATGCTACCAGCTCCAGCTCCAGGATCCAGAGA GTTTGCAAGACAGAGGCGAAGGGAAGGTCGCAACAACAGTTATCTCCAAGATGCTATTTCG TTGAACCCATCCTGGAGGTTTCCAGCTTGCCGACAACCAACTCAACAACCAATTCAGCCA CCAAATAACAGCTAATACCACTGATGAACCCACCACACAACCCACCACAGAGGACCCAG ATCTTCAGGTTTCTGCGATGCAGCACCAGACAGTGCTGGAAGTGACAGAGACTGGGGTGG AGGTGGCTGCAGCCTCCGCCATCTCTGTGGCCCGCACCCTGCTGGTCTTTGAAGTGCAGC AGCCCTTCCTCTTCGTGCTCTGGGACCAGCAGCACAAGTTCCTGTCTTCATGGGGCGAG TATATGACCCCAAGGCGCTGAGACAAG		
	ORF Start: at 3		ORF Stop: TGA at 438
	SEQ ID NO: 84	145 aa	MW at 15697.3kD
NOV26a, CG142003-01 Protein Sequence	GDRASSNPNATSSSSQDPESLQDRGEGKVATTVISKMLFVEPILEVSSLPTTNSTNSAT KITANTTDEPTTQPTTEDPDLQVSAMQHQTVLELTETGVEVAAASAI SVARTLLVFEVQQ PFLFVLWDQQHKFPVFMGRVYDPR		
	SEQ ID NO: 85	436 bp	
NOV26b, 306076006 DNA Sequence	CACCAAGCTTAATCCAAATGCTACCAGCTCCAGCTCCAGGATCCAGAGATTGCAAGA CAGAGGCGAAGGGAAGGTCGCAACAACAGTTATCTCCAAGATGCTATTCGTTGAACCCAT CCTGGAGGTTTCCAGCTTGCCGACAACCAACTCAACAACCAATTCAGCCACCAATAAC AGCTAATACCACTGATGAACCCACCACACAACCCACCACAGAGGACCCAGATCTTCAGGT TTCTGCGATGCAGCACCAGACAGTGCTGGAAGTGACAGAGACTGGGGTGGAGGTGGCTGC AGCCTCCGCCATCTCTGTGGCCCGCACCCTGCTGGTCTTTGAAGTGCAGCAGCCCTTCCT CTTCTGTGCTCTGGGACCAGCAGCACAAGTTCCTGTCTTCATGGGGCGAGTATATGACCC CAGGGCCCTCGAGGGC		
	ORF Start: at 2		ORF Stop: end of sequence
	SEQ ID NO: 86	145 aa	MW at 15765.5kD
NOV26b, 306076006 Protein Sequence	TKLNPATSSSSQDPESLQDRGEGKVATTVISKMLFVEPILEVSSLPTTNSTNSATKIT ANTTDEPTTQPTTEDPDLQVSAMQHQTVLELTETGVEVAAASAI SVARTLLVFEVQQPFL FVLWDQQHKFPVFMGRVYDPRAL		
	SEQ ID NO: 87	223 bp	
NOV26c, 27889088 DNA Sequence	CACCAAGCTTACAGAGGACCCAGATCTTCAGGTTTCTGCGATGCAGCACCAGACAGTGCT GGAAGTGACAGAGACTGGGGTGGAGGTGGCTGCAGCCTCCGCCATCTCTGTGGCCCGCAC CCTGTGGTCTTTGAAGTGCAGCAGCCCTTCCTCTTCGTGCTCTGGGACCAGCAGCACA GTTCCCTGTCTTCATGGGGCGAGTATATGACCCCTCGAGGGC		
	ORF Start: at 2		ORF Stop: end of sequence
	SEQ ID NO: 88	74 aa	MW at 8317.5kD
NOV26c, FPVFMGRVYDPLEG	TKLTEDPDLQVSAMQHQTVLELTETGVEVAAASAI SVARTLLVFEVQQPFLFVLWDQQHK FPVFMGRVYDPLEG		

278889088			
Protein Sequence			
	SEQ ID NO: 89	529 bp	
NOV26d, CG142003-02 DNA Sequence	GAGGAGAAGTTTGGAGTCCGCTGACGTCGCCGCCAGATGGCCTCCAGGCTGACCCTGCT GACCCTCCTGCTGCTGCTGCTGGCTGGGGATAGAGCCTCCTCAAATCCAAATGCTACCAG CTCCAGCTCCCAGGATCCAGAGAGTTTGCAAGACAGAGGCGAAGGGAAGGTCGCAACAAC AGTTATCTCCAAGATGCTATTTCGTTGAACCCATCCTGGAGGTTTCCAGCTTGCCGACAAC CAACTCAACAACCAATTAGCCACCAAAATAACAGCTAATACCACTGATGAACCCACCAC ACAACCCACCACAGAGGACCCAGATCTTCAGGTTTCTGCGATGCAGCACCAGACAGTGCT GGAAGTGCAGAGACTGGGGTGGAGGTGGCTGCAGCCTCCGCCATCTCTGTGGCCCGCAC CCTGCTGGTCTTTGAAGTGCAGCAGCCCTTCCTCTTCGTGCTCTGGGACCAGCAGCACAA GTTCCCTGTCTTCATGGGGCGAGTATATGACCCAGGGCCTGAGACAAG		
	ORF Start: ATG at 38		ORF Stop: TGA at 521
	SEQ ID NO: 90	161 aa	MW at 17434.5kD
NOV26d, CG142003-02 Protein Sequence	MASRLTLLTLLLLLAGDRASSNPNTSSSSQDPESLQDRGEGKVATTVISKMLFVEPIL EVSSLPTTNSTNSATKITANTTDEPTTQPTTEDFDLQVSAMQHQTVLELTETGVEVAAA SAISVARTLLVFEVQQPFLFVLWDQQHKFPVFMGRVYDPRA		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 26B.

Table 26B. Comparison of NOV26a against NOV26b through NOV26d.		
Protein Sequence	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV26b	7..145 4..142	99/139 (71%) 99/139 (71%)
NOV26c	76..143 4..71	58/68 (85%) 58/68 (85%)
NOV26d	1..145 17..161	93/145 (64%) 93/145 (64%)

One polymorphic variant of NOV26a has been identified and is shown in Table 41J.

- 5 Further analysis of the NOV26a protein yielded the following properties shown in Table 26C.

Table 26C. Protein Sequence Properties NOV26a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1555 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV26a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 26D.

Table 26D. Geneseq Results for NOV26a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU02972	Angiotensin converting enzyme (ACEV) splice variant protein #72 - <i>Homo sapiens</i> , 636 aa. [WO200136632-A2, 25-MAY-2001]	1..94 17..109	81/94 (86%) 83/94 (88%)	3e-37
AAW18207	Wild-type C1 inhibitor - <i>Homo sapiens</i> , 500 aa. [US5622930-A, 22-APR-1997]	1..94 17..109	81/94 (86%) 83/94 (88%)	3e-37
AAW18212	Recombinant C1 inhibitor mutein - <i>Homo sapiens</i> , 500 aa. [US5622930-A, 22-APR-1997]	1..94 17..109	81/94 (86%) 83/94 (88%)	3e-37
AAW18218	Recombinant C1 inhibitor mutein - <i>Homo sapiens</i> , 500 aa. [US5622930-A, 22-APR-1997]	1..94 17..109	81/94 (86%) 83/94 (88%)	3e-37
AAW18217	Recombinant C1 inhibitor mutein - <i>Homo sapiens</i> , 500 aa. [US5622930-A, 22-APR-1997]	1..94 17..109	81/94 (86%) 83/94 (88%)	3e-37

In a BLAST search of public sequence databases, the NOV26a protein was found to have homology to the proteins shown in the BLASTP data in Table 26E.

Table 26E. Public BLASTP Results for NOV26a				
Protein Accession Number	Protein/Organism/Length	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96FE0	Serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 - <i>Homo sapiens</i> (Human), 500 aa.	1..94 17..109	81/94 (86%) 83/94 (88%)	8e-37

P05155	Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) - <i>Homo sapiens</i> (Human), 500 aa.	1..94 17..109	81/94 (86%) 83/94 (88%)	8e-37
Q95J12	Complement C1 inhibitor - Pan troglodytes (Chimpanzee), 162 aa (fragment).	2..82 1..80	75/81 (92%) 77/81 (94%)	3e-34
Q16304	C1-inhibitor - <i>Homo sapiens</i> (Human), 83 aa (fragment).	76..145 14..83	67/70 (95%) 68/70 (96%)	7e-32
P97290	Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) - <i>Mus musculus</i> (Mouse), 504 aa.	76..144 435..503	57/69 (82%) 65/69 (93%)	2e-27

PFam analysis predicts that the NOV26a protein contains the domains shown in Table 26F.

Table 26F. Domain Analysis of NOV26a			
Pfam Domain	NOV26a Match Region	Identities/ Similarities for the Matched Region	Expect Value
serpin	76..143	31/74 (42%) 61/74 (82%)	2.5e-25

Example 27.

The NOV27 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 27A.

Table 27A. NOV27 Sequence Analysis			
	SEQ ID NO: 91	1356 bp	
NOV27a, CG142023-01 DNA Sequence	GGCGAGGCCGGCGCGATGCGGCAGCTGTGCCGGGGCCGCGTGCTGGGCATCTCGGTGGCC ATCGCGCACGGGTCTTCTCGGGCTCCCTCAACATCTTGCTCAAGTTCCCTCATCAGCCGC TACCAGTTCTCCTTCCTGACCCTGGTGCACTGCGCTGACCAGCTCCACCGCGGCGCTGAGC CTGGAGCTGCTGCGGCGCCTCGGGCTCATCGCCGTGCCCCCTTCGGTCTGAGCCTGGCG CGCTCCTTCGCGGGGGTTCGCGGTGCTCTCCACGCTGCAGTCCAGCCTCAGGCTCTGGTCC CTGCGCGGCTCAGCCTGCCCATGTACGTGGTCTTCAAGCGCTGCCTGCCCCCTGGTCACC ATGCTCATCGGCGTCTGGTGTCAAGAACGGCGCGCCCTCGCCAGGGGTGTGGCGGCG GTGCTCATCACCACTGCGGCGCCGCCCTGGCAGGTGCCGGCGACCTGACGGGCGACCCC ATCGGGTACGTACGGGAGTGCTGGCGGTGCTGGTGACGCTGCCTACCTGGTGCTCATC CAGAAGGCCAGCGCAGACACCGAGCACGGGCCGCTCACCGCGCAGTACGTATCGCCGTC TCTGCCACCCGCTGCTGGTCTGCTCCTTCGCCAGCACCGACTCCATCCACGCCTGG ACCTTCCCGGGCTGGAAGGACCCGGCCATGGTCTGCATCTTCGTGGCCTGCATCCTGATC GGCTGCGCCATGAACCTTACACAGCTGCACTGCACCTACATCAATTCGGCCGTGACCACC AGCTTCGTGGGTGTGGTGAAGAGCATCGCCACCATCACGGTGGGCATGGTGGCCTTCAGC GACGTGGAGCCCACTCTCTGTTCAATTGCGGCGTGGTGGTGAACACCCCTGGGCTCTATC ATTTACTGTGTGCCCAAGTTCATGGAGACCAGAAAGCAAAGCAACTACGAGGACCTGGAG GCCCAGCCTCGGGGAGAGGAGGCGCAGCTAAGTGGAGACCAGCTGCCGTTCTGTATGGAG GAGCTGCCCGGGAGGGAGGAATGGCCGGTCAGAAGGTGGGGAGGCAGCAGGTGGCCCC		

	GCTCAGGAGAGCAGGCAAGAGGTCAGGGGCAGCCCCGAGGAGTCCCCTGGTGGCTGGG AGCTCTGAAGAAGGGAGCAGGAGGTCGTTAAAAGATGCTTACCTCGAGGTATGGAGGTTG GTTAGGGGAACCAAGGTATATGAAGAAGGATTATTTGATAGAAAACGAGGAGTTACCCAGT CCTTGAGAAGGAGGTGCATGTACGTACCTATGTGCATACACTTATTTTATATGTTAGAAA TGACGTGTTTAAATGAGAGGCCTCCCCGTTTTATTTC		
	ORF Start: ATG at 16		ORF Stop: TGA at 1264
	SEQ ID NO: 92	416 aa	MW at 44181.9kD
NOV27a, CG142023-01 Protein Sequence:	MRQLCRGRVLGISVAIAHGVFSGSLNILLKFLISRYQFSFTLVQCLTSSTAALSLELLR RLGLIAVPPFGLSLARSFAGVAVLSTLQSSLTLSLRGLSLPMYVVFRRCLPLVTMLIGV LVLKNGAPSPGVLA AVLITTCGAALAGAGDLTGDPFGYVTGVLAVLVHAAVLVLIQKASA DTEHGPLTAQYVIAVSATPLLVICSFASDTSIHAWTFPGWKDPAMVCIFVACILIGCAMN FTTLHCTYINSAVTTSPFVGUVKSIATITVGMVAFSDVEPTSLFIAGVVNTLGSIIYCVA KFMETRKQSNYEDLEAQPRGEEAQLSGDQLPFVMEELPGECCGNGRSEGGEAAGGPAQESR QEVRSRPGVPLVAGSSEEGSRRSLKDAYLEVWRLVRGTRYMKKDYLIENEELPSP		

Further analysis of the NOV27a protein yielded the following properties shown in Table 27B.

Table 27B. Protein Sequence Properties NOV27a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 20 and 21

A search of the NOV27a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several
5 homologous proteins shown in Table 27C.

Table 27C. Geneseq Results for NOV27a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV27a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU81226	Human lung cancer protein, Seq ID No 62 - <i>Homo sapiens</i> , 391 aa. [WO200192525-A2, 06-DEC-2001]	1..416 1..391	391/416 (93%) 391/416 (93%)	0.0
AAM47572	Drosophila cell cycle progression protein #1 - <i>Drosophila</i> sp, 373 aa. [WO200172774-A2, 04-OCT-2001]	12..321 64..371	87/316 (27%) 153/316 (47%)	3e-21

ABB60236	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 7500 - <i>Drosophila melanogaster</i> , 373 aa. [WO200171042-A2, 27-SEP-2001]	12..321 64..371	87/316 (27%) 153/316 (47%)	3e-21
AAB88597	Human hydrophobic domain containing protein clone HP03670 #121 - <i>Homo sapiens</i> , 337 aa. [WO200112660-A2, 22-FEB-2001]	8..322 24..329	74/315 (23%) 137/315 (43%)	7e-14
AAB56473	Human prostate cancer antigen protein sequence SEQ ID NO:1051 - <i>Homo sapiens</i> , 341 aa. [WO200055174-A1, 21-SEP-2000]	8..322 28..333	74/315 (23%) 136/315 (42%)	1e-13

In a BLAST search of public sequence databases, the NOV27a protein was found to have homology to the proteins shown in the BLASTP data in Table 27D.

Table 27D. Public BLASTP Results for NOV27a				
Protein Accession Number	Protein/Organism/Length	NOV27a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9CXD4	6230421J19Rik protein - <i>Mus musculus</i> (Mouse), 152 aa.	271..416 1..152	111/152 (73%) 120/152 (78%)	4e-55
Q94B65	Hypothetical 34.6 kDa protein - <i>Arabidopsis thaliana</i> (Mouse-ear cress), 323 aa.	10..319 13..323	93/316 (29%) 163/316 (51%)	8e-34
Q9SB76	Hypothetical 31.9 kDa protein - <i>Arabidopsis thaliana</i> (Mouse-ear cress), 296 aa.	30..319 6..296	90/296 (30%) 151/296 (50%)	1e-31
Q95Y15	UDP-sugar transporter UST74c (Fringe connection protein) - <i>Drosophila melanogaster</i> (Fruit fly), 373 aa.	12..321 64..371	87/316 (27%) 153/316 (47%)	9e-21

Q9NTN3	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter (UDP-GlcA/UDP-GalNAc transporter) - <i>Homo sapiens</i> (Human), 355 aa.	18..309 49..341	80/295 (27%) 132/295 (44%)	1e-16
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PFam analysis predicts that the NOV27a protein contains the domains shown in Table 27E.

Table 27E. Domain Analysis of NOV27a			
Pfam Domain	NOV27a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF6	166..299	21/135 (16%) 87/135 (64%)	0.29

Example 28.

The NOV28 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 28A.

Table 28A. NOV28 Sequence Analysis			
	SEQ ID NO: 93	785 bp	
NOV28a, CG142092-01 DNA Sequence	AAAAAGTCCATCTGGGGCTCTTCATAGAAAAAGGAAAATGGCAGCCTGGCCCTTCTCCAG GCTGTGGAAAGTCTCTGATCCAATTCTTCCAAATGACCTTGATCGCTGCTCTGTTGCC TGCTGTTCTTGGCAATTGTGGTCTCCACCCACTTTATCATTGCTGCCCCGATGGATAT TACGTTGACTGAGACACGCTTCAAACTGGAACACTCTGAAATACACCTGCCTCCCTGG CTACGTCAGATCCCATTCAACTCAGACGCTTACCTGTAATTCTGATGGCGAATGGGTGTA TAACACCTTCTGTATCTACAACGATGCAGACACCCAGGAGATTACGTAATGGGCAAGT AGAGATTAAGACAGATTTATCTTTGGATCACAATAGAATTGAGCTGTTGAGAAGGATT TTTCTTAATTGGCTCAACCACTAGTCGTGTGTAAGTCCAAGATAGAGGAGTTGGCTGGGG TCATCCTCTCCCAATGTGAAATTGTCAAGTGTAAAGCTCCTCCAGACATCAGGAATGG AAGGCACAGCGGTGAAGAAATTTCTACGCATACGGCTTTTCTGTACCTACAGCTGTGA ACAAGTGCTCACAGGCAAAAGACTCATGCAGTGTCTCCCAAACCCAGAGGATGTGAAAT GGCCCTGGAGGTATATAAGCTGTCTCTGGAATTTGAACAACCTGGAACACAGAGAGACAG CGCAAGACAATCCACTTTGGATAAAGAACTATAATTTTCTCAAAGAAGGAGGAAAAGG TGTCT		
	ORF Start: at 2		ORF Stop: TAA at 752
	SEQ ID NO: 94	250 aa	MW at 28139.0kD
NOV28a, CG142092-01 Protein Sequence	KTPSGALHRKRKMAAWPFSRLWKVSDPILFQMTLIAALLPAVLGNCGPPPTLSFAAPMDI TLTEFRFKTGTTLLKYTCPLGVVRSHSTQTLTCNSDGEVYNTFCIYKRCRHPGELRNQV EIKTDLSEFGSIEFSCSEGFLLIGSTTSRCEVQDRGVGWGHPPLPQCEIVKCKPPDIRNG RLSGEENFYAYGFSVTYSCEQVLTGKRLMQCLPNPEDVKMALEVYKLSLEIEQLELQRDS ARQSTLDKEL		
	SEQ ID NO: 95	972 bp	
NOV28b, CG142092-02 DNA Sequence	AAAACTCTGATCTGGGGAGGAACAGGACTACATAGATCAAGGCAGTTTCTTCTTTGAG AAATATCCCAGATATCATCATAGAGTCTTCTGCTCTTCTCAACTACCAAGAAAAACA TCAGCGAAGCAGCAGGCCATGCACCCCCAAAACTCCATCTGGGGCTCTTCATAGAAAA AGGAAAATGGCAGCCTGGCCCTTCTCCAGGCTGTGGAAGTCTCTGATCCAATTCTCTTC CAAATGACCTTGATCGCTGCTGTTGCCTGCTGTTCTTGGCAATTGTGGTCTCCACCC		

	ACTTTATCATTGCTGCCCGATGGATATTACGTTGACTGAGACACGCTTCAAAACTGGA ACTACTCTGAAATACACCTGCCTCCCTGGCTACGTGAGATCCCATCAACTCAGACGCTT ACCTGTAATTCTGATGGCGAATGGGTGTATAACACCTTCTGTATCTACAAACGATGCAGA CAGCCAGGAGAGTTACGTAATGGGCAAGTAGAGATTAAGACAGATTTATCTTTTGGATCA CAAATAGAATTACAGCTGTTTCTGAGAAGGCTGTGAACAAGTGCTCACAGGCAAAAGACTCATG CAGTGTCTCCCCAACCCAGAGGATGTGAAAATGGCCCTGGAGGTATATAAGCTGTCTCTG GAAATTGAACAACCTGGAACCTACAGAGAGACAGCGCAAGACAATCCACTTTGGATAAAGAA CTATAATTTTTCTCAAAAGAAGGAGGAAAAGGTGTCTTGTCTGGCTTGCCTCTTGCAATTC AATACAGATCAGTTTAGCAAATCTACTGTCAATTTGGCAGTGATATTCATCATAATAAAT ATCTAGAAATGATAATTTGCTAAAGTTTAGTGCTTTGAGATTGTGAAATTATTAATCATC CTCTGTGTGGCTCATGTTTTTGTCTTTTCAACACACAAAGCACAAATTTTTTTTCGATTAA AAATGTATGTAT		
	ORF Start: ATG at 139		ORF Stop: TAA at 724
	SEQ ID NO: 96	195 aa	MW at 21984.2kD
NOV28b, CG142092-02 Protein Sequence	MHPPKTPSGALHRRKRKMAAWPFSRLWKVSDPILFQMTLIAALLPAVLGNCGPPPTLSFAA PMDITLTETRFKGTTLKYTCLPGYVRSHSTQTLTNSDGEWYNTFCIYKRCHRPGBLR NGQVEIKTDLFSGSQIEFSCSEGCEQVLTGKRLMQCLPNPEDVKMALEVYKLSLEIEQLE LQRDSARQSTLDKEL		
	SEQ ID NO: 97	681 bp	
NOV28c, CG142092-03 DNA Sequence	AAAACCTGATCTGGGGAGGAACCCAGGACTACATAGATCAAGGCAGTTTCTTCTTTGAG AAACTATCCAGATATCATCATAGAGTCTTCTGCTCTTCTCCTCAACTACCAAAGAAAAACA TCAGCGAAGCAGCAGGCCATGCACCCCCCAAACTCCATCTGGGGCTCTTCATAGAAAA AGGAAAATGGCAGCCTGGCCCTTCTCCAGGCTGTGGAAGTCTCTGATCCAATTCTCTTC CAAATGACCTTGATCGCTGCTGTTGCTGCTGTCTTGGCAATTGTGGTCTCCACCC ACTTTATCATTGCTGCCCCGATGGATATTACGTTGACTGAGACACGCTTCAAACTGGA ACTACTCTGGAATTTGAACAACCTGGAACCTACAGAGAGACAGCGCAAGACAATCCACTTTG GATAAAGAACTATAATTTTTCTCAAAAGAAGGAGGAAAAGGTGTCTTGTCTGGCTTGCCTC TTGCAATTCATACAGATCAGTTTAGCAAATCTACTGTCAATTTGGCAGTGATATTCATC ATAATAAATATCTAGAAATGATAATTTGCTAAAGTTTAGTGCTTTGAGATTGTGAAATTA TTAATCATCCTCTGTGTGGCTCATGTTTTTGTCTTTTCAACACACAAAGCACAAATTTTTT TTGATTAAAAATGTATGTAT		
	ORF Start: ATG at 139		ORF Stop: TAA at 433
	SEQ ID NO: 98	98 aa	MW at 10927.6kD
NOV28c, CG142092-03 Protein Sequence	MHPPKTPSGALHRRKRKMAAWPFSRLWKVSDPILFQMTLIAALLPAVLGNCGPPPTLSFAA PMDITLTETRFKGTTLIEQLELQRDSARQSTLDKEL		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 28B.

Table 28B. Comparison of NOV28a against NOV28b and NOV28c.		
Protein Sequence	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV28b	1..250 5..195	185/250 (74%) 185/250 (74%)
NOV28c	1..74 5..78	73/74 (98%) 74/74 (99%)

Further analysis of the NOV28a protein yielded the following properties shown in Table 28C.

Table 28C. Protein Sequence Properties NOV28a

PSort analysis:	0.6500 probability located in plasma membrane; 0.5046 probability located in mitochondrial inner membrane; 0.3752 probability located in microbody (peroxisome); 0.3000 probability located in Golgi body
SignalP analysis:	Cleavage site between residues 45 and 46

A search of the NOV28a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 28D.

Table 28D. Geneseq Results for NOV28a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR13490	Human C4 binding protein - <i>Homo sapiens</i> , 581 aa. [WO9111461-A, 08-AUG- 1991]	13..218 1..208	190/208 (91%) 193/208 (92%)	e-113
AAB57162	Human prostate cancer antigen protein sequence SEQ ID NO:1740 - <i>Homo sapiens</i> , 110 aa. [WO200055174-A1, 21-SEP- 2000]	62..170 1..109	107/109 (98%) 108/109 (98%)	1e-61
AAW39924	Amino acid sequence of a mouse sperm protein designated sp56 - <i>Mus</i> sp, 579 aa. [WO9800440-A1, 08-JAN-1998]	13..204 1..192	103/193 (53%) 132/193 (68%)	2e-57
AAG68150	Codon modified human DAF protein sequence SEQ ID NO:1 - <i>Homo sapiens</i> , 320 aa. [JP2001211882-A, 07- AUG-2001]	32..217 22..212	74/191 (38%) 106/191 (54%)	3e-32
ABB07542	Amino acid sequence of APT2334 - Synthetic, 271 aa. [WO200204638-A1, 17- JAN-2002]	45..217 65..241	68/177 (38%) 98/177 (54%)	2e-30

- 5 In a BLAST search of public sequence databases, the NOV28a protein was found to have homology to the proteins shown in the BLASTP data in Table 28E.

Table 28E. Public BLASTP Results for NOV28a				
Protein Accession Number	Protein/Organism/Length	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P04003	C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP) - <i>Homo sapiens</i> (Human), 597 aa.	1..218 5..224	202/220 (91%) 205/220 (92%)	e-120
Q28065	C4b-binding protein alpha chain precursor (C4bp) - <i>Bos taurus</i> (Bovine), 610 aa.	1..211 5..217	127/214 (59%) 154/214 (71%)	5e-71
S53711	C4BP alpha chain precursor - rabbit, 597 aa.	1..211 5..217	124/214 (57%) 152/214 (70%)	5e-68
P08607	C4b-binding protein precursor (C4bp) - <i>Mus musculus</i> (Mouse), 469 aa.	5..200 17..210	107/196 (54%) 131/196 (66%)	5e-59
Q91X48	Complement component 4 binding protein - <i>Mus musculus</i> (Mouse), 469 aa.	5..200 17..210	107/196 (54%) 130/196 (65%)	8e-59

PFam analysis predicts that the NOV28a protein contains the domains shown in Table 28F.

Table 28F. Domain Analysis of NOV28a			
Pfam Domain	NOV28a Match Region	Identities/ Similarities for the Matched Region	Expect Value
sushi	46..104	16/68 (24%) 42/68 (62%)	1.3e-10
sushi	109..166	20/64 (31%) 47/64 (73%)	6.2e-14
sushi	171..216	20/64 (31%) 38/64 (59%)	0.012

Example 29.

- 5 The NOV29 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 29A.

Table 29A. NOV29 Sequence Analysis

	SEQ ID NO: 99	1356 bp	
NOV29a, CG171681-01 DNA Sequence	<p>CTGCGCTGCCGAGGCGAGCTAAGCGCCCGCTCGCCATGGGGAGCCCCGCACATCGGCCCG CGCTGCTGCTGCTGCTGCGCCTCTGCTGCTGCTGCTGCTGCTGCGCGTCCC GCCAGCC GCAGCTTCCCAGATATGGAACCTCTAGAATCAAGTGCCCAAGTGTGAAGGAACGCATTG CAGAACCCAACTGACAGTCCGGGTGTCTGGGAGACACCCGAAGGAAGAGACACAG CAGATGGAATTTCTACTGATGTCTTCTAAAAGGCCTCCCCCAGGCTCCAACTTTCCAG AAGGAGACCACAAGATCCAGTACACAGTCTATGACAGAGCTGAGAATAAGGGCACTTGCA AATTTGAGTTAAAGTAAGAGTCAAACGCTGTGGCAAACTCAATGCCCCAGAGAATGGTT ACATGAAGTGTCTCCAGCAGCGGTGATAATTATGGAGCCACCTGTGAGTTCTCTGTCATCG GCGGCTATGAGCTCCAGGGTAGCCCTGCCGAGTATGTCAATCCAACCTGGCTTGGTCTG GCACGGAGGCCACCTGTGCAGCCATGAACGTCAATGTGGGTGTGAGAACGGCAGCTGCAC TTCTGGATCAGTTTTATGAGAAAAGGAGACTCCTCATTGTGTCCACCCACACGCCGAA ACCTCCTTTACCGGCTCCAGTAGGAATGCTGCAGCAAGCAGTGTGGCCTTGATCTTC GACACATACCGTGGTGGAGCTGTGGGTGTGTTCCCGACTCTCATTGGCAGGATAGGAG CAAAGATTATGCCTCCAGCCCTAGCGCTGCAGCTCAGGCTGTTGCTGCGAATCCCACTCT ACTCCTTCAGTATGGTGTAGTGGATAAGCATGGCATGGACAAAGAGCGCTATGTCTCCC TGGTGATGCCTGTGGCCCTGTTCAACCTGATTGACACTTTTCCCTTGAGAAAAGAGAGA TGGTCTCAAGCCGAAATGAGCCAGACCTGTAAACCTGACATGATGGTTCTCTCTTGTG GCAATTCTCTCTTACGTGTACATAGTGACATGCACACGGGAAAGCCTTAAAAATATCCT TGATGTACAGATTTTATTGTAAATTTAAAAGTCTATTTTATTATGAGCTTTCTTGCAC TTAAAAATTAGCATGCTGCTTTTTTGTACTTGGAAAGTGTTTCAAAAAATTATATGACCATA TTTACTCTTTCTAACCTTTCTTTACTCCATCATGGCTGGTTGATTGTTAGAGAAATTAGA ACCCATAACCATACAGAGCTATCAACATGTTATTCAATGTGACACCTAACTCTTTCTTA TTTTGTTTTTAAAGACTTTTTTATTAATAAAACG</p>		
	ORF Start: ATG at 36		ORF Stop: TGA at 999
	SEQ ID NO: 100	321 aa	MW at 35636.4kD
NOV29a, CG171681-01 Protein Sequence	<p>MGSPAHRPALLLLLLPLLLLLLLLRVPPSRSPDMEPPRIKCPVSKERIAEPNKLTVRVSW ETPEGRDADGILTDVILKGLPPGNSFPPEGDHKIQYTVYDRAENKGTCKFRVKVRVKRC KLNAPENGMYMKSSDGDNYGATCEPSCIGGYELQGS PARVCQSNLWSGTEPTCAAMVN VGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLQLGMLQQAQCGLDLRHITVVELVGVF PTLIGRIGAKIMPPALALQLRLLLRIPLYFSFMSVLVDKHGMKDKEYVSLVMPVALFNLID TFPLRKEEMVLQAEMSQTCNT</p>		
	SEQ ID NO: 101	1795 bp	
NOV29b, CG171681-03 DNA Sequence	<p>CTTGGTCTCTTCGGTCTCCTGCCGCCCGGGAAGCGCGCTGCGCTGCCGAGGCGAGCTA AGCGCCCGCTGCCATGGGAGCCCGGCACATCGGCCCGCGCTGCTGCTGCTGCTGCCG CTCTGCTGCTGCTGCTGCTGCTGCGCGTCCC GCCAGCCGAGCTTCCCAGATACCCCGTGGT GCTCCCCCATCAAGGTGAAGTATGGGGATGTGTACTGCAGGGCCCTCAAGGAGGATACT ACAAACAGCCCTGGGAACCAGGTGCGACATTGCTGCCAGAAGGGCTACGAGCTGCATG GCTCTTCCCTACTGATCTGCCAGTCAAACAAACGATGGTGTGACAAGGTCATCTGCAAAC AAAAGCGATGCTCTACCTTGCCATGCCAGCAATGCGAGGGTTAAGTGTGTAGATGGTG CCTACTTTAACTCCCGGTGTGAGTATTATTGTTTACCAGGATACACGTTGAAAGGGGAGC GGACCGTCACATGTATGGACAACAAGGCCTGGAGCGGCCGCCAGCCTCCTGTGTGGATA TGGAACTCCTAGAATCAAGTGCCCAAGTGTGAAGGAACGATTGCAGAACCCAAACAAAC TGACAGTCCGGGTGTCTTGGGAGACACCCGAAGGAAGATACACAGCAGATGGAATCTTA CTGATGTCACTTTAAAGGCCTCCCCCAGGCTCCAACTTTCCAGAAGGAGACCAAGA TCCAGTACACAGTCTATGACAGCTGAGATAAAGGGCACTTGCAAATTTGAGTTAAAG TAAGAGTCAAACGCTGTGGCAAACCTCAATGCCCCAGAGAATGGTTACATGAAGTGTCCA GCGACGGTGATAATTATGGAGCCACCTGTGAGTTCTCCTGCATCGGCGGCTATGAGCTCC AGGGTAGCCCTGCCGAGTATGTCAATCCAACCTGGCTTGGTCTGGCACGGAGCCCACT GTGCAGCCATGAACGTCAATGTGGGTGTGAGAAGCGCAGTGCATCTTGTGATCAGTTTT ATGAGAAAAGGAGACTCCTATTGTGTCCACACCCACAGCCGAAACCTCCTTTACCGGC TCCAGCTAGGAATGCTGCAGCAAGCACAGTGTGGCCTTGATCTTCGACACATCACCGTGG TGGAGCTGGTGGGTGTGTTCCCGACTCTCATTGGCAGGATAGGAGCAAAGATTATGCCTC CAGCCCTAGCGTGCAGCTCAGGCTGTTGCTGCGAATCCCACCTCTACTCCTTCAGTATGG TGCTAGTGGATAAGCATGGCATGGACAAAGAGCGCTATGTCTCCTGGTGTGCTGCTGG CCCTGTTCAACCTGATTGACATTTTCCCTTGAGAAAAGAGAGATGGTCTACAGCCG AAATGAGCCAGACCTGTAAACCTGACATGATGGTTCTCTCTTGGCAATTCCTCTTCAT</p>		

	TGTCTACATAGTGACATGCACACGGGAAAGCCTTAAAAATATCCTTGATGTACAGATTTT ATTTGTAATTTTAAAAGTCTATTTTATTATGAGCTTTCTTTGCACCTTAAAAATTAGCATG CTGCTTTTTGTACTTGGAGTGTTTCAAAAAATTATATGACCATAATTACTCTTTCTAAC TTTCTTTACTCCATCATGGCTGGTTGATTTTGTAGAGAAATTAGAACCATAACCATAACA CAGGCTATCAACATGTTATTCAATGTGACACCTAACTCTTTTCTATTTTGTTTTTTAAGT AAGACTTTTATTAATAAAACAAAATGTTTTGGAGCAAAAAAAAAAAAAAAAAAAAAA		
	ORF Start: ATG at 75	ORF Stop: TGA at 1404	
	SEQ ID NO: 102	443 aa	MW at 49267.9kD
NOV29b, CG171681-03 Protein Sequence	MGSPAHRPALLLLLPPLLLLLLRVPPSRSPDTPWCSPKVKYGDVYCRAPQGGYYKTA GTRCDIRQCQGYELHGSSLLICQSNKRWSKVICQKRCPTLAMPANGGFKCVDGAYFNS RCEYYCSPGYTLKGERTVTCMDNKAWSGRPASCVDMEPPRIKCPVSKERIAEPNKLTVRV SWETPEGRDITADGILTDVILKGLPPGSNFPEDGDKIQYTVYDRAENKGTCKFRVKVRVKR CGKLNAPENGYMKSSDGDNYGATCEFCIGGYELQGS PARVCQSNLAWSGTEPTCAAMN VNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLQLGLMLQQAQCGLDLRHITVVELVG VFPTLIGRIGAKIMPPALALQLRLLLRIPLYSFSMVLVDKHGMDKERYVSLVMPVALFNL LIDTFPLRKEEMVLQAEMSQTNT		
	SEQ ID NO: 103	1798 bp	
NOV29c, CG171681-02 DNA Sequence	CTTGGTCTCTTCGGTCTCCTGCGCCCGGGGAAGCGCGTGCCTGCCGAGGCGAGCTA AGCGCCGCTCGCCATGGGAGCCCCGCACATCGGCCCGCGCTGCTGCTGCTGCCGC CTCTGCTGCTGCTGCTGCTGCTGCGCGTCCCGCCAGCCGAGCTTCCCAGATACCCCGT GGTGCTCCCCCATCAAGGTGAAGTATGGGGATGTGTACTGCAGGGCCCCCTCAAGGAGGAT ACTACAAAACAGCCCTGGGAACAGGTGCGACATTGCTGCCAGAAGGGCTACGAGCTGC ATGGCTCTTCCCTACTGATCTGCCAGTCAAACAACAGATGGTCTGACAAGGTCACTGCA AACAAAAGCGATGTCTACCTTGGCATGCCAGCAAATGGAGGGTTAAGTGTGTAGATG GTGCTACTTTTAACTCCCGGTGTGAGTATTATTGTTTACCAGGATACACGTTGAAAGGGG AGCGGACCGTCACATGTATGGACAACAAGGCCTGGAGCGGCCGCGCCAGCCTCCTGTGTGG ATATGGAACCTCCTAGAATCAAGTGCCCAAGTGTGAAGGAACGCATTGCAGAACCCAACA AACTGACAGTCCGGGTGTCTGGGAGACACCCGAAGGAAGAGACACAGCAGATGGAATTC TTACTGATGTCAATTCTAAAGGCCTCCCCCAGGCTCCAACCTTCCAGAAGGAGACCACA AGATCCAGTACACAGTCTATGACAGAGCTGAGAATAAGGGCACTTGCAAATTTGAGTTA AAGTAAGAGTCAAACGCTGTGGCAAACCTCAATGCCCCAGAGAATGGTTACATGAAGTGCT CCAGCGACGGTGATAATTATGGAGCCACCTGTGAGTTCTCTGCATCGCGGGCTATGAGC TCCAGGGTAGCCCTGCCCGAGTATGTCAATCCAACCTGGCTTGGTCTGGCAGCGAGCCCA CCTGTGCAGCCATGAACGTCAATGTGGGTGTGAGAAGCGCAGCTGCATCTTGGATCAGT TTTATGAGAAAAGGAGACTCTCATTGTGTCCACACCCACAGCCGAAACCTCCTTTACC GGCTCCAGCTAGGAATGCTGCAGCAAGCACAGTGTGGCCTTGATCTTCGACACATCACCG TGGTGGAGCTGGTGGGTGTGTTCCCGACTCTCATTGGCAGGATAGGAGCAAAGATTATGC CTCCAGCCCTAGCGCTGCAGCTCAGGCTGTTGTGCGAATCCCACTCTACTCCTTACGTA TGGTGCTAGTGGATAAGCATGGCATGGACAAAGAGCGCTATGTCTCCCTGGTGATGCCTG TGGCCCTGTGTAACCTGATTGACACTTTCCCTTGAGAAAAGAAGAGATGGTCTTACAAG CCGAAATGAGCCAGACCTGTAACACCTGACATGATGGTTCTCTTGGCAATTCCTCTT CATTTGCTACATAGTGACATGCACACGGGAAAGCCTTAAAAATATCCTTGATGTACAGAT TTTATTTGTAATTTTAAAAGTCTATTTTATTATGAGCTTTCTTTGCACCTTAAAAATTAGC ATGCTGCTTTTTGTACTTGAAGTGTTTCAAAAAATTATATGACCATAATTACTCTTTCT AACTTTCTTTACTCCATCATGGCTGGTTGATTTTGTAGAGAAATTAGAACCATAAACCAT ACACAGGCTATCAACATGTTATTCAATGTGACACCTAACTCTTTTCTATTTTGTTTTTTA AGTAAGACTTTTATTAATAAAACAAAATGTTTTGGAGCAAAAAAAAAAAAAAAAAAAAAA		
	ORF Start: ATG at 75	ORF Stop: TGA at 1407	
	SEQ ID NO: 104	444 aa	MW at 49381.1kD
NOV29c, CG171681-02 Protein Sequence	MGSPAHRPALLLLLPPLLLLLLRVPPSRSPDTPWCSPKVKYGDVYCRAPQGGYYKTA LGRCDIRQCQGYELHGSSLLICQSNKRWSKVICQKRCPTLAMPANGGFKCVDGAYFNS SRCEYYCSPGYTLKGERTVTCMDNKAWSGRPASCVDMEPPRIKCPVSKERIAEPNKLTVR VSWETPEGRDITADGILTDVILKGLPPGSNFPEDGDKIQYTVYDRAENKGTCKFRVKVRVKR RCGKLNAPENGYMKSSDGDNYGATCEFCIGGYELQGS PARVCQSNLAWSGTEPTCAAM NVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLQLGLMLQQAQCGLDLRHITVVELV GVFPTLIGRIGAKIMPPALALQLRLLLRIPLYSFSMVLVDKHGMDKERYVSLVMPVALFNL LIDTFPLRKEEMVLQAEMSQTNT		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 29B.

Table 29B. Comparison of NOV29a against NOV29b and NOV29c.		
Protein Sequence	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV29b	33..321 155..443	273/289 (94%) 273/289 (94%)
NOV29c	33..321 156..444	273/289 (94%) 273/289 (94%)

Two polymorphic variants of NOV29c have been identified and are shown in Table 41K.

- 5 Further analysis of the NOV29a protein yielded the following properties shown in Table 29C.

Table 29C. Protein Sequence Properties NOV29a	
PSort analysis:	0.8200 probability located in outside; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Cleavage site between residues 31 and 32

A search of the NOV29a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 29D.

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Table 29D. Geneseq Results for NOV29a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB07747	A human cancer-associated protein-1 (CAP-1) - <i>Homo sapiens</i> , 465 aa. [WO200043508-A2, 27-JUL-2000]	33..319 178..464	148/287 (51%) 205/287 (70%)	7e-89

AAB59009	Breast and ovarian cancer associated antigen protein sequence SEQ ID 717 -- <i>Homo sapiens</i> , 431 aa. [WO200055173-A1, 21-SEP-2000]	33..319 144..430	148/287 (51%) 205/287 (70%)	7e-89
ABB72149	Rat protein isolated from skin cells SEQ ID NO: 188 - <i>Rattus</i> sp, 118 aa. [WO200190357-A1, 29-NOV-2001]	88..203 3..118	71/116 (61%) 89/116 (76%)	3e-38
AAB55949	Skin cell protein, SEQ ID NO: 188 - <i>Rattus</i> sp, 118 aa. [WO200069884-A2, 23-NOV-2000]	88..203 3..118	71/116 (61%) 89/116 (76%)	3e-38
AAY76010	Rat DRS protein homolog, SEQ ID NO:188 - <i>Rattus</i> sp, 118 aa. [WO9955865-A1, 04-NOV-1999]	88..203 3..118	71/116 (61%) 89/116 (76%)	3e-38

In a BLAST search of public sequence databases, the NOV29a protein was found to have homology to the proteins shown in the BLASTP data in Table 29E.

Table 29E. Public BLASTP Results for NOV29a				
Protein Accession Number	Protein/Organism/Length	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P78539	Sushi repeat-containing protein SRPX precursor - <i>Homo sapiens</i> (Human), 464 aa.	33..321 176..464	289/289 (100%) 289/289 (100%)	e-168
Q63769	Sushi repeat-containing protein SRPX precursor (DRS protein) (Down-regulated by V-SRC) - <i>Rattus norvegicus</i> (Rat), 464 aa.	33..321 176..464	279/289 (96%) 286/289 (98%)	e-164
Q9R0 m3	Sushi-repeat-containing protein - <i>Mus musculus</i> (Mouse), 464 aa.	33..320 176..463	276/288 (95%) 285/288 (98%)	e-163
Q9R0 m2	Sushi-repeat-containing protein - <i>Mus musculus</i> (Mouse), 380 aa.	33..320 92..379	276/288 (95%) 285/288 (98%)	e-163

AAM73690	Sushi-repeat containing protein - <i>Mus musculus</i> (Mouse), 410 aa (fragment).	33..319 123..409	152/287 (52%) 203/287 (69%)	2e-89
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PFam analysis predicts that the NOV29a protein contains the domains shown in Table 29F.

Table 29F. Domain Analysis of NOV29a			
Pfam Domain	NOV29a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HYR	33..114	27/86 (31%) 78/86 (91%)	2.2e-34
sushi	119..174	19/64 (30%) 41/64 (64%)	2.7e-09

Example 30.

The NOV30 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 30A.

Table 30A. NOV30 Sequence Analysis			
	SEQ ID NO: 105	1499 bp	
NOV30a, CG51117-01 DNA Sequence	ACGCGTGTAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATGTCGTTATGGTGGGA GGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTACGCCCTTCTACG TCTTAAGGCAGAGAATAGCCAGGATAAGGTGCCAGCTCAAAGCTGTGTGCCAACCACGAT GCAAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGTTATGCTGGAA AAACCTGGTATTCAAGTTTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGG TGCATGAACACTTACGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCG GATGGTTCTGCTCAAGTGCCCTGACCTGCTCCATGGCAAACGTGTCAGTATGGCTGTGAT GTTGTTAAAGGACAAATACGGTGCCAGTGCCATCCCCTGGCCTGCAGCTGGCTCCTGAT GGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATTT AGGCAATGTGTCAACACTTTGGGAGCTACATCTGCAAGTGTCAAAAGGCTTCGATCTC ATGTATATTGGAGGCAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAGTAT CAGTGCAGCAGCTTTGCTCGATGTTATAACGTACGTGGGTCCTACAAGTGCAAATGTAAA GAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCAAAAGTTATGATTGAACCT TCAGGTCCAATTATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAAT AATAATTGGATTCTGTATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCT CCTATCATTACCAACAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACA CCAATTCCTACTCCACCACCACCACCACCCTGCCAACAGAGCTCAGAACCTCTACCA CCTACAACCCAGAAAGGCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACA CCTCCAGGAGGGATTACAGTTGACACAGGGTACAGACAGACCCTCAGAAACCCAGAGGA GATGTGTTTCAATCCACGGCAACCTTCAAATGACTTGTTTGAAATATTTGAAATAGAAAGA GGAGTCAGTGCAGACGATGAAGCAAAGGATGATCCAGGTGTTCTGGTACACAGTTGTAAT TTTGACCATGGACTTTTGTGGATGGATCAGGGAGAAAGACAATGACTTGCATGGGAACCA ATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGCAGCCAAAGCCCCAGGGGGA AAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTCATGCATTACGGGGACCTGTGCCTG TCATTTCAGGCACAAGGTGACGGGGGTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAA		
	ORF Start: at 148		ORF Stop: at 1498
	SEQ ID NO: 106	450 aa	MW at 48855.5kD

NOV30a, CG51117-01 Protein Sequence	GASSKLCANHDANMVNVSGQTSASVILVMLEKPGIQVLNECGLKPRPCKHRCMNTYGSYK CYCLNGYMLMPDGCSSALTCSMANQYGCDEVVKQIRQCPSGLQLAPDGRTCVDVDE CATGRASCPRFRQCVNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCY NVRGSYKCKCKEGYQGDGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGS TWWPPKTPYIPPIITNRPTSKPTTRPTPKPTPIPTPPPPPLPTELRLPLPTTTPERTT GLTTIAPAASPPGGITVDNRVQTDPOKPRGDVFIHQPSNDLFEIERGVSADEAK DDPGVLVHSCNFDHGLCGWIREKNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLP GRLMHSGDLCLSFHVKVTGLHSGTLQVFVR		
	SEQ ID NO: 107	1638 bp	
NOV30b, CG51117-05 DNA Sequence	GAGTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATGTCGTTATGGT GGGAGGATGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTACGCCTGTG TGCCAACCACGATGCAACATGGTGAATGTATCGGGCCAAACAAGTGAAGTGTATCCT GGTTATGCTGGAAAACTGTATTCAAGTTTAAATGAGTGTGGCCTGAAGCCCCGGCCC TGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTGTACTGTCTCAACGGATAT ATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTGCTCCATGGCAAAGTGTGAG TATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCTGCAG CTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCC TGCCCTAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCAATAA GGCTTCGATCTCATGTATATTGGAGGCAAATATCAATGTCATGACATAGACGAATGTCTCA CTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAACGTACGTGGGTCTTACAAG TGCAAATGTAAAGAAGGATACAGGGTGATGGACTGACTTGTGTGTATATCCCAAAAGTT ATGATTGAACCTTCAGGTCCAATTCATGTACCAAAAGGAAATGGTACCATTTTAAAGGGT GACACAGGAAATAAATTTGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACA CCATATATCTCTCTATCATTACCAACAGGCTACTTCTAAGCCAAACAAGACCTACACA CCAAAGCCAAACACCAATTCCTACTCCACCACCACCACCACCCTGCCAACAGAGCTCAGA ACACCTCTACCACCTACAACCCAGAAAGGCCAACACCGGACTGACAACTATAGACCA GCTGCCAGTACACCTCCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACCCTCAG AAACCCAGAGGAGATGTGTTTCAATCCACGGCAACCTTCAAATGACTTGTGTTGAAATATTT GAAATAGAAAGAGGAGTCAGTGCAGACGATGAAGCAAAGGATGATCAGGTGTTCTGGTA CACAGTTGTAATTTTACCATGACTTTGTGGATGGATCAGGGAGAAAGACAATGACTTG CACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGCAGCCAAA GCCCCAGGGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTTATGCATTACAGG GACCTGTGCTGTCTATTACGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTG TTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGC TGGAGGCAAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGTCGTCTTCAAAGGT GAAAAAAGGCGTGGTCACACTGGGGAGATTGGATTAGATGATGTGAGCTTGAAAAAGGC CACTGCTCTGAAGAACGC		
	ORF Start: at 1	ORF Stop: end of sequence	
	SEQ ID NO: 108	546 aa	MW at 59854.9kD
NOV30b, CG51117-05 Protein Sequence	EFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCPKCKHGEICPNKCKCHP GYAGKTCIQVLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGCSSALTCSMANQ YGCDEVVKQIRQCPSGLQLAPDGRTCVDVDECATGRASCPRFRQCVNTFGSYICKCHK GFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLTCVYIPK MIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPTTRPT PKPTPIPTPPPPPLPTELRLPLPTTTPERTTGLTTIAPAASPPGGITVDNRVQTDPO KPRGDVFIHQPSNDLFEIERGVSADEAKDDPGVLVHSCNFDHGLCGWIREKNDL HWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFHVKVTGLHSGTLQV FVRKHGAHGAALWGRNGHGWRTQITLRGADIKSVVFKGEKRRGHTGEIGLDDVSLKKG HCSEER		
	SEQ ID NO: 109	2245 bp	
NOV30c, CG51117-06 DNA Sequence	GGACACTGACATGGACTGAAGGAGTAGAAAAGAAGGGAGCGGGAGGGGGCTCCGGGCGCC GCGCAGCAGACCTGCTCCGGCGCGCCTCGCCGCTGTCTCCGGAGCGGCAGAGTA GCCCGGGCGGGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCG CCCAACACCCCAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCGCTGCCCA ACATGGATTTTCTCTGGCGCTGGTGCTGGTATCCTCGCTCTACTGACAGGCGCGCGCG AGTTCGACGGGAGTAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATGTCGTTATG GTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGACAGTGTACGCCTT		

	TCTACGTCTTAAGGCAGAGAATAGCCAGGATAAGGTGCCAGCTCAAAGCTGTGTGCCAAC CACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATG CTGGAAAAACCTGTAATCAAGACGAGCACATCCCAGCTCCTCTTGACCAAGGCAGTGAAC AGCCTCTTTTTCCAACCCCTGGATCACCAAGCCACAAGTTTGCCTTCAAGGGATCTAAATG AGTGTGGCCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACA AGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGTCTCAAGTGCCCTGA CCTGCTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCC AGTGCCCATCCCCTGGCTGCAGCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATG AATGTGCTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACACTTTTGGA GCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGGCAATATCAAT GTCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTT ATAACATACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGA CTTGTGTGTATATCCAAAAGTTATGATTGAACCTTCAGGTCCAATTTCATGTACCAAAGG GAAATGGTACCATTTTAAAGGGTGACACAGGAAATAATAATTGGATTCTGTATGTTGGAA GTACTTGGTGGCCTCCGAAGACACCATATATTCCTCTCATATTACCAACAGGCCTACTT CTAAGCCAACAACAAGACTACACCAAAGCCAAACCAATTCTACTCCACCACCACCAC CACCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCA CCGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACA ACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTTCATTCCACGGCAACCTT CAAATGACTTGTGTTGAAATATTTGAAATAGAAAGAGGAGTCACTGCAGACGATGAAGCAA AGGATGATCCAGGTGTTCTGGTACACAGTTGTAATTTGACCATGGACTTGTGGATGGA TCAGGGAGAAAGACAATGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAAT ATCTGACAGTGTCCGCAGCCAAAGCCCCAGGGGAAAAGCTGCACGCTTGGTGCTACCTC TCGGCCGCTTATGCATTACAGGGGACCTGTGCCTGTCTATTAGGCACAAGGTGACGGGGC TGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGT GGGGAAGAAATGGTGGCCATGGCTGGAGGCAAAACAGATCACCTTCCGAGGGGCTGACA TCAAGAGCGTCGTCTTCAAAGGTGAAAAAAGGCGTGGTCACACTGGGGAGATTGGATTAG ATGATGTGAGCTTGAAAAAGGCCACTGCTCTGAAGAACGCTAACAACTCCAGAACTAAC AATGAACCTCTATGTTGCTCTATCCTCTTTTTCCAATTCTCATCTTCTCTCTCTCTCC CTTTATCAGGCCTAGGAGAAGAGTGGGTGAGTGGGTGAGAAGGAAGTCTATTGTTGGTGAC CCAGGTTCTTCTGGCCTGCTTTGT		
	ORF Start: ATG at 243		ORF Stop: TAA at 2082
	SEQ ID NO: 110	613 aa	MW at 67416.5kD
NOV30c, CG51117-06 Protein Sequence	MDFLLALVLVSSLYLQAAEFDGSRWPRQIVSSI GLCRYGGRIDCCWGWARQSWGQCQPF YVLRQRIARIRCQLKAVCPQRCKHGECIGPNKCKCHPGYAGKTCNQDEHIPAPLDQGSSEQ PLFQPLDHOATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALT CSMANCQYGCDDVVKQIRQCPSPLGLQLAPDGRCTVDVDECATGRASCPRFRCVNTFGS YICKCHKGFDLMIYGGKYQCHDIDCSLGQYQCSSFARCYNIRGSYKCKCKEYQGDGLT CVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNWIPDVGSTWPPKTPYIPPIITNRPTS KPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDN RVQTDPPQKPRGDVFI PRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGWI REKNDNLHWEPI RDPAGGYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFRHKVTGL HSGTLQVFVRKHGAHGAALWGRNGGHWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLD DVSLKKKGHCSEER		
	SEQ ID NO: 111	2194 bp	
NOV30d, CG51117-07 DNA Sequence	GGACACTGACATGGACTGAAGGAGTAGAAAAAGAGGAGCGGGAGGGGGCTCCGGGCGCC GCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAGCAGTA GCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGGC CCCACCACCCCAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCA ACATGGATTTTCTCTGGCGCTGGTGCTGCTATCTCGCTCTACTGCAAGCGGGCGCCGCG AGTTGCAAGCGGGAGTAGGTGGCCAGGCAATAGTGTATCGATTGGCCTATGTCGTTATG GTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCCTG TGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGAAGTGTATC CTGGTTATGCTGAAAAACCTGTAATCAAGACGAGCACATCCCAGCTCCTCTTGACCAAG GCAGTGAACAGCCTCTTTTCCAACCCCTGGATCACCAAGCCACAAGTTTGCCTTCAAGGG ATCTAAATGAGTGTGGCCTGAAGCCCCGCCCTGTAAAGCACAGGTGCATGAACACTTACG GCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAA GTGCCCTGACCTGCTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAA		

	TACGGTGCCAGTGCCCATCCCCTGGCCTGCAGCTGGCTCCTGATGGGAGGACCTGTGTAG ATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACA CTTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGGCA AATATCAATGTCTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTG CTCGATGTTATAACATACGTGGGTCTTACAAGTGCAATGTAAGAAGGATACCAAGGCTG ATGGACTGACTTGTGTGTATATCCCAAAGTTATGATTGAACCTCAGGTCCAATTCATG TACCAAAGGGAATGGTACCATTTTAAAGGGTGACACAGGAAATAATAATTGGATTCTCTG ATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCTATCATTACCAACA GGCCTACTTCTAAGCCAACAACAGACCTACACCAAAGCCAACACCAATTCTCTACTCCAC CACCACCACACCCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAA GGCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTA CAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTCCAC GGCAACCTTCAATGACTTGTGAAATATTTGAAATAGAAAGAGGAGTCAGTGCAGACG ATGAAGCAAAGGATGATCCAGGTGTTCTGGTACACAGTTGTAATTTGACCATGGACTTT GTGGATGGATCAGGGAGAAAGACAATGACTTGCACTGGGAACCAATCAGGGACCCAGCAG GTGGACAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGGGGAAAAGCTGCACGCTTGG TGCTACCTCTCGGCCGCTTATGCATTGAGGGACCTGTGCCTGTCTTACAGGCACAAGG TGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACAGGTGCCACGGAG CAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAG GGGCTGACATCAAGAGCGTCGTCTTCAAAGGTGAAAAAGGCGTGGTCACACTGGGGAGA TTGGATTAGATGATGTGAGCTTGAAAAAGGCCACTGCTCTGAAGAACGCTAACAACTCC AGAACTAACAAATGAACCTCTATGTGCTCTATCCTCTTTTCCAATTCTCATCTCTCTC CTCTTCTCCCTTTTATCAGGCCCTAGGAGAAGAGTGGGTGAGTGGGTGAGAAGAGTCTA TTTGGTGACCCAGGTTCTTCTGGCTGCTTTTGT		
	ORF Start: ATG at 243	-	ORF Stop: TAA at 2031
	SEQ ID NO: 112	596 aa	MW at 65299.9kD
NOV30d, CG51117-07 Protein Sequence	MDFLLALVLVSSLYLQAAAEFDGSRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPV CQPRCKHGEICIPNKCKCHPGYAGKTCNQDEHI PAPLDQSGEQPLFQPLDHQATSLPSRD LNECGLKPRPKHRMNTYGSYKCYCLNGYMLMPDGCSSALTCSMANQYGCVDVVKQI RCQCPSPGLQLAPDGRCTVDVDECATGRASCPRFRQCVNTFGSYICKCHKGFDLMYIGGK YQCHDIDECSLQYQCSSFARCYNIRGSYKCKKEGYQDGLTCVYIPKVMIEPSGPIHV PKNGTILKGDGTGNNWIPDVGSTWPPKTPYIPPIITNRPTSKPTTPKPTPIPTPP PPPLPLTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDNRVQTDPOKPRGVDVFI PR QPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAG GQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSPRHKVTGLHSGTLQVFRKHGAHGA ALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLDDVSLKKGHCSER		
	SEQ ID NO: 113	2112 bp	
NOV30e, CG51117-03 DNA Sequence	GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGGCGCGCGCTCGCCGCTGTC CTCCGGGAGCGGCAGCAGTAGCCGGCGCGAGGGCTGGGGGTTCTCTGAGACTCTCAG AGGGGCGCTCCCATCGGCGCGCCACCACCCCAACCTGTTCTCTCGCGCCACTGCGCTGC GCCCCAGGACCCGCTGCCCAACATGGATTTTCTCTGCGCTGGTGCTGGTATCCTCGCT CTACCTGCAGGCGCGCGCGAGTTTACAGCGGAGGTGGCCAGGCAAATAGTGTCTATCGAT TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTG GGGACAGTGTGAGCCTTTCTACGTCTTAAGGCAGAGAATAGCCAGGATAAGGTGCCAGCT CAAAGCTGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAA GTGTCATCCTGGTTATGCTGGAAAAACCTGTATTCAAGTTTTAAATGAGTGTGGCCTGAA GCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTGCTACTGTCT CAACGGATATATGCTCATGCCGATGGTTCTGCTCAAGTGCCCTGACCTGCTCCATGGC AAACTGTGATGAGTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCC TGGCCTGCAGCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGATGATGCTACAGG AAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAA GTGTCATAAAGGCTTCGATCTCATGTATATTGGAGGCAAATATCAATGTCTATGACATAGA CGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAACGTACGTGG GTCCTACAAGTGCAAAATGTAAGAAGGATACCAAGGTGATGGACTGACTTGTGTGTATAT CCCAAAGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAGGGAATGGTACCAT TTTAAAGGGTGACACAGGAAATAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCC TCCGAAGACACCATATATTCCTCTATCATTACCAACAGGCCTACTTCTAAGCCAACAAC AAGACCTACACCAAAGCCAACCAATTCTACTCCACCACCACCACCACCTGCCAAC		

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CG51117-04	KCKC
Protein Sequence	HPGYAGKTCNQAVGFERCMVPAGRRGSTL
	SEQ ID NO: 119 1804 bp
NOV30h, CG51117-08 DNA Sequence	<p>CACCGGATCCATGGATTTTCTCCTGGCGCTGGTGTGCTGCTATCCTCGCTCTACCTGCAGGC GGCCGCCGAGTTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATGTCTG TTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTCA GCCTGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTG TCATCCTGGTTATGCTGGAAAACCTGTAATCAAGACGAGCACATCCCAGCTCCTCTTGA CCAAGGCAGTGAACAGCCTCTTTTCCAACCCCTGGATCACCAGCCACAAGTTTGCTTC AAGGGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACAC TTACGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTTG CTCAAGTGCCCTGACCTGCTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGG ACAAATACGGTGCCAGTGCCCATCCCCCTGGCCTGCACCTGGCTCCTGATGGGAGGACCTG TGTAAGTGTGTAATGTGTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGT CAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAGGCTTCGATCTCATGTATATTGG AGGCAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAG CTTTGCTCGATGTTATAACGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACCA GGGTGATGGACTGACTTGTGTGTATATCCAAAAGTTATGATTGAACCTTCAGGTCCAAT TCATGTACCAAAGGGAATGGTACCATTTTAAAGGTTGACACAGGAAATAATAATTGGAT TCCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACCATATATCTCTCCTATCATTAC CAACAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCTTAC TCCACCACCACCACCACCCCTGCCAACAGAGCTCAGAACACCTTACCACCTACAACCCC AGAAAGGCCAACACCACCGGACTGACAACATAGCACCAGCTGCCAGTACACCTCCAGGAGG GATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTTAT TCCACGGCAACCTTCAAATGACTTGTGTTGAAATATTGAAATAGAAAGAGGAGTCAAGTG AGACGATGAAGCAAAGGATGATCCAGGTGTTCTGGTACACAGTTGTAATTTTGACCATGG ACTTTGTGGATGGATCAGGGAGAAAGACAATGACTTGCACTGGGAACCAATCAGGGACCC AGCAGGTGGACAATATCTGACAGTGTGCGCAGCCAAAGCCCCAGGGGAAAAGCTGCACG CTTGGTGCTACCTCTCGGCCCCCTCATGCATTGAGGGGACCTGTGCTGTCTATTCAGGCA CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACAGGTGCCCA CGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTGGAGGCAAAACACAGATCACCTT GCGAGGGGCTGACATCAAGAGCGTCTGTTCAAAGGTGAAAAAAGGCGTGGTCACTGG GGAGATTGGATTAGATGATGTGAGCTTGAAAAAAGGCCACTGCTCTGAAGAACGCGTCTGA CGGC</p>
	ORF Start: ATG at 11 ORF Stop: at 1796
	SEQ ID NO: 120 595 aa MW at 65207.8kD
NOV30h, CG51117-08 Protein Sequence	<p>MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSI GLCRYGGRIDCCWGWARQSWGQCQPV QPRCKHGEICIGPNKCKCHPGYAGKTCNQDEHIPAPLDQGGSEQLFQPLDHQATSLPSRDL NECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALTCSMANQYQCDVVKQIR CQCPSPGLHLAPDGRCTVDVDECATGRASCPRFRQCVNTFGSYICKCHKGFGLMYIGGKY QCHDIDECSLGQYQCSSFARCYNVRGSYKCKKEGYQGDGLTCVYIPKVMIEPSGPIHVP KNGTILKGD TGNNWIPDVGSTWPPKTPYIPPIITNRPTSKPTTRPTKPTPIPTPPP PPPLPTLRLTLPPTTTPERTTGLTTIAPAASTPPGGITVDNRVQTDQPKPRGDFVPIPRQ PSNDLFEIFEIERGVSADEAKDDPGVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGG QYLTVSAAKAPGGKAARLVLPGLRLMHSGLCLSPRHKVTGLHSGTLQVVFVRKHGAHGAA LWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLDDVSLKKGHCSEER</p>
	SEQ ID NO: 121 1858 bp
NOV30i, CG51117-09 DNA Sequence	<p>CACCGGATCCATGGATTTTCTCCTGGCGCTGGTGTGCTGCTATCCTCGCTCTACCTGCAGGC GGCCGCCGAGTTTCGACGGGAGTAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATG TCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTG TCAGCCTTTCTACGTCTTAAGGCAGAGAATAGCCAGGATAAGGTGCCAGCTCAAAGCTGT GTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTCTATCC TGGTTATGCTGGAAAACCTGTAATCAAGACGAGCACATCCCAGCTCCTCTTGACCAAGG CAGTGAACAGCCTCTTTTCCAACCCCTGGATCACCAGCCACAAGTTTGCTTCAAGGGA TCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGG CAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAAG TGCCCTGACCTGCTCCATGGCAAACCTGTGATGCTGCTGATGTTGTTAAAGGACAAAT</p>

	ACGGTGCCAGTGCCCATCCCCTGGCCTGCAGCTGGCTCCTGATGGGAGGACCTGTGTAGA TGTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACAC TTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATGGAGGCAA ATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGC TCGATGTTATAACGTACGTGGGTCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGA TGGACTGACTTGTGTGTATATCCCAAAAGTTATGATTGAACCTTCAGGTCCAATTCATGT ACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAATAATAATTGGATTCTCTGA TGTGGAAGTACTTGGTGGCTCCGAAGACACCATATATTCCTCTATCATTACCAACAG GCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCTACTCCACC ACCACCACCACCCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAG GCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTAC AGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGGAGATGTGTTTATTCCACG GCAACCTTCAAATGACTTGTGTTGAAATATTTGAAATAGAAAGAGGAGTCAGTGCAGACGA TGAAGCAAAGGATGATCCAGGTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTTG TGGATGGATCAGGGAGAAAGACAATGACTTGCCTGGGAACCAATCAGGGACCCAGCAGG TGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGGGGAAAAGCTGCACGCTTGGT GCTACCTCTCGGCCGCCTCATGCATTACAGGGGACCTGTGCCTGTCACTCAGGACACAAGT GACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGC AGCCCTGTGGGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCAGAGG GGCTGACATCAAGAGCGTCGCTTCAAAGGTGAAAAAAGGCGTGGTGCACACTGGGGAGAT TGGATTAGATGATGTGAGCTTGAAGAAAGGCCACTGCTCTGAAGAACGCGTCGACGGC
	ORF Start: ATG at 11 ORF Stop: at 1850
	SEQ ID NO: 122 613 aa MW at 67402.4kD
NOV30i, CG51117-09 Protein Sequence	MDFLLALVLVSSLYLQAAAEFDGSRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPF YVLRQRIARIRCQLKAVCQPRCKHGEICGPNKCKCHPGYAGKTCNQDEHIPAPLDQGSEQ PLFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALT CSMANCQYGCDVVKQIRQCPSGLQLAPDGRTCDVDDECATGRASCPRFRQCVNTFGS YICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT CVYIPKVMIEPSGPIHVPKNGTILKGD TGNNWIPDVGSTWWPPKTPYIPIITNRPTS KPTTRPTPKPTPIPTPPPPPLPTELRLTPLPTTTPERTTGLTTIAPAASTPPGGITVDN RVQTDPOKPRGDVFI PRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGWI REKNDLHWEP IRDPAGGQYLTVSAAKAPGGKAARLVPLPLRLMHSGDLCLSFHRKVTGL HSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLD DVSLKKGHCSEER

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 30B.

Table 30B. Comparison of NOV30a against NOV30b through NOV30i.		
Protein Sequence	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV30b	32..240 65..273	207/209 (99%) 207/209 (99%)
NOV30c	1..240 98..340	210/244 (86%) 217/244 (88%)
NOV30d	1..240 81..323	210/244 (86%) 217/244 (88%)
NOV30e	32..240 101..309	207/209 (99%) 207/209 (99%)

NOV30f	184..196 88..100	8/13 (61%) 8/13 (61%)
NOV30g	167..196 33..64	14/32 (43%) 15/32 (46%)
NOV30h	1..240 80..322	210/244 (86%) 216/244 (88%)
NOV30i	1..240 98..340	211/244 (86%) 217/244 (88%)

Further analysis of the NOV30a protein yielded the following properties shown in Table 30C.

Table 30C. Protein Sequence Properties NOV30a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV30a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several
5 homologous proteins shown in Table 30D.

Table 30D. Geneseq Results for NOV30a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB70549	Clone 16467945.0.85-S261.D protein sequence SEQ ID NO:82 - <i>Homo sapiens</i> , 546 aa. [WO200110902-A2, 15-FEB-2001]	32..450 65..483	417/419 (99%) 417/419 (99%)	0.0
AAB70547	Human PRO17 protein sequence SEQ ID NO:34 - <i>Homo sapiens</i> , 582 aa. [WO200110902-A2, 15-FEB-2001]	32..450 101..519	417/419 (99%) 417/419 (99%)	0.0
AAB80265	Human PRO334 protein - <i>Homo sapiens</i> , 509 aa. [WO200104311-A1, 18-JAN-2001]	36..450 88..473	383/415 (92%) 383/415 (92%)	0.0

AAU29049	Human PRO polypeptide sequence #26 - <i>Homo sapiens</i> , 509 aa. [WO200168848-A2, 20-SEP-2001]	36..450 88..473	383/415 (92%) 383/415 (92%)	0.0
AAY13397	Amino acid sequence of protein PRO334 - <i>Homo sapiens</i> , 509 aa. [WO9914328-A2, 25-MAR-1999]	36..450 88..473	383/415 (92%) 383/415 (92%)	0.0

In a BLAST search of public sequence databases, the NOV30a protein was found to have homology to the proteins shown in the BLASTP data in Table 30E.

Table 30E. Public BLASTP Results for NOV30a				
Protein Accession Number	Protein/Organism/Length	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC33425	Sequence 33 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 582 aa.	32..450 101..519	417/419 (99%) 417/419 (99%)	0.0
Q91V88	POEM (NEPHRONECTIN short isoform) - <i>Mus musculus</i> (Mouse), 561 aa.	36..450 88..502	363/416 (87%) 386/416 (92%)	0.0
Q91ZD3	Nephronectin long isoform - <i>Mus musculus</i> (Mouse), 578 aa.	36..450 105..519	363/416 (87%) 386/416 (92%)	0.0
Q91XL5	Nephronectin - <i>Mus musculus</i> (Mouse), 592 aa.	38..450 121..533	362/414 (87%) 385/414 (92%)	0.0
Q923T5	Nephronectin - <i>Mus musculus</i> (Mouse), 609 aa.	38..450 138..550	362/414 (87%) 385/414 (92%)	0.0

PFam analysis predicts that the NOV30a protein contains the domains shown in

5 Table 30F.

Table 30F. Domain Analysis of NOV30a			
Pfam Domain	NOV30a Match Region	Identities/ Similarities for the Matched Region	Expect Value
EGF	41..75	15/47 (32%) 27/47 (57%)	0.84

EGF	81..115	10/47 (21%) 24/47 (51%)	0.034
EGF	166..201	12/47 (26%) 29/47 (62%)	4.9e-06

Fig. 1 shows that NOV30b (G51117-05) is expressed as about 66 kDa protein secreted by 293 cells.

Example 31.

5 The NOV31 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 31A.

Table 31A. NOV31A Sequence Analysis		
	SEQ ID NO: 123	3336 bp
NOV31a, CG51264-01 DNA Sequence	CGCCGGTGGCTCGGCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCTAC CTCCAGCTCCTCTCTCCCTCTCTCTCGCTCTCTCTCTCTCTCCATCTGCTGTGGTTA TGGCCTGTGCTGGAGCACAAAAGAGTCTCCGCGGTGGAGGTCTGCGTGTCTTGTCTTT TCCTCGTGGGGTGACGCTTGTGGAGAGACTCCAGAGCAAATACGAGACCAAGTGGCA TAATCACAAGCCCAGGCTGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGTTCA TAAGGGCAAACCCAGGCGAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAGGAT CCAGAAGGTGCAATTTGGACTGGTTGACAATAGAAACATACAGAATAATTGAAAGTTACA GAGCTTGTGGTTCCACAATTCCACCTCCGTATATCTCTTCACAAGACCACATCTGGATTA GGTTTCATTTCGGATGACAACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTTCAGGGA AATCTGAGGAACCAAATTTGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAAGTGATAC CAGAAGCCTGGAATGCAATAACATGGATGAATGTGGAGATAGTTCGGATGAAGAGATCT GTGCCAAAGCAAGCAATCTCCAACCTGCTGCTGTTTTCAACCTGTGCTTACAACCAAGT TCCAGTGTATATCCCGTTTTACCAAAGTTTACACTTGCTCTCCCGAATCTTTAAATGTG ATGGGAACATTGACTGCCTTGACCTAGGAGATGAGATAGACTGTGATGTCCAACATGTG GGCAATGGCTAAATATTTTTATGGTACTTTTTAATCTCCCAATTATCCAGACTTTTATC CTCCTGGAAGCAATTGCACCTGGTTAATAGACTGGTGAACCCGTAAGCTCATTTTAC GCTTCACTGACTTTAAACTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATG GATTAGAGGAGAATCCACACAAGCTTTTGGTGTGTTGACAGCTTTTGATTCTCATGCAC CTCTTACAGTTGTTTCTTCTCTGGACAGATAAGGGTACATTTTTGTGCTGATAAAGTGA ATGCTGCAAGGGGATTTAATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAA TACCCTGTGGAGGTAACCTGGGGGTTTATACTGAGCAGCAGCGTGTGATGGGTATTGGC ATTGCCAAATGGAAGGGATGAACCAATTGTACCATGTGCGCAAGGAAGAAATTTCCAT GTTCCCGAAATGGTGTCTGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCC CAAATGGCTCAGATGAAAAAACTGCTTTTTTTGCCAACCAGGAAATTTCCATTGTAAAA ACAATCGTTGTGTGTTTGAAGATTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCA GCGATGAAGAAAATTGCCAGTAATCGTGCCTACAAGAGTCATCACTGCTGCCGCTCATAG GGAGCTCATCTGTGGCCTGTACTCGTCATAGCATCTGGGATGTACTTGAAGCTTTAT CTCTGAGAATGTTTGAAGAAGATCATTGAAACACAGTTGTCAAGAGTGGAAGCAGAAT TGTTAAGAAGAGAAGCTCCTCCCTCGTATGGACAATTGATTGCTCAGGGTTTAATCCAC CAGTTGAAGATTTTCTGTTGTTACCTAATCAGGCTTCTGTTTTGAAAAATCTGAGGC TAGCGGTACGATCTCAGCTTGGATTTACTTCAGTCAGGCTTCTCTATGGCAGGCAGATCAA GCAACATTTGGAACCGTATTTTTAATTTTGGCAAGATCAGCTCATTCTGGGTCAATTGGCTT TGGTCTCAGCAGATGGAGATGAGGTTGTCCCTAGTCAGAGTACCAGTAGAGAACCTGAGA GAAATCATACTACAGAAGTTGTTTTCCGTGGAGTCTGATGATACAGACACAGAAAATG AGAGAAGAGATATGGCAGGAGCATCTGGTGGGGTTGACAGTCTTTGCTCAAAAAGTCC CTCCCAACAACGGCAGTAGAAGCGACAGTAGGAGCATGTGCAAGTCTCTCAACTCAGAGTA CCCGAGGTGGTCATGCAGATAATGAAGGGATGTGACAAGTGTGGAACCCCAAGTGTGA GTCCAGCAGCTCACCAGCTTACAAGTGCACCTCAGTCGTATGACTCAGGGGTACGCTGGG	

[illegible]

	CCGCGAATGGTCTGTTCTTCTCTGATCGTCTGCAACTACCAGAAATCATGCCAA ATGGCAAACAGAACCATCTACTTGGTAAGTAGCATTAAATCCCCTTGCAGCATTAC		
	ORF Start: ATG at 120		ORF Stop: TAA at 1467
	SEQ ID NO: 126	449 aa	MW at 50654.0kD
NOV31b, CG51264-03 Protein Sequence	MACRWSTKESPRWRSALLLLFLAGVYNGALAEHSENVHISGVSTACGETPEQIRAPSGI ITSPGWPSSEYPKINCSWFRANPGEIITISFQDFDIQSSRRCNLDWLTITIETYNIESYR ACGSTIPPPYISSQDHIWIRFHSDDNISRKGFRLAYFSKGSEEPNCACDQFRGNGKCIP EAWKCNMNMDECGDSSDEEICAKEANPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCD GNIDCLDLGDEIDCDVPTCGQWLKYFYGTFFNSPNYPDFYPPGNSNCTWLIDTGDHRKVILR FTDFKLDTGTYGQDVYKIIDGLEENPHKLLRVLTAFDSSHAPLTVVSSSGQIRVHFCADKVN AARGFNATYQVDGFCPLPWEIPCGGNWGCYTEQQRDDGYWHCPNGRDETNTMCQKEEFP SRNGVCYPRSDRCNYQNHCPNGKQNPSTW		
	SEQ ID NO: 127	1441 bp	
NOV31c, CG51264-04 DNA Sequence	CGCCGGTGGCTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCTAC CTCCAGCTTCTCTCTCCCTCTCTCTCGTCTCTCTCTCTCTCTCTCCATCTGCTGTGGTTA TGGCCTTGTCTGAGACACAAAAGAGTCTCCGCGGTGGAGGTCTGCGTGTCTCTTGCTTT TCCTCGCTGGGGGTGACGCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCA TAATCAACAAGCCAGGCTGGCTTCTGAATATCTCTGCAAAATCAAACTAGCTGGTTTCA TAAGGGCAAACCCAGGCGAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGAT CCAGAAGGTGCAATTTGGACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACA GAGCTTGTGGTTCCACAATCCACCTCCGTATATCTCTTCAAGACCACATCTGGATTA GGTTTCATTCCGATGACAACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTTCAGGGA AATCTGAGGAACCAAATTTGCTTGTGATCAGTTTCGTTGGTGAATGGAAGTGTATAC CAGAAGCCTGGAATGTAAATACATGGATGAATGTGGAGATAGTTCCGATGAAGAGATCT GTGCCAAAGAAGCAAATCTCCAAGTCTGCTGCTTTTCAACCTGTGCTTACAACCAAGT TCCAGTGTTTATCCCGTTTACCAAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTG ATGGGAACATTGACTGCCTTTGACCTAGGAGATGAGATAGACTGTGATGTGCGCAACATGTG GGCAATGGCTAAAATTTTATGTGACTTTTAACTTCCCAATTCAGACTTTCAGACTTTTATC CTCCTGGAAGCAATTGCACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTAC GCTTCACTGACTTTAACTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATG GATTAGAGGAGAATCCACACAAGCTTTTGCCTGTGTTGACAGCTTTTGATTCTCATGCAC CTCTTACAGTTGTTTCTTCTTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGA ATGCTGCAAGGGGATTAATGCTACTTACCAAGTAGATAGTGTCTGTTTGGCATGGGAAA TACCCTGTGGAGGTAACGGGGGTGTATACCTGAGCAGCAGCGCTCGTGATGGGTATTGGC ATTGCCCAAATGGAAGGGATGAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCAT GTTCCCGAAATGGTGTCTGCTATCTCTGCTCTGATCGCTGCAACTACAGAATCATTGCC CAAATGGCAAACAGAACCCATCTACTTGGTAAGTAGCATTAAATCCCCTTGCAGCATTCA C		
	ORF Start: ATG at 120		ORF Stop: TAA at 1410
	SEQ ID NO: 128	430 aa	MW at 48793.0kD
NOV31c, CG51264-04 Protein Sequence	MACRWSTKESPRWRSALLLLFLAGVYACGETPEQIRAPSGIITSPGWPSSEYPKINCSWFR IRANPGEIITISFQDFDIQSSRRCNLDWLTITIETYNIESYRACGSTIPPPYISSQDHIWI RFHSDDNISRKGFRLAYFSKGSEEPNCACDQFRGNGKCIPCAWKCNMNMDECGDSSDEE ICAKEANPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTC GQWLKYFYGTFFNSPNYPDFYPPGNSNCTWLIDTGDHRKVILRFTDFKLDTGTYGQDVYKIID GLEENPHKLLRVLTAFDSSHAPLTVVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCPLPWE IPCGGNWGCYTEQQRDDGYWHCPNGRDETNTMCQKEEFP SRNGVCYPRSDRCNYQNHCPNGKQNPSTW		
	SEQ ID NO: 129	3021 bp	
NOV31d, CG51264-06 DNA Sequence	CTCCTCTCTCGTCTCTCTCTCTCTCTCATCTGCTGTGGTTATGGCGTGTCTGCTGGAGC ACAAAAGAGTCTCCGCGGTGGAGGTCTGCGTGTCTCTTGCTTTTCTCGCTGGGGTGTAC GCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCAAGCCAGGC TGGCCTTCTGAATATCCTGCAAAATCAACTGTAGCTGGTTATGAAGGGCAAACCCAGGC GAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTG GACTGGTTGCAATAGAAACATACAAGAATATTGAAAGTTACAGAGTTGTGGTTCCACA ATTCACCTCCGTATATCTCTTCAAGACCACATCTGGATTAGGTTTCATTCCGATGAC		

	AACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATCTGAGGAACCAAAAT TGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAAGTGTATACCAGAAGCCTGGAAATGT AATAACATGGATGAATGTGGAGATAGTTCGGATGAAGAGATCTGTGCCAAAGAAGCAAAT CCTCCAACCTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAAGTTCAGTGTTTATCCCGT TTTACCAAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGC CTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAAATGTGGGCAATGGCTAAATAT TTTTATGGTACTTTTAATTCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGC ACCTGGTTAATAGACACTGGTGATACCGTAAAGTCATTTTACGCTTCACTGACTTTAAA CTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATGGATTAGAGGAGAATCCA CACAAGCTTTTGGCGTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTC TCTTCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTT AATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCCTGTGGAGGTAAC TGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCAAATGGAAGG GATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTC TGTTATCCTCGTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAA AAAAACTGCTTTTTTTGCCAACAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTT GAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGTGATGCGCAGCGATGAAGAAAATTGC CCAGTAATCGTGCCTACAAGAGTCATCACTGCTGCCGTATAGGGAGCCTCATCTGTGGC CTGTTACTCGTCATAGCATTTGGGATGTACTTGTAAAGCTTTATCTCTGAGAATGTTTGAA AGAAGATCATTGAAACACAGTTGTCAAGAGTGGAAAGCAGAATTGTTAAGAAGAGAAGCT CCTCCCTCGTATGGACAATTGATTGCTCAGGGTTTAATTCACCAAGTTGAAGATTTTCT GTTTGTTCACTAATCAGGCTTCTGTTTGGAAAATCTGAGGCTAGCGGTACGATCTCAG CTTGGAATTTACTTCAGTCAGGCTTCTATGGCAGGCAGATCAAGCAACATTGGAACCGT ATTTTTAATTTGCAAGATCACGTATTCTGGGTCAATTGGCTTTGGTCTCAGCAGATGGA GATGAGGTTGTCCTTAGTCAGAGTACCAGTAGAGAACCTGAGAGAAATCATACTACAGA AGTTTGTTTTTCCGTGGAGTCTGATGATACAGACAGAAAATGAGAGAAGAGATATGGCA GGAGCATCTGGTGGGGTTGCAGCTCCTTTGCCCTCAAAAAGTCCCTCCACAAACGGCAGTG GAAGCGACAGTAGGAGCATGTGCAAGTTCCTCAACTCAGAGTACCCGAGGTGGTCATGCA GATAATGGAAGGGATGTGACAAGTGTGGAACCCCCAAGTGTGAGTCCAGCACGTACCAG CTTACAAGTGCACCTCAGTCGTATGACTCAGGGGCTACGCTGGGTACGTTTTACATTAGGA CGATCAAGTTCCTAAGTCAGAACCAGAGTCTTTGAGACAACCTGATAATGGGGTAAGT GGAAGAGAAGATGATGATGATGTTGAAATGCTAATTC AATTTCTGATGGATCTTCAGAC TTTGATGTGAATGACTGCTCCAGACCTCTTCTTGATCTTGCCTCAGATCAAGGACAAGGG CTTAGACAACCATATAATGCAACAAATCCTGGAGTAAGGCCAAGTAATCGAGATGGCCCC TGTGAGCGCTGTGGTATTGTCCACACTGCCAGATACCAGACACTTGCTTAGAAGTAACA CTGAAAAACGAAACGAGTGATGATGAGGCTTTGTTACTTTGTTAGGTACGAATCACATAA GGGAGATTGTATACAAGTTGGAGCAATATCCATTTATTATTTGTACTTTACAGTTAAA CTAGTTTTAGTTTAAAAAGAAAAATGCAGGGTGATTTCTTATTATTATATGTTAGCCTG CATGGTTAAATTCGACAACCTGTAACCTATGAACCTAGAGTTTACTATTTTAGCAGCTA AAAATGCATCACATATTGCATATTGTTCAATAATGGTCCTTTTCAATTTGTTTCTGATTGTT TTCATCCTGATACTGTAGTTCACTGTAGAAATGTGGCTGCTGAAACTCATTGTATTGTCA TTTTTATCTATCCTATGTTTAAATGGTTTGTGTTTTACAAAATAATACCTTATTTTAATTGA AACGTTTATGCTTTTGCCAAGCACATCTTGTAACTTAATATAGCTAGATGTTAAGGTTGT TAATGTACCAAAAAAAAAAAAA		
	ORF Start: ATG at 43		ORF Stop: TAG at 2563
	SEQ ID NO: 130	840 aa	MW at 93121.8kD
NOV31d. CG51264-06 Protein Sequence	MACRWSTKESPRWRSALLLFLAGVYACGETPEQIRAPSGIITS PGWPSEYPKINC SWF IRANPGEIITISFQDFDIQGSRRCLDWLTIEYKNIESYRACGSTIPPPYISSQDHIWI RFHSDDNISRKGFRLAYFSGKSEEPNCADQFRCGNGKCIPEAWKCNMDECGDSSDEBI CAKEANPPTAAAFQPCAYNQFQLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTC GQWLKIFYGTFNSPNYPDFYPPGSNCTWLIDTGDHRKVI LRFTDFKLDGTGYDGVKIYD GLEENPHKLLRVLTAFD SHAPLTVSSSGQIRVHFCADKVNAARGFVQYDGFCLPWE IPCGGNWGCYTEQQRCDGYWHCPNGRDETNTMCQKEEFPCSRNGVCYPRSDRCNYQNHC PNGSDEKNCFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSDEENCPIVIVPTRVITAAVI GSLICGLLLVIALGCTCKLYSLRMFERRSFETQLSRVEAELLRREAPPSYQGLIAQGLIP PVEDFPVCSNPQASVLENLRLAVRSQLGFTSVRLPMAGRSSNIWNRI FNFARSRHSGSLA LVSADGDEVVPSQSTSREPERNHTRSLFSVESDDTD TENERNDMAGASGGVAAPLPQKV PPTTAVEATVGACASSSTQSTRGGHADNGRDVTSVEPPSVSPARHQLTSALSRMTQGLRW		

	VRFTLGRSSSLQNSPLRQLDNGVSGREDDDDVEMLIPISDGSSDFDVNDCSRPLLDLA SDQGGQLRQYPYNATNPGVRPSNRDGPCECGIVHTAQIPDTCLEVTLKNETSDDEALLLC
	SEQ ID NO: 131 3012 bp
NOV31e, CG51264-07 DNA Sequence	<p>CTCCTCCTCCGTCCTCCTCTCTCTCATCTGCTGTGGTTATGGCCTGTCGCTGGAGC ACAAAAGAGTCTCCGCGGTGGAGGTCTGCGTTGCTTTTCTCCTCGCTGGGGTGTAC GCTGTGAGAACTCAACAATACAGCACAAAGTGGCATAATCACAGCCCAGGCTGGCCTTCT GAATATCCTGCAAAAATCAACTGTAGCTGGTTTATAAGGGCAAACCCAGGCGAAATCATT ACTATAAGTTTTTCAAGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTGGACTGGTTG ACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACAATCCACCT CCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTCATTCCGATGACAACATCTCT AGAAAGGGTTTTCAAGCTGGCATATCTTTCAGGCAAATCTGAGGAACCAAATTTGTGCTTGT GATCAGTTTCGTTGTGGTAATGGAAGTGTATACCAGAAGCCTGGAAATGTAATAACATG GATGAATGTGGAGATAGTTCCGATGAAGAGATCTGTGCCAAAGCAAACTCTCCAACCT GCTGCTGCTTTTCAACCTGTGCTTACAACAGTTCAGTGTATTATCCCGTTTACCAAA GTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGCCTTGACCTA GGAGATGAGATAGACTGTGATGTGCCAATGTGGCAATGGCTAAATATTTTATGGT ACTTTAATTCTCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGCACCTGGTTA ATAGACACTGGTGATCACCCTAAAGTCATTTACGCTTCACTGACTTTAACTTGATGGT ACTGGTTATGGTGATTATGTCAAATATATGATGGATTAGAGGAGAATCCACACAAGCTT TTGCGTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCTTCTTCTGGA CAGATAAGGGTACATTTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTTAATGCTACT TACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCCTGTGGAGGTAACTGGGGGTGT TATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGGATGAAACC AATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTCTGTTATCCT CGTTCTGATCGCTGCAACTACCAGAATCATTTGCCCAAATGGCTCAGATGAAAAAACTGC TTTTTTTGCCAACCAGGAAATTTCCATTGTAACCAATCGTTGTGTGTTTGAAGTTGG GTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGCCAGTAATC GTGCTTACAAGAGTCATCACTGCTGCCGTCATAGGGAGCCTCATCTGTGGCCTGTTACTC GTCATAGCATTGGGATGTACTGTAAAGCTTTATTCTCTGAGAATGTTTGAAGAAGATCA TTTGAACACAGTTGTCAAGAGTGGAAGCAGAATTGTTAAGAAGAGAAGCTCCTCCCTCG TATGGACAATTGATTGCTCAGGGTTTAATCCACCAGTTGAAGATTTTCTGTTTGTTC CCTAATCAGGCTTCTGTTTTGGAAAATCTGAGGCTAGCGGTACGATCTCAGCTTGGATT ACTTCAGTCAGGCTTCTATGGCAGGCAGATCAAGCAACATTTGGAACCGTATTTTAAAT TTTGCAAGATCAGCTCATTCTGGGTCATTGGCTTTGGTCTCAGCAGATGGAGATGAGGTT GTCCCTAGTCAGAGTACCAGTAGAGAACCTGAGAGAAATCATACTACAGAACTTTGTTT TCCGTGGAGTCTGATGATACAGACACAGAAAATGAGAGAAGAGATATGGCAGGAGCATCT GGTGGGGTTGCAGCTCCTTTGCCCTCAAAAAGTCCCTCCCAACCGGAGTGGAAGCGACA GTAGGAGCATGTGCAAGTCTCTCAACTCAGAGTACCCGAGGTGGTATGCAGATAATGGA AGGATGTGACAAGTGTGGAACCCCAAGTGTGAGTCCAGCACGTCCAGCTTACAAGT GCACTCAGTCGTATGACTCAGGGGCTACGCTGGGTACGTTTTACATTAGGACGATCAAGT TCCCTAAGTCAGAACAGAGTCTTTGAGACAACCTGATAATGGGGTAAGTGAAGAGAA GATGATGATGATGTTGAAATGCTAATTTCAATTTCTGATGGATCTTCAGACTTTGATGTG AATGACTGCTCCAGACCTCTTCTTGATCTTGCCTCAGATCAAGGACAAGGGCTTAGACAA CCATATAATGCAACAAATCCTGGAGTAAGGCCAAGTAATCGAGATGGCCCTGTGAGCGC TGTGGTATTGTCCACACTGCCAGATACCAGACACTTGCTTAGAAGTAACACTGAAAAAC GAAACGAGTGATGATGAGGCTTTGTTACTTTGTTAGGTACGAATCACATAAGGGAGATTG TATACAAGTTGGAGCAATATCCATTTATTATTTTGTAACTTTACAGTTAACTAGTTTTA GTTTAAAAAGAAAAATGCAGGGTGATTCTTATTATTATATGTAGCCTGCATGGTTAA ATTGACAACCTGTAACTCTATGAACCTTAGAGTTTACTATTTTAGCAGCTAAAAATGCAT CACATATTGCATATTGTTCAATAATGGTCCTTTTCAATTTGTTTCTGATTGTTTTCATCCTG ATACTGTAGTTCACTGTAGAATGTGGCTGCTGAACTCATTGATTGTCTTTTTATCT ATCCTATGTTAAATGGTTTGTTTTACAAAATAATACCTTATTTAATTGAACGTTTAT GCTTTTGCCAAGCACATCTTGAACCTAATATAGCTAGATGTTAAGGTTGTTAATGTACC AAAAAAAAAAAA</p>
	ORF Start: ATG at 43 ORF Stop: TAG at 2554
	SEQ ID NO: 132 837 aa MW at 92869.5kD
NOV31e, CG51264-07	MACRWSTKESPRWRSALLLLFLAGVYVRTQYSTSGIITS PGW PSEYPAKINC SWFIRA NPGEIITISFQDFDIQGSRRCNLDWLTITETYNIESYRACGSTIPPPYISSQDHIWIRFH

Protein Sequence	SDDNI SRKGFRLAYLSGKSEEPNCADQFRCNGNKCIPEAWKCNMDECGDSSDEEICA EANPPTAAAFQPCAYNQFCLSRFTKVYTCLPESLKCNDGIDCLDLGDEIDCDVPTCGQW LKYFYGTFSNPYPDFYPPGSNCTWLIDTGDHRKVLIRFTDFKLDGTGYGDYVKIYDGL ENPHKLLRVLTAFD SHAPLTVVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCPLWEIPC GGNWGCYTEQQRCDDGYWHCPNGRDETNTMCQKEEFPCSRNGVCYPRSDRCNYQNHCPG SDEKNCFCCQPGNFHCKNNRCVFESWVCDSDQDCGDSBENCVPVITRVITAAVIGSL ICGLLLVIALGCTTKYLSRMFERRSFETQLSRVEAELLRREAPPSYQGLIAQGLIPPVE DFPVCSNPQASVLENLRLAVRSQLGFTSVRLPMAGRSSNIWNRI FNFARSRHSGSLALVS ADGDEVVPSQSTREPERNHTRSLFSVESDDTDTENERRDMAGASGGVAAPLPQKVPP TAVEATVGACASSSTQSTRGGHADNGRDVTSEPPSPVSPARHQLTSALSRMTQGLRWVR TLGRSSSLSQNSPLRQLDNGVSGREDDDDVEMLIPI SDGSSDLDVNDCSRPLDLASD GQGLRQPYNATNPGVPRNSRDGCPERCIVHTAQIPDTCLEVVTLKNETSDDEALLLC		
	SEQ ID NO: 133	1441 bp	
NOV31f, CG51264-02 DNA Sequence	CGCGCGGTGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGCTCGTCTAC CTCACAGCTTCTCCTCCCTCCTCCTCCGTCTCCTCCTCCTCCTCCTCATCTGCTGTGGTTA TGGCTGTGCTGGAGCACAAAGAGTCTCCGCGGTGGAGGTCTGCGTTGCTCTTGCTTT TCCTCGCTGGGGTGACGCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCA TAATCACAAGCCCAGGCTGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTTCA TAAGGGCAAACCCAGGCGAAATCATTACTATAAGTTTTAGGATTTTGATATTCAGGAT CCAGAAGGTGCAATTTGGACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACA GAGCTTGTGGTTCACAATCCACCTCCGTATATCTCTTACAAGACCACATCTGGATTA GGTTTCATTCCGATGACACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGA AATCTGAGGAACCAAATTTGTGCTTGTGATCAGTTTCGGTGTGGTATGGAAGTGTATAC CAGAGCGTGAAGATGTAAATACATGGATGAATGTGGATAGTTCGATGAAGAGACTCT GTGCCAAAGAAGCAAATCCTCCAAGTGTGCTGCTTTTCAACCTGTGCTTACAACCAAGT TCCAGTGTATATCCGTTTACCAAAGTTTACACTTGCTCCCCGAATCTTTAAATGTG ATGGGAACATTGACTGCCTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATATG GGCAATGGACTAAAATTTTATGGTACTTTTAATCTCCCAATTCAGACTTTTATC CTCTGGAAGCAATTCACCTGGTTAATAGACACTGGTATCACCCTAAAGTCAATTTTAC GCTTCACTGACTTTAACTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATG GATTAGAGGAGAATCCACACAAGCTTTTGCCTGTGTTGACAGCTTTTGATTCTCATGCAC CTCTTACAGTTGTTTCTTCTTCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGA ATGCTGCAAGGGGATTAAATGCTACTTACCAAGTAGATGGGTCTGTTTGCCATGGGAAA TACCTTGAGAGGTAACTGGGGGTGTATACTGAGCAGACGCTCGTATGGGTATTGGC ATTGCCCAAATGGAAGGGATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCAT GTTCCCGAAATGGTGTCTGCTATCCTCGCTGATCGCTGCAACTACCAGAATCATTGCC CAAATGGCAAACAGAACCCATCTACTTGGTAAGTAGCATTAAATCCCTTGCACGACATTCA C		
	ORF Start: at 3		ORF Stop: TAA at 1410
	SEQ ID NO: 134	469 aa	MW at 53338.2kD
NOV31f, CG51264-02 Protein Sequence	PVARRRRRRRRRRRRRLPPASPPSSSVSSSLSPSAVMACRWSTKESPRWRSAALLLLF LAGVYACGETPEQIRAPSGIITSPGWSEYPKINCNSWIFIRANPGEIITISFQDFDIQGS RRCNLDWLTIEPTQYKNIESYRACGSTIPPPYISSQDIWIRFHSDDNISRKGFRLAYFSGK SEBENCADQFRCNGNKCIPEAWKCNMDECGDSSDEEICA EANPPTAAAFQPCAYNQF QCLSRFTKVYTCLPESLKCNDGIDCLDLGDEIDCDVPTCGQWLKYFYGTFSNPYPDFYF PGSNCTWLIDTGDHRKVLIRFTDFKLDGTGYGDYVKIYDGLEENPHKLLRVLTAFD SHAP LTVVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCPLWEIPC GGNWGCYTEQQRRDGYWH CPNGRDETNTMCQKEEFPCSRNGVCYPRSDRCNYQNHCPNGKQNPSTW		
	SEQ ID NO: 135	3078 bp	
NOV31g, CG51264-05 DNA Sequence	CTCCTCCTCCGTCTCCTCCTCCTCCTCCTCATCTGCTGTGGTTATGGCCTGTGCTGGAGC ACAAAAGAGTCTCCGCGGTGGAGGTCTGCTTGTCTTGTCTTTTCTCGCTGGGGTGAC GGAATGGTGCTCTTGAGAACATTCTGAAAATGTGCATATTTAGGAGTGTCAACTGCT TGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGCTGG CCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTTTATAGGGGCAACCCAGGCGAA ATCATTACTATAAGTTTTAGGATTTTATGATTCAAGGATCCAGAAGGTGCAATTTGGAC TGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCCAATT CCACCTCCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTTCATTCCGATGACAA		

	ATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATCTGAGGAACCAAATTGT GCTGTGATCAGTTTCGTTGTGGAATGGAAGTGTATACCAGAAGCCTGGAAATGCAAT AACATGGATGAATGTGGAGATAGTTCGATGAAGAGATCTGTGCCAAAGAAGCAAATCCT CCAACTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAGTTCAGTGTATCCCCGTTTT ACCAAAGTTTACACTTGCCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGCCTT GACCTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGCAATGGCTAAAATATTTT TATGGTACTTTTAATTCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGCACC TGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTTCACTGACTTTAACTT GATGGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCACAC AAGCTTTTGGTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCTTCT TCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTTAAT GCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCCTGTGGAGGTAAGTGG GGGTGTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGGGAT GAAACCAATGTACCATGTGCCAGAAGGAAGAAATTTCCATGTTCCCGAAATGGTGCTGT TATCCTCGTTCTGATCGCTGCACTACCAGAATCATTGCCCAAATGGCTCAGATGAAAAA AACTGCTTTTGTGCAACCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTGAA AGTTGGGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGCCCA GTAATCGTGCTTACAAGAGTCATCACTGCTGCCGTATAGGGAGCCTCATCTGTGCCTG TTAATCGTCATAGCATTTGGGATGTACTTGTAAAGCTTTATCTCTGAGAAATGTTTGAAAGA AGATCATTTGAAACACAGTTGTCAAGAGTGGGAAGCAGAATTGTTAAGAAGAGAAGCTCCT CCTCGTATGGACAATTGATTGCTCAGGGTTTAATCCACAGTTGAAGATTTTCTGTT TGTTACCTAATCAGGCTTCTGTTTGGAAAATCTGAGGCTAGCGGTACGATCTCAGCTT GGATTTACTTCAGTCAGGCTTCTATGGCAGGCAGATCAAGCAACATTGGAACCGTATT TTAATTTTGCAAGATCACGTCAATCTGGGTATTGGCTTGGTCTCAGCAGATGGAGAT GAGGTTGTCCCTAGTCAGAGTACCAGTAGAGAACCTGAGAGAAATCATACTCAGAGAAGT TTGTTTTCCGTGGAGTCTGATGATACAGACACAGAAAATGAGAGAAGATATGGCAGGA GCATCTGGTGGGTTGCAGCTCCTTGCCTCAAAAAGTCCCTCCCAACCGCAGTGGA GCGACAGTAGGAGCATGTGCAAGTTCCTCAACTCAGAGTACCCGAGGTGGTCTATGCAGAT AATGGAAGGGATGTGACAAGTGTGGAACCCCCAAGTGTGAGTCCAGCACGTCAACAGCTT ACAAGTGCACCTCAGTCGTATGACTCAGGGGTACGCTGGGTACGTTTTACATTAGGACGA TCAAGTTCCTAAGTCAGAACAGAGTCTTTGAGACAACTTGATAATGGGGTAAAGTGA AGAGAAGATGATGATGATGTTGAAATGCTAATTCCAATTTCTGATGGATCTTCAGACTTT GATGTGAATGACTGCTCCAGACCTCTTCTTGATCTTGCCTCAGATCAAGGACAAGGGCTT AGACAACCATATAATGCAACAAATCCTGGAGTAAGGCCAAGTAATCGAGATGGCCCTGT GAGCGCTGTGGTATTGTCCACACTGCCAGATACCAGACACTTGCTTAGAAGTAACACTG AAAAAACGAAACGAGTGATGATGAGGCTTTGTTACTTTGTAGGTACGAATCACATAAGGG AGATTGTATACAAGTTGGAGCAATATCCATTATTATTGTAACCTTACAGCTTAAACTA GTTTTAGTTTAAAAAGAAAAATGCAGGGTGATTCTTATTATTATATGTTAGCCTGCAT GGTAAATTCGACAACTTGTAACCTATGAACTTAGAGTTACTATTTTAGCAGCTAAAA ATGCATCACATATTGCATATTGTTCAATAATGGTCTCTTCAATTTGTTTCTGATTGTTTT ATCCTGATACTGTAGTTCACTGTAGAAATGTGGCTGCTGAACTCATTGATTGTCAATT TTATCTATCCTATGTTAAATGTTTGTGTTTTACAAAATAATACCTTATTTTAATTGAAAC GTTTATGCTTTTGCCAAGCACATCTTGTAACTTAATATAGCTAGATGTTAAGGTTGTTAA TGTACCAAAAAAAAAA		
	ORF Start: ATG at 43		ORF Stop: TAG at 2620
	SEQ ID NO: 136	859 aa	MW at 94982.7kD
NOV31g, CG51264-05 Protein Sequence	MACRWSTKESPRWRSALLLLFLAGVYNGALAEHSENVHISGVSTACGETPEQIRAPSGI ITSPGWBPSEYPKINCSWFIRANPGEIITISFQDFDIQGSRRCNLDWLTIEYKNIESYR ACGSTIPPPYISSQDHIWIRFHSDDNISRKGFRLAYFSKGSEEPNACDQFRCNGNKCIP EAWKCNMDECGDSSDEEICAKEANPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCD GNIDCLDLGDEIDCDVPTCGQWLKYFYGTFFNSPNYPDFYPPGSNCTWLIDTGDHRKVILR FTDFKLDGTGYGDYVKIYDGLEENPHKLLRVLTAFDASHAPLTVVSSGGQIRVHFCADKVN AARGFNATYQVDGFCLPWEIPCGGNWGCYTEQQRCDGYWHCPNGRDETNTMCQKEEFP SRNGVCYPRSDRCNYQNHCPNGSDEKNCFFCQPGNFHCKNNRCVFESWVCDSDQDCGDS DEENCPIVIVPRVITAAVIGSLICGLLLVIALGCTCKLYSLRMFERRSFETQLSRVEAEL LRREAPPSYQGLIAQGLIPPVEDFPVCSNPQASVLENLRLAVRSQLGFTSVRLPMAGRSS NIWNRI FNFARSRHSGSLALVSADGDEVVPSQSTSREPERNHTRSLFVSDDTDENE RRD MAGASGGVAAFLPQKVPPTTAVEATVGACASSSTQSTRGGHADNGRDVTSEPPSVS		

	PARHQLTSALSRTQGLRWVRFTLGRSSLSQNSPLRQLDNGVSGREDDDDVEMLIPI DGSSDFDVNDCSRPLDLASDQGLRQPYNATNPGVRPSNRDGPCECGIVHTAQIPDT CLEVTLKNETSDDEALLC
	SEQ ID NO: 137 1389 bp
NOV31h, CG51264-08 DNA Sequence	AATGGTGCTCTTGCAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAACTGCTTGT GGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGCTGGCCT TCTGAATATCCTGCAAAAACCACTGTAGCTGGTTCATAAGGGCAAACCCAGGCGAAATC ATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTGGACTGG TTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACAATTCCA CCTCCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTCATTCCGGATGACAACATC TCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATCTGAGGAACCAAATTTGTGCT TGTGATCAGTTTCGTTGTGGTAATGGAAAGTGTATACCAGAAGCCTGGAATGTAATAAC ATGGATGAATGTGGAGATAGTTCCGATGAAGAGATCTGTGCCAAAGAAGCAAATCCTCCA ACTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAGTTCAGTGTTTATCCCGTTTACC AAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGCCTTGAC CTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAATATTTTTAT GGTACTTTTAAATCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGCACCTGG TTAATAGACACTGGTGATCACCCTAAAGTCATTTTACGCTTCACTGACTTTAACTTGAT GGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCACACAAG CTTTTGCCTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCTTCTCT GGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTTAATGCT ACTTACCAAGTAGATGGGTCTGTTTGCATGGGAAATACCTGTGGAGGTAAGTGGGGG TGTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGGGATGAA ACCAATTGTACCATGTGTGCGAGGAAGAATTTCCATGTTCCCGAAATGGTGTCTGTTAT CCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAAAAAAC TGCTTTTTTGGCAACCAGGAAATTTCCATTGTAAAAACAATCGTGTGTGTTTGAAAGT TGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGCCAGTA ATCGTGCCT
	ORF Start: at 1 ORF Stop: end of sequence
	SEQ ID NO: 138 463 aa MW at 52053.1kD
NOV31h, CG51264-08 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWPSEYPAKTNCSWFIRANPGEI ITISFQDFDIQGSRRCLNDWLTIEYKNIESYRACGSTIPPPYISSQDHIWIRFHSDDNI SRKGFRLAYFSKSEEPNACDQFRGNGKCIPEAWKCNMDECGDSSDEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTCLESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDLEENPHK LLRVLTAFDHAPLTVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCLPWEIPCGGNWG CYTEQQRCDGYWHCPNGRDETNTMCQKEEFPCSRNGVCYPRSDRCNYQNHCPNGSDEKN CFFCQPGNFHCKNNRNVFESWVCDSDDCGDSDEENCPVIVP
	SEQ ID NO: 139 1389 bp
NOV31i, CG51264-09 DNA Sequence	AATGGTGCTCTTGCAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAACTGCTTGT GGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGCTGGCCT TCTGAATATCCTGCAAAAACCACTGTAGCTGGTTCATAAGGGCAAACCCAGGCGAAATC ATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTGGACTGG TTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACAATTCCA CCTCCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTCATTCCGGATGACAACATC TCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATCTGAGGAACCAAATTTGTGCT TGTGATCAGTTTCGTTGTGGTAATGGAAAGTGTATACCAGAAGCCTGGAAATGTAATAAC ATGGATGAATGTGGAGATAGTTCCGATGAAGAGATCTGTGCCAAAGAAGCAAATCCTCCA ACTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAGTTCAGTGTTTATCCCGTTTACC AAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGCCTTGAC CTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAATATTTTTAT GGTACTTTTAAATCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGCACCTGG TTAATAGACACTGGTGATCACCCTAAAGTCATTTTACGCTTCACTGACTTTAACTTGAT GGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCACACAAG CTTTTGCCTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCTTCTCT GGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTTAATGCT ACTTACCAAGTAGATGGGTCTGTTTGCATGGGAAATACCTGTGGAGGTAAGTGGGGG

	TGT TACTATCTAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAATGGAAGGGATGAA ACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCGCGAAATGGTGTCTGTTAT CCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAAAAAAC TGCTTTTTTTGCCAACCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTTGAAAGT TGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGCCAGTA ATCGTGCCT		
	ORF Start: at 1		ORF Stop: end of sequence
	SEQ ID NO: 140	463 aa	MW at 52053.1kD
NOV31i, CG51264-09 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWPSEYPAKTNCSWFIRANPGEI ITISFQDFDIQGSRRCLDWLTIETYKNIESYRACGSTIPPPYISSQDHIWIRFHSDDNI SRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNMDECGDSSDEEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTCPLPESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDShAPLTVVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCLPWEIPCGGNWG CYTEQQRCDGYWHCPNGRDETNCMTQKKEFP CSRNGVCYPRSDRCNYQNHCPNGSDEKN CFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSDEENCPIVIP		
	SEQ ID NO: 141	1401 bp	
NOV31j, CG51264-10 DNA Sequence	GGTACCAATGGTGCTCTTGCAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAACT ACTTGTGGAGAGACTCCAGGGCAAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGC TGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTTCATAAGGGCAAACCCAGGC GAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTG GACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACA ATTCCACCTCCGTATATCTCTTCACAAGACCACATCTGGATTAGGTTTCATTCCGGATGAC AACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATCTGAGGAACCAAT TGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAGTGTATACCAGAAGCCTGGAATGT AATAACATGGATGAATGTGGAGATAGTTCGGATGAAGAGATCTGTGCCAAGAAGCAAT CCTCCAACCTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAAGTTCAGTGTATTATCCCGT TTTACCAAGTTTACACTGCTCCCTCCCGAATCTTTAAATGTGATGGGAACATTGACTGC CTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAAATAT TTTTATGGTACTTTTAATTCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGC ACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTTCACTGACTTTAA CTTGATGGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCA CACAAGCTTTTGCCTGTGTGTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCT TCTTCTGGACAGATAAGGGTACATTTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTT AATGCTACTTACCAAGTAGATGGGTCTGTTTGCCATGGGAAATACCCTGTGGAGGTAAC TGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGG GATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTC TGTTATCCTCGTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAA AAAACTGCTTTTTTTTGCCAACCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTT GAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGC CCAGTAATCGTGCCTCGGCCG		
	ORF Start: at 7		ORF Stop: at 1396
	SEQ ID NO: 142	463 aa	MW at 52023.1kD
NOV31j, CG51264-10 Protein Sequence	NGALAEHSENVHISGVSTTCGETPGQIRAPSGIITSPGWPSEYPAKINCSWFIRANPGEI ITISFQDFDIQGSRRCLDWLTIETYKNIESYRACGSTIPPPYISSQDHIWIRFHSDDNI SRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNMDECGDSSDEEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTCPLPESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDShAPLTVVSSSGQIRVHFCADKVNAAARGFNATYQVDGFCLPWEIPCGGNWG CYTEQQRCDGYWHCPNGRDETNCMTQKKEFP CSRNGVCYPRSDRCNYQNHCPNGSDEKN CFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSDEENCPIVIP		
	SEQ ID NO: 143	1401 bp	
NOV31k, CG51264-11 DNA Sequence	GGTACCAATGGTGCTCTTGCAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAACT GCTTGTGGAGAGACTCCAGAGCAAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGC TGGCCTTCTGAATATCCTGCAAAAACCAACTGTAGCTGGTTCATAAGGGCAAACCCAGGC GAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTG		

	GACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACA ATTCCACCTCCGTATATCTCTTACACAAGACCACATCTGGATTAGGTTTCATTCCGATGAC AACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTTCAGGGAAATCTGAGGAACCAAAT TGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAGTGTATACCAGAAGCCTGGAAATGT AATAACATGGATGAATGTGGAGATAGTCCGATGAAGAGATCTGTGCCAAAGAAGCAAAT CCTCCAAGTGTGCTGCTTTTTCAACCCTGTGCTTACAACAGTTCAGTGTTTATCCCGT TTTACCAAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGC CTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAAATAT TTTTATGGTACTTTTAATCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGC ACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTTCACTGACTTTAAA CTTGATGGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCA CACAAGCTTTTGCCTGTGTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCT TCTTCTGGACAGATAAGGGTACATTTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTT AATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCTGTGGAGGTAAC TGGGGGTGTTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGG GATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTC TGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAA AAAACTGCTTTTTTTTGCCAACCCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTT GAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGC CCAGTAATCGTGCTCTCGGCCG		
	ORF Start: at 7		ORF Stop: at 1396
	SEQ ID NO: 144	463 aa	MW at 52053.1kD
NOV31k, CG51264-11 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITS PGWSEYPAKTNCSWFI RANPGEI ITISFQDFDIQGSRRCLNDWLT IETYKNIESYRACGSTIPPPYISSQDHIWIRFHSDDNI SRKGFRLAYFSGKSEEPNCADQFR CGNGKCIPEAWKCNMDECGDSSDEEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTC LPESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDSDHAPLTVVSSSGQIRVHF CADKVNAARGFNATYQVDGFCLPWEIPCGGNWG CYTEQQRCDGYWHCPNGRDETNCTMCQKEEFP CSRNGVCYPRSDRCNYQNHCPNGSDEKN CFFCQPGNFHCKNNRCVFESWVCDSDDCGDSDEENCPIVIP		
	SEQ ID NO: 145	1401 bp	
NOV311. CG51264-12 DNA Sequence	GGTACCAATGGTGCTCTTG CAGAACATTCTGAAAATGTGCATATTT CAGGAGTGTCAACT GCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCCAGGC TGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTTCTAAGGGCAAACCCAGGC GAAATCATTACTATAAGTTTT CAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTG GACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACA ATTCCACCTCCGTATATCTCTT CACAAGACCACATCTGGATTAGGTTTCATTCCGATGAC AACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTTCAGGGAAATCTGAGGAACCAAAT TGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAGTGTATACCAGAAGCCTGGAATGT AATAACATGGATGAATGTGGAGATAGTTCGATGAAGAGATCTGTGCCAAAGAAGCAAAT CCTCCAAGTGTGCTGCTTTTTCAACCCTGTGCTTACAACAGTTCAGTGTATTATCCCGT TTTACCAAAGTTTACACTTGCCTCCCCGAATCTTTAAATGTGATGGGAACATTGACTGC CTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAAATAT TTTTATGGTACTTTTAATCTCCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGC ACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTTCACTGACTTTAAA CTTGATGGTACTGGTTATGGTGATTATGTCAAAATATATGATGGATTAGAGGAGAATCCA CACAAGCTTTTGCCTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCT TCTTCTGGACAGATAAGGGTACATTTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTT AATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCTGTGGAGGTAAC TGGGGGTGTTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGG GATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTC TGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAA AAAACTGCTTTTTTTTGCCAACCCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTT GAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGC CCAGTAATCGTGCTCTCGGCCG		
	ORF Start: at 7		ORF Stop: at 1396
	SEQ ID NO: 146	463 aa	MW at 52065.2kD

NOV31l, CG51264-12 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWPSEYPAKINC SWFIRANPGEI ITISFQDFDIQGSRRCNLDWLTITETKYNIESYRACGSTIPPPYISSQDHIWIRFHSDNI SRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNMDECGDSSDEEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFD SHAPLTVVSSSGQIRVHFCADKVNAARGFNATYQVDGFCLPWEIPCGGNWG CYTEQQRCDGYWHCPNGRDETNCMTQKKEFPCSRNGVCYPRSDRCNYQNHCPNGSDEKN CFFCQPGNFHCKNNRCVFESWVCDSDQDDCGDGSDEENCPVIVP
	SEQ ID NO: 147 1401 bp
NOV31m, CG51264-13 DNA Sequence	GGTACCAATGGTGTCTTTCGAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAAC TGCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCAG GCTGGCCTTCTGAATATCCTGCAAAAATCACTGTAGCTGGTTTCATAAGGGCAAACCA GGCGAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAA TTTGGACTGGTTGACAATAGAAACATACAGAATATTGAAAGTTACAGAGCTTGTGGTT CTACAATCCACCTCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTCATTG GATGACAACATCTCTAGAAAGGTTTCAGACTGGCATATTTTCAGGGAAATCTGAGGA ACCAAATTTGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAAGTGTATACCAGAAGCCT GGAAATGTAATAACATGGATGAATGTGGAGATAGTTCCGATGAAGAGATCTGTGCCAAA GAAGCAAATCCTCCAACCTGCTGTGCTTTTCAACCCTGTGCTTACAACCAAGTTCCAGTG TTTATCCCGTTTACCAAAGTTTACACTTGCCTCCCCGAATCTTAAATGTGATGGGA ACATTGACTGCCTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGC TGGCTAAATATTTTTATGGTACTTTTAATCTCCCAATTATCCAGACTTTTATCCTCC TGGGAAGCAATTGCACCTGGTTAATAGACACTGGTGATCACCGTAAAGCATTTTACGCT TCACTGACTTTAACTTGATGGTACTGGTTATGGTGATTATGTCAAAATATATGATGA TTAGAGGAGAATCCACACAAGCTTTTGCCTGTGTTGACAGCTTTTGATTCTCACGCACC TCTTACAGTTGTTTCTTCTTGACAGATAAGGGTACATTTTGTGCTGATAAAGTGA ATGCTGCAAGGGGATTTAATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAA ATACCCTGTGGAGGTAACCTGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTG GCATTGCCCAAATGGAAGGGATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTT CATGTTCCCGAAATGGTGTCTGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCAT TGCCCAAATGGCTCAGATGAAAAAACTGCTTTTGTGCCAACCAGGAAATTTCCATTG TAAAAACAATCGTTGTGTGTTTGAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTG ATGGCAGCGATGAAGAAAATTGCCAGTAATCGTGCCTCGGCCG
	ORF Start: at 7 ORF Stop: at 1396
	SEQ ID NO: 148 463 aa MW at 52065.2kD
NOV31m, CG51264-13 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWPSEYPAKINC SWFIRANPGEI IITISFQDFDIQGSRRCNLDWLTITETKYNIESYRACGSTIPPPYISSQDHIWIRFHSDNI NISRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNMDECGDSSDEEICAKEA NPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTCGQWL KYFYGTNSPNYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLE ENPHKLLRVLTAFD SHAPLTVVSSSGQIRVHFCADKVNAARGFNATYQVDGFCLPWEIP CGGNWGCYTEQQRCDGYWHCPNGRDETNCMTQKKEFPCSRNGVCYPRSDRCNYQNHCP NGSDEKNCFQCQPGNFHCKNNRCVFESWVCDSDQDDCGDGSDEENCPVIVP
	SEQ ID NO: 149 1401 bp
NOV31n, CG51264-14 DNA Sequence	GGTACCAATGGTGTCTTTCGAGAACATTCTGAAAATGTGCATATTTTCAGGAGTGTCAACT GCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAAGTGGCATAATCACAAGCCAGGC TGGCCTTCTGAATATCCTGCAAAAATCACTGTAGCTGGTTTCATAAGGGCAAACCCAGGC GAAATCATTACTATAAGTTTTTCAGGATTTTGATATTCAAGGATCCAGAAGGTGCAATTTG GACTGGTTGACAATAGAAACATACAGAATATTGAAAGTTACAGAGCTTGTGGTTCCACA ATTCCACCTCCGTATATCTCTTACAAGACCACATCTGGATTAGGTTTCATTGCGATGAC AACATCTCTAGAAAGGTTTCAGACTGGCATATTTTCAGGGAAATCTGAGGAACCAAT TGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAAGTGTATACCAGAAGCCTGGAAATGT AATAACATGGATGAATGTGGAGATAGTTCCGATGAAGAGATCTGTGCCAAAGAAGCAAAT CCTCCAACCTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAAGTTCCAGTGTATCCCGT TTTACCAAAGTTTACACTTGCCTCCCCGAATCTTAAATGTGATGGGAACATTGACTGC CTTGACCCAGGAGATGAGATAGACTGTGATGTGCCAACATGTGGGCAATGGCTAAATAT TTTTATGGTACTTTTAATCTCCAATTATCCAGACTTTTATCCTCCTGGAAGCAATTGC

	ACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTTCACTGACTTTAAA CTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATGGATTAGAGGAGAATCCA CACAAGCTTTTGGCGTGTGTTGACAGCTTTTGATTCTCATGCACCTCTTACAGTTGTTTCT TCTTCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGCTGCAAGGGGATTT AATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACCCTGTGGAGGTGAC TGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTGCCCAAATGGAAGG GATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTCCCGAAATGGTGTC TGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAATGGCTCAGATGAA AAAACTGCTTTTTTTTGCCAACCAGGAAATTTCCATTGTAAAAACAATCGTTGTGTGTTT GAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGATGAAGAAAATTGC CCAGTAATCGTGCCTCGGCCG		
	ORF Start: at 7		ORF Stop: at 1396
	SEQ ID NO: 150	463 aa	MW at 52050.1kD
NOV3In, CG51264-14 Protein Sequence	NGALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWPEYPAKINCSWFIRANPGEI ITISFQDFDIQGSRRCNLDWLTIIETYNIESYRACGSTIPPPYISSQDHIWIRFHSDDNI SRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNMDECGDSSDEEICAKEANPP TAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCNDGIDCLDPGDEIDCDVPTCGQWLKYFY GTFNSPNYPDFYPPGSNCTWLIDTGDHRKVI LRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDASHAPLTVSSSGQIRVHFCAKDVNAARGFNATYQVDGFCPLWEIPCGGDWG CYTEQQRCDGYWHCPNGRDETNCMCQKEEFCSRNGVCYPRSDRNYQNHCPNGSDEKN CFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSDSEENCPIVIP		
	SEQ ID NO: 151	2592 bp	
NOV3Io, CG51264-15 DNA Sequence	GGCCTGTCGCTGGAGCACAAAAGAGTCTCCGCGGTGGAGGTCTGCGTTGCTCTTGCTTTT CCTCGCTGGGGTGACGGAATGGTGCTCTTGCAGAACATTCTGAAAATGTGCATATTTT AGGAGTGTCAACTGCTTGTGGAGAGACTCCAGAGCAAATACGAGCACCAGTGGCATAAT CACAAGCCCAGGCTGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTTCATAAG GGCAAACCCAGGCGAAATCATTACTATAAGTTTTCAGGATTTTGATATTCAAGGATCCAG AAGGTGCAATTTGGACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTACAGAGC TTGTGGTTCACAATTCACCTCCGTATATCTCTTCACAAGACCACATCTGGATTAGGTT TCATTCCGATGACAACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGGGAAATC TGAGGAACCAAATTGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAGTGTATACCAGA AGCCTGGAATGTAATAACATGGATGAATGTGAGATAGTTCGATGAAGAGATCTGTGC CAAAGAAGCAAATCCTCCAACCTGCTGCTGCTTTTCAACCCTGTGCTTACAACCAAGTTCCA GTGTTTATCCCGTTTTTACCAAAGTTTACACTTGCTCCCGAATCTTTAAAATGTGATGG GAACATTGACTGCCTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAATGTGGGCA ATGGCTAAAATATTTTATGGTACTTTTAATTCTCCCAATTATCCAGACTTTTATCCTCC TGGGAAGCAATTGCACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTTACGCTT CACTGACTTTAACTTGATGGTACTGGTTATGGTGATTATGTCAAATATATGATGGATT AGAGGAGAATCCACACAAGCTTTTGGCGTGTGTTGACAGCTTTTGATTCTCATGCACCTCT TACAGTTGTTTCTTCTTCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGTGAATGC TGCAAGGGGATTTAATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGAAATACC CTGTGGAGGTAACTGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTGGCATTG CCCAAATGGAAGGGATGAAACCAATTGTACCATGTGCCAGAAGGAAGAATTTCCATGTTT CCGAAATGGTGTCTGTTATCCTCGTTCTGATCGCTGCAACTACCAGAATCATTGCCCAAA TGGCTCAGATGAAAAAACTGCTTTTTTTTGCCAACCAGGAAATTTCCATTGTAAAAACAA TCGTTGTGTGTTGAAAGTTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGGCAGCGA TGAAGAAAATTGCCAGTAATCGTGCTTACAAGAGTCATCACTGCTGCCGTATAGGGAG CCTCATCTGCGGCCTGTTACTCGTCATAGCATTGGGATGTACTTGTAAGCTTTATTCTCT GAGAATGTTTGAAGAAGATCATTGAAACACAGTTGTCAAGAGTGGAGCAGAATTGTT AAGAAGAGAAGCTCCTCCCTCGTATGGACAATTGATTGCTCAGGGTTTAATTCCACCAGT TGAAGATTTTCTGTTTGTTCACCTAATCAGGCTTCTGTTTGGAAAATCTGAGGCTAGC GGTACGATCTCAGCTTGATTGTTTACTTCAGTCAGGCTTCTATGGCAGGCAGATCAAGCAA CATTTGGAACCGTATTTTTTAATTTTGCAAGATCACGTCATTCTGGGTCAATGGCTTTGGT CTCAGCAGATGGAGATGAGGTTGTCCCTAGTCAGAGTACCAGTAGAGAACCTGAGAGAAA TCATACTCACAGAAGTTTGTTTTCCGTGGAGTCTGATGATACAGACACAGAAAATGAGAG AAGAGATATGGCAGGAGCATCTGGTGGGGTTCAGCTCCTTTGCCTCAAAAAGTCCCTCC CACAACGGCAGTAGAAGCGACAGTAGGAGCATGTGCAAGTTCCTCAACTCAGAGTACCCG AGGTGGTCATGCAGATAATGGAAGGGATGTGACAAGTGTGGAACCCCAAGTGTGAGTCC		

	AGCACGTCACCAGCTTACAAGTGCACCTCAGTCGTATGACTCAGGGGCTACGCTGGGTACG TTTTACATTAGGACGATCAAGTTCCTTAAGTCAGAACAGAGTCCTTTGAGACAACTTGA TAATGGGGTAAGTGAAGAGAAGATGATGATGATGTTGAAATGCTAATTCGAATTTCTGA TGGATCTTTCAGACTTTGATGTGAATGACTGCTCCAGACCTCCTCTTGATCTTGCCCTCAGA TCAAGGACAAGGGCTTAGACAACCATATAATGCAACAAATCCTGGAGTAAGGCCAAGTAA TCGAGATGGCCCCCTGTGAGCGCTGTGGTATTGTCCACACTGCCAGATACCAGACACTTG CTTAGAAGTAACACTGAAAAACGAAACGAGTGGTGATGAGGCTTTGTTACTTTGTTAGGT ACGAATCACATA		
	ORF Start: at 2	ORF Stop: TAG at 2576	
	SEQ ID NO: 152	858 aa	MW at 94777.5kD
NOV31o, CG51264-15 Protein Sequence	ACRWSTKESPRWRSALLLFLAGVYNGALAEHSENVHISGVSTACGETPEQIRAPSGII TSPGWSEYPKINCSWIFIRANPGEIITISFQDFDIQSRRCNLDWLTIETYKNIESYRA CGSTIPPPYISSQDHIWIRFHSDDNISRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPE AWKCNMDECGDSSDEEICAKEANPPTAAAFQPCAYNQFCLSRFTKVYTCLPESLKCDG NIDCLDLGDEIDCDVPTCGQWLKYFYGTFSNPYPDFYPPGSNCTWLIDTGDHRKVILRF TDFKLDGTGYGDYVKIYDGLEENPHKLLRLVLTAFDASHAPLTVVSSSGQIRVHFCADKVNA ARGFNATYQVDGFCLPWEIPCGGNWGCYTEQQRCDGYWHCPNGRDETNCMTCKKEFPSCS RNGVCYPRSDRCNYQNHCPNGSDEKNCFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSD EENCPIVIVPTRVITAAVIGSLICGLLLVIALGCTCKLYSLRMFERRSFETQLSRVEAELL RREAPPSYQGLIAQGLIPPVEDFPVCSPNQASVLENLRLAVRSQLGFTSVRLPMAGRSSN IWNRI FNFARSRHSGSLALVSADGDEVVPSQSTSREPERNHTRSLFSVESDDTDENER RDMAGASGGVAAPLPQKVPPTTAVEATVGACASSSTQSTRGGHADNDRDVTSEPPSVSP ARHQLTSALSMTQGLRWVFTLGRSSSLSONQSPLRQLDNGVSGREDDDDVEMLIPI SD GSSDFDVNDCSRPLDLASDQGGQLRQPYNATNPGRPSNRDGPCECERGIVHTAQIPDTC LEVTLKNETSGDEALLC		
	SEQ ID NO: 153	12560 bp	
NOV31p, CG51264-16 DNA Sequence	TATGGCCTGTCGCTGGAGCACAAAGAGTCTCCGCGTGGAGGCTGCGTTGCTCTTGCT TTTCCTCGCTGGGGTGACGCTTGTGGAGAGACTCCAGGGCAAATACGAGCACCAAGTGG CATAATCACAAAGCCAGGCTGGCCTTCTGAATATCCTGCAAAAATCAACTGTAGCTGGTT CATAAGGGCAAACCCAGGCGAAATCATTACTATAAGTTTTCAGGATTTTGATATTCAAGG ATCCAGAAGGTGCAATTTGGACTGGTTGACAATAGAAACATACAAGAATATTGAAAGTTA CAGAGCTTGTGGTTCCACAATTCCACCTCCGTATATCTCTTACAAAGACCACATCTGGAT TAGGTTTCATTTCGATGACAACATCTCTAGAAAGGGTTTCAGACTGGCATATTTTTCAGG GAAATCTGAGGAACCAAATTTGTGCTTGTGATCAGTTTCGTTGTGGTAATGGAAGTGTAT ACCAGAAGCCTGGAAATGTAATAACATGGATGAATGTGGAGATAGTTCGATGAAGAGAT CTGTGCCAAAGAAGCAAATCCTCCAACCTGCTGCTGCTTTTCAACCCCTGTGCTTACAACCA GTTCCAGTGTATATCCCGTTTACCAAAGTTTACACTTGCCTCCCCGAATCTTTAAAATG TGATGGGAACATTGACTGCCTTGACCTAGGAGATGAGATAGACTGTGATGTGCCAACATG TGGGCAATGGCTAAAATATTTTATGGTACTTTTAATCTCCCAATTTACGACTTTTA TCCTCCTGGAAGCAATTGCACCTGGTTAATAGACACTGGTGATCACCGTAAAGTCATTTT ACGCTTCACTGACTTTTAACTTGATGGTACTGGTTATGGTGATTATGTCAAAATATATGA TGGATTAGAGGAGAATCCACACAAGCTTTTTCGCTGTGTTGACAGCTTTTGATTCTCATGC ACCTCTTACAGTTGTTTCTTCTTCTGGACAGATAAGGGTACATTTTGTGCTGATAAAGT GAATGCTGCAAGGGGATTTAATGCTACTTACCAAGTAGATGGGTTCTGTTTGCCATGGGA AATACCCTGTGGAGGTAACCTGGGGGTGTTATACTGAGCAGCAGCGTTGTGATGGGTATTG GCATTGCCCAAATGGAAGGGATGAAACCAATGTACCATGTGCCAGAAGGAAGAATTTCC ATGTTCCCGAAATGGTGTCTGTTATCCTCGTTCGTGATCGCTGCAACTACCAGAATCATTG CCCAAATGGCTCAGATGAAAAAACTGCTTTTTTGGCAACCAGGAAATTTCCATTGTAA AAACAATCGTTGTGTGTTTGAAGATTGGGTGTGTGATTCTCAAGATGACTGTGGTGATGG CAGCGATGAAGAAAATTGCCCAAGTAATCGTGCCTACAAGAGTCATCACTGCTGCCGTCAT AGGGAGCCTCATCTGTGGCCTGTTACTCGTCATAGCATTGGGATGTACTGTGAAGCTTTA TTCTCTGAGAATGTTTGAAGAAGATCATTTGAAACACAGTTGTCAAGAGTGGAAGCAGA ATTGTTAAGAAGAGAAGCTCCTCCCTCGTATGGACAATTGATTGCTCAGGGTTTAATTC ACCAGTTGAAGATTTTCTGTTTGTTCACCTAATCAGGCTTCTGTTTTGGAAAATCTGAG GCTAGCGGTACGATCTCAGCTTGATTTACTTCAGTCAGGCTTCCTATGGCAGGCAGATC AAGCAACATTTGGAACCGTATTTTAATTTTGCAAGATCAGCTCATTCTGGGTCAATTGGC TTTGGTCTCAGCAGATGGAGATGAGGTTGTCCCTAGTCAGAGTACCAGTAGAGAACCTGA GAGAAATCATACTCACAGAAGTTTGTTCCTGGAGTCTGATGATACAGACACAGAAAA		

	TGAGAGAAGAGATATGGCAGGAGCATCTGGTGGGGTTGCAGCTCCTTTGCCTCAAAAAGT CCCTCCCACAACGGCAGTAGAAGCGACAGTAGGAGCATGTGCAAGTTCCTCAACTCAGAG TACCCGAGGTGGTCATGCAGATAATGGAAGGGATGTGACAAGTGGAACCCCAAGTGT GAGTCCAGCACGTCACCAGCTTACAAGTGCACTCAGTCGTATGACTCAGGGGCTACGCTG GGTACGTTTTTACATTAGGACGATCAAGTTCCTAAGTCAGAACCAGAGTCCTTTGAGACA ACTTGATAATGGGGTAAGTGAAGAGAAGATGATGATGATGTTGAAATGCTAATTCGAAT TTCTGATGGATCTTCAGACTTTGATGTGAATGACTGCTCCAGACCTCTTCTTGATCTTGC CTCAGATCAAGGACAAGGGCTTAGACAACCATATAATGCAACAAATCCTGGAGTAAGGCC AAGTAATCGAGATGGCCCCCTGTGAGCGCTGTGGTATTGTCCACACTGCCAGATACCAGA CACTTGCTTAGAAGTAACACTGAAAAACGAAACGAGTGATGATGAGGCTTTGTACTTTG TTAGGTACGAATCACATAAGGGCGATTCCAGCACCTGGCT		
	ORF Start: ATG at 2		ORF Stop: TAG at 2522
	SEQ ID NO: 154	840 aa	MW at 93049.7kD
NOV31p, CG51264-16 Protein Sequence	MACRWSTKESPRWRSALLLFLAGVYACGETPGQIRAPSGIITSPGWPSEYPKINCSEF IRANPGEIITISFQDFDIQGSRRCNLDWLTITETYNIESYRACGSTIPPPYISSQDHIWI RFHSDDNISRKGFRLAYFSGKSEEPNCACDQFRGNGKCIPEAWKCNNMDECGDSSDEEI CAKEANPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTC GQWLKYFYGTFFNSPNYPDFYPPGSNCTWLIIDTGDHRKVILRFTDFKLDGTGYGDYVKIYD GLEENPHKLLRLVLTAFDSHAPLTVVSSSGQIRVHFCADKVNAARGFNATYQVDFCLPWE IPCGGNWGCYTEQQRCDGYWHCPNGRDETNCTMCQKEEFPCSRNGVCYPRSDRCNYQNH PNGSDEKNCFFCQPGNFHCKNNRCVFESWVCDSDDCGDSDEENCPVIVPTRVITA AVI GSLICGLLLVIALGCTCKLYSLRMFERRSFETQLSRVEAELLRREAPPYQGLIAQGLIP PVEDFPVCSPNQASVLENLRLAVRSQLGFTSVRLPMAGRSSNIWNRIFFNARSRHSGSLA LVSADGDEVVPSQSTSREPERNHTRSLFSVESDDTDENERRDMAGASGGVAAPLPQKV PPTTAVEATVGACASSSTQSTRGGHADNGRDVTSVEPPSVSPARHQLTSALSRTQGLRW VRFTLGRSSSLSQNSPLRQLDNGVSGREDDDDVEMLIPI SDGSSDFDVNDCSRPLDLA SDQGGQLRQPYNATNPGVRPSNRDGPCECERGIVHTAQIPDTCLEVLTKNETSDDEALLLC		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 31B.

Table 31B. Comparison of NOV31a against NOV31b through NOV31p.		
Protein Sequence	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV31b	1..423 1..442	422/442 (95%) 422/442 (95%)
NOV31c	1..423 1..423	422/423 (99%) 422/423 (99%)
NOV31d	1..840 1..840	826/840 (98%) 826/840 (98%)
NOV31e	1..840 1..837	815/840 (97%) 816/840 (97%)
NOV31f	1..423 40..462	422/423 (99%) 422/423 (99%)
NOV31g	1..840 1..859	826/859 (96%) 826/859 (96%)
NOV31h	27..471 19..463	430/445 (96%) 430/445 (96%)

NOV31i	27..471 19..463	430/445 (96%) 430/445 (96%)
NOV31j	28..471 20..463	429/444 (96%) 429/444 (96%)
NOV31k	27..471 19..463	430/445 (96%) 430/445 (96%)
NOV31l	27..471 19..463	431/445 (96%) 431/445 (96%)
NOV31m	27..471 19..463	431/445 (96%) 431/445 (96%)
NOV31n	27..471 19..463	429/445 (96%) 430/445 (96%)
NOV31o	2..840 1..858	823/858 (95%) 823/858 (95%)
NOV31p	1..840 1..840	825/840 (98%) 825/840 (98%)

Further analysis of the NOV31a protein yielded the following properties shown in Table 31C.

Table 31C. Protein Sequence Properties NOV31a	
PSort analysis:	0.4600 probability located in plasma membrane; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Cleavage site between residues 28 and 29

- A search of the NOV31a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 31D.

Table 31D. Geneseq Results for NOV31a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB70544	Human PRO14 protein sequence SEQ ID NO:28 - <i>Homo sapiens</i> , 840 aa. [WO200110902-A2, 15-FEB-2001]	1..840 1..840	840/840 (100%) 840/840 (100%)	0.0

AAO20441	Protein of the human cancer suppressor gene 98 - <i>Homo sapiens</i> , 894 aa. [CN1328030-A, 26-DEC-2001]	1..840 36..894	840/859 (97%) 840/859 (97%)	0.0
AAU14316	Human novel protein #187 - <i>Homo sapiens</i> , 859 aa. [WO200155437-A2, 02-AUG-2001]	1..840 1..859	840/859 (97%) 840/859 (97%)	0.0
AAB42317	Human ORFX ORF2081 polypeptide sequence SEQ ID NO:4162 - <i>Homo sapiens</i> , 859 aa. [WO200058473-A2, 05-OCT-2000]	1..840 1..859	840/859 (97%) 840/859 (97%)	0.0
AAY02381	Polypeptide identified by the signal sequence trap method - <i>Homo sapiens</i> , 859 aa. [WO9918126-A1, 15-APR-1999]	1..840 1..859	840/859 (97%) 840/859 (97%)	0.0

In a BLAST search of public sequence databases, the NOV31a protein was found to have homology to the proteins shown in the BLASTP data in Table 31E.

Table 31E. Public BLASTP Results for NOV31a				
Protein Accession Number	Protein/Organism/Length	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC33422	Sequence 27 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 840 aa.	1..840 1..840	840/840 (100%) 840/840 (100%)	0.0
Q9Y561	ST7 protein - <i>Homo sapiens</i> (Human), 859 aa.	1..840 1..859	840/859 (97%) 840/859 (97%)	0.0
Q9BE74	Hypothetical 73.8 kDa protein - <i>Macaca fascicularis</i> (Crab eating macaque) (Cynomolgus monkey), 672 aa.	169..840 1..672	663/672 (98%) 666/672 (98%)	0.0
CAC38967	Sequence 19 from Patent WO0119856 - <i>Homo sapiens</i> (Human), 430 aa.	1..423 1..423	422/423 (99%) 422/423 (99%)	0.0
CAC33423	Sequence 29 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 449 aa.	1..423 1..442	422/442 (95%) 422/442 (95%)	0.0

Pfam analysis predicts that the NOV31a protein contains the domains shown in Table 31F.

Table 31F. Domain Analysis of NOV31a			
Pfam Domain	NOV31a Match Region	Identities/ Similarities for the Matched Region	Expect Value
CUB	28..137	41/119 (34%) 89/119 (75%)	3.9e-31
ldl_recept_a	145..183	19/43 (44%) 30/43 (70%)	2.1e-10
ldl_recept_a	194..237	17/47 (36%) 27/47 (57%)	6.6e-05
CUB	240..350	42/120 (35%) 83/120 (69%)	6.6e-23
ldl_recept_a	354..393	15/43 (35%) 23/43 (53%)	0.072
ldl_recept_a	394..431	17/44 (39%) 27/44 (61%)	0.045
ldl_recept_a	432..468	21/43 (49%) 32/43 (74%)	1.4e-11

Example 32.

- 5 The NOV32 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 32A.

Table 32A. NOV32 Sequence Analysis			
	SEQ ID NO: 155	2365 bp	
NOV32a, CG52423-01 DNA Sequence	ACGCGTTCGATATCCGCCCGAGCTCCGGCGCAGCTCCTCCACCTTGGAGCTCATGAGAG CAGGCCTGGTGGTGAGCAGGGACGGTGCACCGGACGGCGGGATCGAGCAAATGGGTCTGG CCATGGAGCACGGAGGGTCTACGCTCGGGCGGGGGCAGCTCTCGGGGCTGCTGGTATT ACCTGCGCTACTTCTTCTCTTCTGCTCTCCCTCATCCAATTCCTCATCATCCTGGGGCTCG TGCTCTTCATGGTCTATGGCAACGTGCACGTGAGCACAGAGTCCAACTGCAGGCCACCG AGCGCCGAGCCGAGGGCCTATACAGTCAGCTCCTAGGGCTCACGGCCTCCCACTCCA TGACCAAGGAGCTCAACTTCACCAACCGCGCCAAGGATGCCATCATGCAGATGTGGCTGA ATGCTCGCCGCGACCTGGACCGCATCAATGCCAGCTTCCGCCAGTGCCAGGGTGACCGGG TCATCTACACGAACAATCAGAGGTACATGGCTGCCATCATCTTGAGTGAGAAGCAATGCA GAGATCAATTCAAGGACATGAACAAGAGCTGCGATGCCTTGCTCTTCATGTGAATCAGA AGGTGAAGACGCTGGAGGTGGAGATAGCCAAGGAGAAGACCATTTGCACTAAGGATAAGG AAAGCGTGCTGTGAACAAACGCGTGGCGGAGGAACAGCTGTTGAATGCGTGAAAACCC GGGAGCTGCAGCACCAAGAGCGCCAGCTGGCCAAGGAGCAACTGCAAAAAGGTGCAAGCCC TCTGCCTGCCCCCTGGACAAGGACAAGTTTGAGATGGACCTTCGTAACCTGTGGAGGGACT CCATTATCCACGACGCTGGACAACCTGGGTTACAACCTCTACCATCCCCTGGGCTCGG AATTGGCCTCCATCCGCAGAGCCTGCGACCACATGCCAGCCTCATGAGCTCCAAGGTGG		

	AGGAGCTGGCCCGGAGCCTCCGGGCGGATATCGAACGCGTGGCCCGGAGAACTCAGACC TCCAACGCCAGAAGCTGGAAGCCCAGCAGGGCCTGCGGGCCAGTCAGGAGGCGAAACAGA AGGTGGAGAAGGAGGCTCAGGCCCGGAGGCCAAGCTCCAAGCTGAATGCTCCCGGCAGA CCCAGCTAGCGCTGGAGGAGAAGGCGGTGCTGCGGAAGGAACGAGACAACCTGGCCAAGG AGCTGGAAGAGAAGAAGAGGGAGGCGGAGCAGCTCAGGATGGAGCTGGCCATCAGAACT CAGCCCTGGACACCTGCATCAAGACCAAGTCGACGCCGATGATGCCAGTGTCAAGGCCCA TGGGCCCTGTCCCAACCCCCAGCCCATCGACCCAGCTAGCCTGGAGGAGTTCAAGAGGA AGATCCTGGAGTCCCAGAGGCCCTGTCAGGCATCCCTGTAGCCCCATCCAGTGGCTGAG GAGGCTCCAGGCCTGAGGACCAAGGGATGGCCCGACTCGGCGGTTTTCGGGAGGATGCAGG GATATGCTCAGCGCCCGACACAACCCCTCCCGCCGCCCAACCAACCCAGGGCCACC ATCAGACAACTCCCTGCATGCAAACCCCTAGTACCCTCTCACACCCGCACCCGCGCTCA CGATCCCTCACCCAGAGCACACGGCCGCGGAGATGACGTCACCCAAGCAACGGCGCTGAC GTCACATATACCGTGGTGATGGCGTCACGTGGCCATGTAGACGTCACGAAGAGATATAG CGATGGCGTCGTGCAGATGCAGCAGCTCGCACACAGACATGGGGAACTTGGCATGACGTC ACACCGAGATGCAGCAACGACGTCACGGGCCATGTGACGTCACACATATTAATGTCACA CAGACGCGGCGATGGCATCACACAGACGGTGATGATGTACACACAGACACAGTGCACAAC ACACACCATGACAACGACACCTATAGATATGGCACCAACATCACATGCACGCATGCCCTT TCACACACACTTTCTACCCAATTCTCACCTAGTGTACGTTCCCCGACCCTGGCACACG GGCCAAGGTACCCACAGGATCCCATCCCTCCCGCACAGCCCTGGGCCCCAGCACCTCCC CTCCTCCAGCTTCCTGGCCTCCAGCCACTTCCTCACCCCCAGTGCCTGGACCCGGAGGT GAGAACAGGAAGCCATTACCTCCGCTCCTTGAGCGTGAGTGTTCAGGACCCCTCGG GGCCCTGAGCCGGGGTGAGGGTCACCTGTTGTGCGGAGGGGAGCCACTCCTTCTCCCC AACTCCAGCCCTGCCTGTGGCCGTTGAAATGTTGGTGGCACTTAATAAATATTAGTAA ATCCTTAAAAAAAAAAAAAAAAAAAA
	ORF Start: ATG at 54 SEQ ID NO: 156 461 aa ORF Stop: TGA at 1437 MW at 52503.8kD
NOV32a, CG52423-01 Protein Sequence	MRAGLVVSRDGPAGDGGIEQMGLAMEHGGSYARAGGSSRGWYYLRYFFLVSLIQFLIIL GLVLFMVYGNVHVSTESNLQATERRAEGLYSQLLGLTASQSNLTKELNFTTRAKDAIMQM WLNARRDLDRINASFRQCQGDRIYVYTNQRYMAAIIILSEKQCRDQFKDMNKS CDALLFML NQKVKTLEVEIAKEKTICTKDKEVLLNKRVAEEQLVECVKTRQLQHQERQLAKEQLQKV QALCLPLDKDKFEMDLRLNLWRDSTIPRSLDNLGYNLYHPLGSELASIRACDHMPSLMSS KVEELARSLRADIERVARENSDLQRQKLEAQQGLRASQEAQKQVEKEAQAREAKLQAECS RQTQLALEEKAVLRKERDNLAKELEKKREAEQLRMELAIRNSALDTCIKTKSQPMMPVS RPMGPVPNPQPIDPASLEEFKRKILESQRPPAGIPVAPSSG

Twenty polymorphic variants of NOV32a have been identified and are shown in Table 41L. Further analysis of the NOV32a protein yielded the following properties shown in Table 32B.

Table 32B. Protein Sequence Properties NOV32a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.6000 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.3000 probability located in Golgi body
SignalP analysis:	Cleavage site between residues 70 and 71

A search of the NOV32a protein against the Geneseq database, a proprietary
5 database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 32C.

Table 32C. Geneseq Results for NOV32a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB42154	Human ORFX ORF1918 polypeptide sequence SEQ ID NO:3836 - <i>Homo sapiens</i> , 479 aa. [WO200058473-A2, 05-OCT-2000]	1..461 19..479	461/461 (100%) 461/461 (100%)	0.0
AAM41619	Human polypeptide SEQ ID NO 6550 - <i>Homo sapiens</i> , 457 aa. [WO200153312-A1, 26-JUL-2001]	7..461 3..457	454/455 (99%) 454/455 (99%)	0.0
AAE06600	Human protein having hydrophobic domain, HP10787 - <i>Homo sapiens</i> , 442 aa. [WO200149728-A2, 12-JUL-2001]	20..461 1..442	442/442 (100%) 442/442 (100%)	0.0
AAM39833	Human polypeptide SEQ ID NO 2978 - <i>Homo sapiens</i> , 442 aa. [WO200153312-A1, 26-JUL-2001]	20..461 1..442	439/442 (99%) 439/442 (99%)	0.0
AAY12280	Human 5' EST secreted protein SEQ ID NO:311 - <i>Homo sapiens</i> , 105 aa. [WO9906548-A2, 11-FEB-1999]	20..124 1..105	104/105 (99%) 104/105 (99%)	3e-54

In a BLAST search of public sequence databases, the NOV32a protein was found to have homology to the proteins shown in the BLASTP data in Table 32D.

Table 32D. Public BLASTP Results for NOV32a				
Protein Accession Number	Protein/Organism/Length	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAD39027	Hypothetical protein - <i>Homo sapiens</i> (Human), 456 aa (fragment).	6..461 1..456	456/456 (100%) 456/456 (100%)	0.0
Q9BX97	PV1 protein - <i>Homo sapiens</i> (Human), 442 aa.	20..461 1..442	442/442 (100%) 442/442 (100%)	0.0
Q9BZD5	Fenestrated-endothelial linked structure protein - <i>Homo sapiens</i> (Human), 442 aa.	20..461 1..442	441/442 (99%) 441/442 (99%)	0.0

BAC04681	CDNA FLJ38711 fis, clone KIDNE2003507, highly similar to <i>Homo sapiens</i> PV1 protein (PLVAP) mRNA - <i>Homo sapiens</i> (Human), 437 aa.	20..461 1..437	436/442 (98%) 436/442 (98%)	0.0
Q91VC4	MECA32 (Similar to PLASMALEMMA vesicle associated protein) - <i>Mus musculus</i> (Mouse), 438 aa.	20..461 1..438	273/442 (61%) 351/442 (78%)	e-156

PFam analysis predicts that the NOV32a protein contains the domains shown in Table 32E.

Table 32E. Domain Analysis of NOV32a			
Pfam Domain	NOV32a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 33.

The NOV33 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 33A.

Table 33A. NOV33 Sequence Analysis			
	SEQ ID NO: 157	1482 bp	
NOV33a, CG52919-01 DNA Sequence	CCAGGCGCTGGCCGTGGTGTGATTCTGTCTAGGCGCTGGCGGCGGCAGCGGCGGTGACGG CTGCGGCCCCGCTCCCTCTACCCGGCCGACCCGGCTCTGCCCCGCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCGCGGTCCAGCCCAGGGCGCGGCCGCAACCAGCACCATG CGCCCGGTAGCCCTGCTGCTCCTGCCCTCGCTGTGGCGCTCCTGGCTCACGGACTCTCT TTAGAGGCCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGTCAACAGCC CCACCTTGAAGCTGCTCAACCACCACCCGCTGCTTGAGGAATTCCTACAAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC TTCACCCCAAGTCCCCTTCCCGCCTGGCCAACCAGGACAGCCGCCCTGTCTTTACCAGC CCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAAGGAGGGACCCTGGAGT CCGGAGTCAGAGTCCCCTATGCTTCGAATCACAGCTCCCCTACCTCCAGGGCCAGCATG GCAGTGCCCAACCCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCCAAGAGGGTCTGAGACATGGGAAGGCCGTGGGTGTCAGAGGTTGTGTCC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCTCCACAGCTTCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGTCAGCTACCTGCTGGCTTGAGATGTGGAATGGGGATGGGGGAGGCTGCGGGCCCC TAAAAGCCTGTCTGTGACACTGTGCCAGCCTGCCCTGCCCTTTGGCACCAGGGCCAGCC TGCAGGAGGCATGTAGATTGGACCCAGATAGACCTGAGCTCAAATCCTGATTCTTCAGCC AAGTACAGTGGCTCATGCTGTAATCCAGCACTTTGGGAGGCAGAGGCCAGTGGATCAT CTGAGGTGAGGAGTTCAAGACCTCCTGGCCAACATGGCGAAACACCATCTCTACTAAAA ATACAAAAATGAGCCGGGCATGGTGGTGGGCACCTGTAATCCAGCTACTCGGAGGCTG AGGCAGGAGAATCACTCAAACCTGGGAGGCAGAGGTGTCAGTGAGCTGAGATTGCACCAT TGCACTCCAGCCTGGGCAACAGAGCGAGACTCTGTCTCAAAAAGAAAAAATCTTGATTCT TTCCAACATAACATGACCTAGGAATTCATTTAACATCTCATCTCTGAGCCTCATCTG		

	TAAATGGCAATAAGAAAATAAACTTCTGGCTAGAAAAAAA		
	ORF Start: ATG at 178		ORF Stop: TAA at 961
	SEQ ID NO: 158	261 aa	MW at 27471.8kD
NOV33a, CG52919-01 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKQAPGIEETDGLTAAPTPEQPERGVHVVTT APTLKLLNHHPLLEEFLOEGLKGDDELRPALPFQPDPPAPFTPSPLRLANQDSRPVFT SPTPMAAAVPTQPQSKEGPWSPESPSMLRITAPLPPGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWWAEVVSQAGIGIQGTITSSTASGDDEETTTTTTIIITTTITTVQT PGQLPAGLQMWKMGWGRLLRGP		
	SEQ ID NO: 159	2127 bp	
NOV33b, CG52919-02 DNA Sequence	CCAGGCGCTGGCCGTGGTGCTGATCTGTGTCAGGCGCTGGCGGGCGGCAGCGGCGGTGACGG CTGCGGGCCCGCTCCCTCTACCCGGCCGGACCCGGCTCTGCCCCCGCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCGCGGTCCAGCCAGGGCGGGCGGCACACAGCACCATG CGCCCGGTAGCCCTGCTGCTCCTGCGCTCGCTGCTGGCGCTCCTGGCTCACGGACTCTCT TTAGAGGCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGTACACAACAGCC CCCACCTTGAAGCTGCTCAACCACACCCGCTGCTTGAGGAATTCCTACAAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC TTCACCCCAAGTCCCTTCCCGCTGGCCAAACAGGACAGCCCGCTGTCTTTACAGC CCCACTCCAGCATGGCTGCGGTACCACTCAGCCCCAGTCCAAGAGGGACCCCTGGAGT CCGGAGTCAGAGTCCCCTATGCTTGAATCACAGTCCCCTACCTCCAGGGCCAGCATG GCAGTGGCCACCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCCAAGAGGGTCTGGAGACATGGGAAGGCCGTGGGTGACAGGTTGTGTCC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCACAGCTTCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGCCCTTGTAGCTGGAATTTCTCAGGCCAGAGGGCTCTCTGGACTCCCTACAGACCTC AGCTCCCCCACTGATGTGGCCTGGACTGCTTCTCTACATCTCTGTCTACCTGGCTAT GGCGTGGAAATCAAGGTCCAGAATATCAGCCTCCGGAAGGGGAGACAGTACTGTGGAA GGCCTGGGGGGCCTGACCACTGCCCTGGCCAAACAGTCTTCTGCTGCGGGGCCAA GTATCCCGCAGCCCCACCAAGCGGCCCTGAGGTTCCAGAGCCTCCCGCCACCGGCT GGCCCTGGCACCTTCCATTTCCATTACCAAGCCTATCTCCTGAGCTGCCACTTTCCCGCT CGTCCAGCTTATGGAGATGTGACTGTCAACAGCCTCCACCCAGGGGGTAGTGCCCGCTTC CATTTGTGCACTGGCTACCAGCTGAAGGGCGCCAGGCATCTCACCTGTCTCAATGCCACC CAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGGCGGAGTGATCCGC AATGGCACCAACCGGCCGATCGTCTCTCCAGGCTTCCCGGGCACTACAGCAACAACCTC ACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGGCTACACCTGCATTTGAGAG GTTTCCCTGGCAGAGGATGATGACAGGCTCATCATTCGCAATGGGACAACTGGAGGCC CCACCACTGGGAAAAAGCTCCCTGCAGCTGCCCCGCCCCCGCCCCGCCCCCTACAACCG ATTACCATAGAGTCAGCGTTTGACAATCCAATTACGAGACTGGAGAGACGAGAGAATAT GAAGTCTCCATCTAGGTGGGGCAGTCTAGGGAAGTCAACTCAGACTTGCAACACAGTCC AGCAGCAAGGCTCCTTGCTTCTGCTGTCCCTCCACCTCCTGTATATACCACCTAGGAGG AGATGCCACCAAGCCCTCAAGAAGTTGTGCCCTTCCCGCCTGCGATGCCACCATGGCC TATTTCTTGGTGTCATTGCCCACTTGGGGCCCTTGCAATTGGGCCATGTACAGGGGGCAT CTACCTGTGGGGAAGAACATAGCTGGGAGCACAGCTTCAACAGCCAGCATTCCTTGAGC CTCCTTCATGGCCCTGGGACCAAGCTGGGGAACACANTTAGGCAGGAGCAGGGAGTTACC TTGTTTCACATGACCACCAACCATTC		
	ORF Start: ATG at 178		ORF Stop: TAG at 1753
	SEQ ID NO: 160	525 aa	MW at 56283.7kD
NOV33b, CG52919-02 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKQAPGIEETDGLTAAPTPEQPERGVHVVTT APTLKLLNHHPLLEEFLOEGLKGDDELRPALPFQPDPPAPFTPSPLRLANQDSRPVFT SPTPMAAAVPTQPQSKEGPWSPESPSMLRITAPLPPGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWWAEVVSQAGIGIQGTITSSTASGDDEETTTTTTIIITTTITTVQT PGPCSWNFSGPEGLSDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVQNISLREGETVT EGLGGPDPLPLANQSFLLRQGVIRSPHTQAALRFQSLPPAGPGTFHFHYQAYLLSCHFP RRPAYGDVTVTSLHPGGSARFHCATGYQLKGARHLTCLNATQPFWDKPEVCIAACGGVI RNGTGRIVSPGFPNYSNNLTCHWLLLEAPEGQRLHLHFEKVSLEADDDRLIIRNGDNVE APPVGKSSLQLPRPRPRPNRITIESAFDNPTYETGETREYEVSI		

	SEQ ID NO: 161	2127 bp	
NOV33c, CG52919-03 DNA Sequence	CCAGGCGCTGGCCGTGGTGTGATTCTGT CAGGCGCTGGCGGCGGCAGCGCGGTGACGG CTGCGGCCCCGCTCCCTCTACCCGGCCGACCCGGCTCTGC CCCC GCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCCGCGGTCCAGCCCAGGGCGCGGCGCAACCAGCACCATG CGCCCGGTAGCCCTGCTGCTCCTGCCCTCGCTGCTGGCGCTCCTGGCTCAGGACTCTCT TTAGAGGCCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGT CACAACAGCC CCACCTTGAAGCTGCTCAACCACCCCGCTGCTTGAGGAATTCTACAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC TTCACCCCAAGTCCCCTTCCCGCCTGGCCAACCAGGACAGCCGCCCTGTCTTTACCAGC CCCACTCCAGCCATGGCTGCGGTACCACTCAGCCCCAGTCCAGGAGGGACCCCTGGAGT CCGGAGTCAGAGTCCCCTATGCTTCGAATCACAGTCCCCTACCTCCAGGGCCAGCATG GCAGTGCCCAACCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCCAAGAGGGTCTGGAGACATGGGAAGGCCGTGGGTTGCAGAGGTTGTGTCC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCACAGCTTCCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGCCCTTGTAGCTGGAATTTCTCAGGCCAGAGGGCTCTCTGGACTCCCCTACAGACCTC AGTCCCCCACTGATGTTGGCCTGGACTGCTTCTTCTACATCTCTGTCTACCTGGCTAT GGCGTGGAATCAAGGTCCAGAATATCAGCCTCCGGGAAGGGGAGACAGTACTGTGGAA GGCCTGGGGGGCCTGACCACTGCCCTGGCCAACAGTCTTTCTGCTGCGGGGCCAA GTCATCCGCAGCCCCACCCACCAAGCGGCCCTGAGGTTCCAGAGCCTCCCGCCACCGGCT GGCCCTGGCACCTTCCATTTCATTACCAAGCCTATCTCTGAGCTGCCACTTTCCCCTG CGTCCAGCTTATGGAGATGTGACTGT CACCAGCCTCCACCCAGGGGTAGTCCCGCTTC CATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCATCTCACCTGTCTCAATGCCACC CAGCCCTTCTGGGATTCAAGGAGCCCGTCTGCATCGCTGCTTGGCGCGGAGTGATCCGC AATGGCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTC ACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGGCTACACCTGCCTTTGAGAAG GTTCCCTGGCAGAGGATGATGACAGGCTCATCATTCGCAATGGGGACAACCTGGAGGCC CCACCACTGTATGATTCTATGAGGTGGAATACCCGCCCCGCCCCGCCCCCTACAACCGC ATTACCATAGAGTCAGCGTTTGACAATCCAACCTACGAGACTGGAGAGACGAGAGAATAT GAAGTCTCCATCTAGGTGGGGCAGTCTAGGGAAAGTCAACTCAGACTTGCACCACAGTCC AGCAGCAAGGCTCCTTGCTTCCTGCTGTCCCTCCACCTCCTGTATATACCACCTAGGAGG AGATGCCACCAAGCCCTCAAGAAGTTGTGCCCTTCCCGCCTGCGATGCCCACTAGGCC TATTTTCTTGTTGCTATTGCCCACTTGGGGCCCTTGCAATTGGGCCATGTACAGGGGGCAT CTACCTGTGGGGAAGAACATAGCTGGGAGCACAGCTTCAACAGCCAGCATTCTTGTAGC CTCCTTCATGGCCCTGGGACCAGCCTGGGGAACACANTTAGGCAGGAGCAGGGAGTTACC TTGTTTCACATGACCACCAACCATTC		
	ORF Start: ATG at 178		ORF Stop: TAG at 1753
	SEQ ID NO: 162	525 aa	MW at 56462.7kD
NOV33c, CG52919-03 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKQAPGIEETDGE LTAAPTPEQPERGVHFVTT APTLKLLNHHPLLEEFLQEGLEKGDDELRPALPFQPDPPAPFTPSPLRLANQDSRPVFT SPTPMAAVPTQPQSKEGPWSPESSESPMLRITAPLPGPSMAVPTLGPGEIASTTPPSRA WPTQEGPGDMGRPWVAEVVSQAGIGIQGTITSSSTASGDDEETTTTTIITTTITTVQT PGPCSWNFSGPEGSLDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVQNISLREGETVTV EGLGGPDPLPLANQSFLLRQVIRSPTHQAALRFQSLPPPAGPGTFHFHYQAYLLSCHFP RRPAYGDVTVTSLHPGGSARFHCATGYQLKGARHLTCLNATQPFWDSPKEPVCIACGGVI RNGTTGRIVSPGFPGNYSNNLTCHWLLAEPEGQRLHLHFKEVSLAEDDDRLLIRNGDNVE APPVYDSYEVEYPPRPRPYNRITIESAFDNPTYETGETREYEVSI		
	SEQ ID NO: 163	1988 bp	
NOV33d, CG52919-04 DNA Sequence	CCAGGCGCTGGCCGTGGTGTGATTCTGT CAGGCGCTGGCGGCGGCAGCGCGGTGACGG CTGCGGCCCCGCTCCCTCTACCCGGCCGACCCGGCTCTGC CCCC GCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCCGCGGTCCAGCCCAGGGCGCGGCGCAACCAGCACCATG CGCCCGGTAGCCCTGCTGCTCCTGCCCTCGCTGCTGGCGCTCCTGGCTCAGGACTCTCT TTAGAGGCCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGT CACAACAGCC CCACCTTGAAGCTGCTCAACCACCCCGCTGCTTGAGGAATTCTACAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC		

	<p>TTACCCCAAGTCCCCTTCCCGCCTGGCCAACCAGGACAGCCGCCCTGTCTTTACCAGC CCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAAGGAGGGACCCTGGAGT CCGGAGTCAGAGTCCCCTATGCTTCGAATCACAGCTCCCCTACCTCCAGGGCCCCAGCATG GCAGTGCCCAACCCTAGGCCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCCAAGAGGGTCCCTGGAGACATGGGAAGGCCGTGGGTTGCAGAGGTTGTTC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCACAGCTTCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGCCCTTGCTAGCTGGAATTTCTCAGGCCCAGAGGGCTCTCTGGACTCCCCTACAGACCTC AGCTCCCCCACTGATGTTGGCCTGGACTGCTTCTTCTACATCTCTGTCTACCTGGCTAT GGCGTGGAATCAAGGTCCAGAATATCAGCCTCCGGGAAGGGGAGACAGTGAATGTGGAA GGCTGGGGGGGCTGACCACTGCCCCCTGGCCAACCAGTCTTTCTGCTGCGGGGCCAA GTCATCCGCAGCCCCACCAAGCGGCCCTGAGGTTCCAGAGCCTCCGCCACCGGCT GGCCCTGGCACCTTCCATTTCCATTACCAAGCCTATCTCTGAGCTGCCACTTTCCCGT CGTCCAGCTTATGGAGATGTGACTGTCACCAGCCTCCACCCAGGGGGTAGTGCCCGCTTC CATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCATCTCACCTGTCTCAATGCCACC CAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGGCGGAGTGATCCGC AATGGCACCACCGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTC ACCTGCTACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGCTACACCTGCATTTGAGAAG GTTTCCTGGCAGAGGATGATGACAGGCTCATCATTGCAATGGGGACAACGTGGAGGCC CCACAGTGATGATTCCTATGAGGTGGAATACCCGCCCGCCCCCGCCCTACAACCGC ATTACCATAGAGTCAGCGTTTGAACAATCCAACCTACGAGACTGGAGAGACGAGAGAATAT GAAGTCTCCATCTAGGTGGGGCAGTCTAGGGAAGTCAACTCAGACTTGCACCACAGTCC AGCAGCAAGGCTCCTGCTTCTGCTGTCCCTCCACCTCCTGTATATACCACCTAGGAGG AGATGCCACCAAGCCACTTTGTACATGTAATGTATTATATGGGGTCTGGGCTCCAGCCAG AGAACAATCTTTATTTCTGTTGTTTCTTATTAAATGGTGTTTTGGAAAAA AAAAAAA</p>		
	<p>ORF Start: ATG at 178 ORF Stop: TAG at 1753</p>		
	<p>SEQ ID NO: 164 525 aa MW at 56462.7kD</p>		
NOV33d, CG52919-04 Protein Sequence	<p>MRPVALLLLPSLLALLAHGLSLEAPTGVKGQAPGIEETDDELTAAPTPEQPERGVHFVTT APTLKLNNHHPLLEEFLEQLEKGDDELRPALPFQDPFPAPFTPSPLRLANQDSRPVFT SPTPMAAAVPTQPQSKGPPSPESPMRLRITAPLPGPSMAVPTLGPGEIASTTPPSRA WPTQEGPGDMGRPWVAEVVSQAGIGIQGTITSSTASGDDEETTTTTTIITTTITTVQT PGPCSWNFSGPEGLSDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVQNISLREGETVTV EGLGGPDPLPLANQSFLLRQVIRSPTHQAALRFQSLPFPAGPGTFHFHYQAYLLSCHFP RRPAYGDTVTVTSLHPGGSARFHCATGYQLKGARHLTCLNATQPFWDSKEPVCIACGGVI RRGTTGRIIVSPGFPNGYSNNLTCHWLLEAPEGQRLHLHFKEVSLAEDDDRLLIRNGDNVE APPVDSYEVEYPPRPRPNRITIESAFDNPTVETGETREYEVS I</p>		
	<p>SEQ ID NO: 165 2143 bp</p>		
NOV33e, CG52919-05 DNA Sequence	<p>CCAGGCGCTGGCCGTGGTGCTGATTCTGTACAGGCGCTGGCGGCGGCAGCGGCGGTGACGG CTGCGGCCCCGCTCCCTCTACCCGGCCGACCCGGCTCTGCCCCGCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCCCGGCTCCAGCCCCAGGGCGCGGCCGCAACCAGCACCATG CGCCCCGTAGCCCTGCTGCTCCTGCCCTCGCTGCTGGCGCTCCTGGCTCACGGACTCTCT TTAGAGGCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGTCAACACAGCC CCCACCTTGAAGCTGCTCAACCACCACCCGCTGCTTGAGGAATTCCTACAAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC TTCACCCCAAGTCCCCTTCCCGCCTGGCCAACCAGGACAGCCGCCCTGTCTTTACCAGC CCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAAGGAGGGACCTGGAGT CCGAGTCAGAGTCCCCTATGCTTCGAATCACAGCTCCCCTACCTCCAGGAGGACCTGATG GCAGTGCCCAACCCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCCAAGAGGGTCTTGAGACATGGGAAGGCCGTGGGTTGCAGAGGTTGTGTCC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCACAGCTTCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGCCCTTGCTAGCTGGAATTTCTCAGGCCCAGAGGGCTCTCTGGACTCCCCTACAGACCTC AGCTCCCCCACTGATGTTGGCCTGGACTGCTTCTTCTACATCTCTGTCTACCTGCTAT GGCGTGGAATCAAGGTCCAGAATATCAGCCTCCGGGAAGGGGAGACAGTGAATGTGGAA GGCTGGGGGGGCTGACCACTGCCCTGGCCAACCAGTCTTCTGCTGCGGGGCCAA GTCATCCGCAGCCCCACCAAGCGGCCCTGAGGTTCCAGAGCCTCCGCCACCGGCT</p>		

	GGCCCTGGCACCTTCCATTTCATTACCAAGCCTATCTCCTGAGCTGCCACTTTCCCGT CGTCCAGCTTATGGAGATGTGACTGTACCAGCCTCCACCCAGGGGGTAGTGCCCGCTTC CATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCATCTCACCTGTCTCAATGCCACC CAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGCGGCGGAGTGATCCGC AATGGCACCACCGGCCCGCATCGTCTCTCCAGGTTCCCGGGCAACTACAGCAACAACCTC ACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGGTACACCTGCCTTTGAGAAG GTTTCCCTGGCAGAGGATGATGACAGGCTCATCATTGCAATGGGGACAACGTGGAGGCC CCACCACTGGGAAAAAGCTCCCTGCAGCTGCCCCGCCCCCGCCCCGCCCTACAACCGC ATTACCATAGAGTCAGCGTTTGACAATCCAACCTACGAGACTGGATCTCTTTCTTTTGCA GGAGACGAGAGAATATGAAGTCTCCATCTAGGTGGGGCAGTCTAGGGAAGTCAACTCAG ACTTGCAACCACAGTCCAGCAGCAAGGCTCCTTGCTTCTGCTGTCCCTCCACCTCCTGT TATACCACCTAGGAGGAGATGCCACCAAGCCCTCAAGAAGTTGTGCCCTTCCCGCCTGC GATGCCACCATGGCCTATTTTCTTGGTGTCTATTGCCCACTTGGGGCCCTTGCAATTGGGC CATGTACAGGGGGCATCTACCTGTGGGGAAGAATAGCTGGGAGCACAAGCTTCAACAG CCAGCATTCCTTGAGCCTCCTTCATGGCCCTGGGACCAGCCTGGGGAACACANTTAGGCA GGAGCAGGGAGTTACCTTGTTCACATGACCACCAACCATTCC		
	ORF Start: ATG at 178		ORF Stop: TGA at 1756
	SEQ ID NO: 166	526 aa	MW at 56252.6kD
NOV33e, CG52919-05 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGETAAPTPEQPERGVHFTT APTLKLLNHHPLLEEFLOEGLEKGDDELRPALPFQDPDPAPFTPSPLRLANQDSRPVFT SPTPAMAAPVTPQPSKEGPWSPSESPMLRITAPLPFGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWAIEVVSQAGIGIQGTITSSTASGDDEETTTTTTIIITTTITVQT PGPCSWNFSGPEGLSDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVQNISLREGETVTV EGLGGPDPLPLANQSFLLRGQVIRSPTHQAALRFQSLPPPAGPGTFHFHYQAYLLSCHFP RRPAYGDVTVTSLHPGGSARFHCATGYQLKGARHLTCLNATQPFWDSEKPEVCIAACGGVI RNGTTGRIVSPGFPGNYSNNLTCHWLEAPEGQRLHLHFEKVSLEAEDDDRLIIRNGDNVE APPVGKSSLQLPRPRPRPNRITIESAFDNPTYETGSLSFAGDERI		
	SEQ ID NO: 167	1694 bp	
NOV33f, CG52919-06 DNA Sequence	CAGGGCGCGGCCGCAACCAGCACCATGCGCCCGGTAGCCCTGCTGCTCCTGCCCTCGCTG CTGGCGCTCCTGGCTCACGGACTCTCTTAGAGGCCCCAACCGTGGGGAAAGGACAAGCC CCAGGCATCGAGGAGACAGATGGCGAGCTGACAGCAGCCCCACACCTGAGCAGCCAGAA CGAGGCGTCCACTTTGTCAACAACAGCCCCACCTTGAAGCTGCTCAACCACCACCCGCTG CTTGAGGAATTCCTACAAGAGGGGCTGGAAAAGGAGATGAGGAGCTGAGGCCAGCACTG CCCTTCCAGCCTGACCCACCTGCACCTTCACCCCAAGTCCCCTTCCCGCTTGGCCAAC CAGGACAGCCGCTGTCTTTACCAGCCCCACTCCAGCCATGGCTGCGGTACCCACTCAG CCCCAGTCCAAGGAGGGACCTGGAGTCCGGAGTCAGAGTCCCTATGCTTGAATCACA GCTCCCCTACCTCCAGGGCCAGCATGGCAGTGCCACCCTAGGCCAGGGGAGATAGCC AGCACTACACCCCCAGCAGAGCCTGGACACCAACCAAGAGGGTCTGGAGACATGGGA AGGCCGTGGGTTCAGAGAGTTGTGTCCAGGGCGCAGGGATCGGGATCCAGGGGACCATC ACCTCCTCCACAGCTTCAGGAGATGATGAGGAGACCACCACTACCACCACCATCATCAC ACCACCATCACCAAGTCCAGACACCAGGCCCTTGTAGCTGGAATTTCTCAGGCCAGAG GGCTCTCTGGACTCCCCTACAGACCTCAGCTCCCCCACTGATGTTGGCCTGGACTGCTTC TTCTACATCTCTGTCTACCCTGGCTATGGCGTGGAATCAAGGTCCAGAATATCAGCCTC CGGGAAGGGGAGACAGTACTGTGGAAGGCCTGGGGGGGCTGACCCACTGCCCTGGCC AACCAGTCTTTCTGCTGCGGGGCCAAGTCATCCGAGCCCCACCCACCAAGCGGCCCTG AGGTTCCAGAGCCTCCCGCCACCGGCTGGCCCTGGCACCTTCCATTTCCATTACCAAGCC TATCTCCTGAGCTGCCACTTTCCCGTCTGTCAGCTTATGGAGATGTGACTGTACCAGC CTCCACCCAGGGGGTAGTGCCCGCTTCCATTGTGCCACTGGCTACCAGCTGAAGGGCGCC AGGCATCTCACCTGTCTCAATGTCAACCAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGC ATCGTGTCTTGGCGGAGTGATCCGCAATGCCACACCGGCCGATCGTCTCTCCAGGC TTCCCGGGCAACTACAGCAACAACCTCACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGC CAGCGGCTACACCTGCCTTTGAGAAGGTTTCCCTGGCAGAGGATGATGACAGGCTCATC ATTGCAATGGGGACAACGTGGAGGCCCCACAGTGTATGATTCTTATGAGGTGGAATAC CTGCCATTGAGGGCCTGCTCAGCTCTGGCAACACTTCTTTGTTGAGCCCCGCCCCCGC CCCCGCCCTACAACCGCATTACCATAGAGTCAGCGTTTGACAATCCAACCTACGAGACT GGATCTCTTTCCCTTGAGGAGACGAGAGAATATGAAGTCTCCATCTAGGTGGGGCAGT CTAGGGAAGTCAAC		

	ORF Start: ATG at 25		ORF Stop: TGA at 1654
	SEQ ID NO: 168	543 aa	MW at 58351.0kD
NOV33f, CG52919-06 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGELTAAPTPEQPERGVHFTT APTLKLLNHHPLLEEFLEQEGLEKGEELRPALPFQDPDPAPFTPSPLPRLANQDSRPVFT SPTPMAAVPTQPQSKEGPWSPESESPMLRITAPLPPGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWVAEVVSQAGIGIQGTITSSTASGDDEETTTTTTIITTTITTVQT PGPCSWNFSGPEGLSDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVQNISLREGETVTV EGLGGPDPLPLANQSFLLRGQVIRSPTHQAALRFQSLPPAGPGTFHFHYQAYLLSCHFP RRPAYGDVTVTSLHPGGSARFHCATGYQLKGARHLTCLNVTQPFWDSPVCIAACGGVI RNATTGRIVSPGFPNGYSNNLTCHWLLEAPEGQRLHLHFVKVSLAEDDDRLLIIRNGDNVE APPVYDSYEVEYLPLEGLSSGKHFFVEPRPRPRPNRITTESAFDNPTYETGSLSLAGD ERI		
	SEQ ID NO: 169	1482 bp	
NOV33g, CG52919-01 DNA Sequence	CCAGGCGCTGGCCGCTGGTGCTGATTCTGTCTAGGCGCTGGCGGCGGCAGCGCGGTGACGG CTGCGGCCCCGCTCCCTCTACCCGGCCGGACCCGGCTCTGCCCCCGCGCCCAAGCCCCAC CAAGCCCCCGCCCTCCCGCCGCTCCAGGCCAGGGCGCGGCCGACCATG CGCCCCGCTAGCCCTGTGCTCCTCGCCCTCGCTGCTGGCGCTCCTGGCTCAGGACTCTCT TTAGAGGCCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGAGGAGACAGATGGCGAG CTGACAGCAGCCCCCACCTGAGCAGCCAGAACGAGGCGTCCACTTTGTCAACACAGCC CCCACCTGAAGCTGTCAACCACCACCCGCTGCTTGAGGAATTCCTACAAGAGGGGCTG GAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCCTGACCCACCTGCACCC TTCACCCCAAGTCCCTTCCCGCCTGGCCAAACAGGACAGCCGCGCTGTCTTTACAGC CCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAAGGAGGGACCTGGAGT CCGGAGTCAGAGTCCCTATGCTTCGAATCACAGCTCCCTACCTCCAGGGCCAGCATG GCAGTGCCACCCCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGG ACACCAACCAAGAGGGTCTTGAGACATGGGAAGGCCGTGGGTTCGACAGGTTGTGTCC CAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCACAGCTTCAGGAGATGAT GAGGAGACCACCACTACCACCACCATCATCACCACCACCATCACCACAGTCCAGACACCA GGTCAGCTACCTGCTGGCTTGACAGATGTGGAATGGGGATGGGGGAGGCTGCGGGGCCCC TAAAAGCCTGTCTCTGACACTGTGCCAGCCTGCCCTGCCCTTTGGCACCAGGGGCCAGCC TGCAGGAGGCATGTAGATTGGACCCAGATAGACCTGAGCTCAAATCCTGATTCTTCAGCC AAGTACAGTGGCTCATGCTGTAATCCAGCACTTTGGGAGGCAGAGGCCAGTGATCAT CTGAGGTGAGGAGTTCAAGACCTCCTGGCCAAACATGGCGAAAACCATCTCTACTAAAA ATACAAAAATGAGCCGGGCATGGTGGTGGGCACCTGTAATCCAGCTACTCGGGAGGCTG AGGCAGGAGAATCACTCAAACCTGGGAGGCAGAGGTTGAGTGAGCTGAGATTGCACCAT TGCACTCCAGCCTGGGCAACAGAGCGAGACTCTGTCTCAAAAAAGAAAAATCTTGATTG TTCCAATAATAACATGACCTAGGAATTCTATTAAACATCTCATCTGAGCCTCATCTG TAAAATGGCAATAAGAAAAATAAATTCTGGCTAGAAAAAAA		
	ORF Start: ATG at 178		ORF Stop: TAA at 961
	SEQ ID NO: 170	261 aa	MW at 27471.8kD
NOV33g, CG52919-01 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGELTAAPTPEQPERGVHFTT APTLKLLNHHPLLEEFLEQEGLEKGEELRPALPFQDPDPAPFTPSPLPRLANQDSRPVFT SPTPMAAVPTQPQSKEGPWSPESESPMLRITAPLPPGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWVAEVVSQAGIGIQGTITSSTASGDDEETTTTTTIITTTITTVQT PGQLPAGLQMWKGGWRLRGP		
	SEQ ID NO: 171	840 bp	
NOV33h, CG52919-07 DNA Sequence	TCCAGGGCGCGGCCGCAACCAGCACCATGCGCCCGGTAGCCCTGCTGCTCCTGCCCTCGC TGCTGGCGCTCCTGGCTCAGGACTCTCTTTAGAGGCCCAACCGTGGGGAAGGACAAG CCCCAGGCATCGAGGAGACAGATGGCGAGCTGACAGCAGCCCCACACCTGAGCAGCCAG AACGAGGCTCCACTTTGTCAACAACAGCCCCACCTTGAAGCTGTCAACCAACCCCGC TGCTTGAGGAATTCCTACAAGAGGGGCCGAAAAGGGAGATGAGGAGCTGAGGCCAGCAC TGCCCTTCCAGCCTGACCCACCTGCACCTTACCCCAAGTCCCCTTCCCGCCTGGCCA ACCAGGACAGCCGCCCTGTCTTTACCAGCCCCACTCCAGCCATGGCTGCGGTACCCACTC AGCCCCAGTCCAAGGAGGGACCTGGAGTCCGGAGTCAGAGTCCCCTATGCTTCGAATCA CAGCTCCCCTACCTCCAGGGCCAGCATGGCAGTGCCACCTAGGCCAGGGGAGATAG CCAGCACTACACCCCCAGCAGACCTGGACACCAACCAAGAGGGTCTGGAGACATGG		

	GAAGGCCGTGGGTTGCAGAGTGTGTGCCAGGGCGCAGGGATCGGGATCCAGGGGACCA TCACCTCCTCCACAGCTTCAGGAGATGATGAGGAGACCACCCTACCACCACCATCATCA CCACCACCATCACCACAGTCCAGACACCAGTCACTACCTGCTGGCTTGAGATGTGGA AATGGGGATGGGGGAGGCTGCGGGGGCCCCCTAAAAGCCTGTCTCTGACACTGTGCCAGCCA		
	ORF Start: ATG at 27	ORF Stop: TAA at 810	
	SEQ ID NO: 172	261 aa	MW at 27455.8kD
NOV33h, CG52919-07 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGETAAPTPEQPERGVHFVTT APTLKLLNHHPLLEEFLEQEGPEKGDDELRPALPFQPDPPAPFTPSPLPRLANQDSRPVFT SPTPMAAAVPTQPQSKEGPWSPESPESEPMRLITAPLPFGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWVAEVVSQAGAGIGIQTITSSSTASGDDEETTTTTTITTTITTVQT PGQLPAGLQMWKNGWRLRGP		
	SEQ ID NO: 173	1654 bp	
NOV33i, CG52919-08 DNA Sequence	CACCAGATCTCCACCATGCGCCCGGTAGCCCTGCTGCTCCTGCCCTCGTGCTGGCGCT CCTGGCTCACGGAATCTCTTTAGAGGCCCAACCGTGGGGAAGGACAAGCCCCAGGCAT CGAGGAGACAGATGGCGAGCTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGT CCACTTTGTCAACAGCCCCACCTTGAAGCTGCTCAACCACCACCCGCTGCTTGAGGA ATTCTCTACAAGAGGGGCTGGAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCA GCCTGACCCACCTGCACCCCTTACCCCAAGTCCCTTCCCGCCTGGCCCAACGAGCAG CCGCCCTGTCTTTACCAGCCCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTC CAAGGAGGGACCCCTGGAGTCCGGAGTCAGAGTCCCCTATGCTTGAATCAGACTCCCCT ACCTCCAGGGCCCAGCATGGCAGTGCCACCCCTAGGCCCAGGGGAGATAGCCAGCACTAC ACCCCCCAGCAGAGCCTGGACACCAACCCAAGAGGGTCTTGGAGACATGGGAAGGCCGTG GGTTGCAGAGGTTGTGTCCCAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTC CACAGCTTCAGGAGATGATGAGGAGACCACCACTACCACCACCATCATCACCACCACCAT CACCACAGTCCAGACACCAGGCCCTTGTAGCTGGAATTTCTCAGGCCCAGAGGGTTCTCT GGACTCCCCTACAGACCTCAGTCCCCCACTGATGTTGGCCTGGACTGCTTCTTCTACAT CTCTGTCTACCCTGGCTATGGCGTGGAAATCAAGGTCCAGAATATCAGCCTCCGGGAAGG GGAGACAGTGAAGTGTGGAAGGCCCTGGGGGGGCTGACCCACTGCCCTGGCCCAACCATG TTTCCTGCTGCGGGGCCAAGTATCCGAGCCCCACCAACCAAGCGGCCCTGAGGTTCCA GAGCCTCCCGCCACCGGCTGGCCCTGGCACCTTCCATTTCATTACCAAGCCTATCTCCT GAGCTGCCACTTTCCCGCTCGTCCAGCTTATGGAGATGTGACTGTACACAGCCTCCACCC AGGGGGTAGTGCCCGCTTCCATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCATCT CACCTGTCTCAATGTACCCAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGC TTGCGGCGGAGTGATCCGCAATGCCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGG CAACTACAGCAACAACCTCACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGGCT ACACCTGCACCTTTGAGAAGGTTTCCCTGGCAGAGGATGATGACAGGCTCATCATCTCGAA TGGGGACAACGTGGAGGCCCTTCAAGTGTATGATTCTATGAGGTGGAATACCTGCCCAT TGAGGGCCTGCTCAGCTCTGGCAAACTTCTTTGTTGAGCCCCGCCCCGCCCCGCC CTACAACCGCATTACCATAGAGTCAGCGTTTGACAATCCAATTACGAGACTGGATCTCT TTCCCTTGACAGGAGACGAGAGAATACTCGAGGGC		
	ORF Start: ATG at 17	ORF Stop: at 1646	
	SEQ ID NO: 174	543 aa	MW at 58351.0kD
NOV33i, CG52919-08 Protein Sequence	MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGETAAPTPEQPERGVHFVTT APTLKLLNHHPLLEEFLEQEGLEKGDDELRPALPFQPDPPAPFTPSPLPRLANQDSRPVFT SPTPMAAAVPTQPQSKEGPWSPESPESEPMRLITAPLPFGPSMAVPTLGPGEIASTTPPSRA WTPTQEGPGDMGRPWVAEVVSQAGAGIGIQTITSSSTASGDDEETTTTTTITTTITTVQT PGPCSWNFSGPEGSLDSDPTDLSSPTDVLDCFFYISVYPGYGVEIKVQNISLREGETVT EGLGGPDPLPLANQSFLLRGQVIRSPTHQAALRFQSLPPPAGPGTFHFHYQAYLLSCHFP RRPAYGDVTVTSLHPGGSARFHCATGYQLKGARHLTCLNVTQPFWDSEKPVCTAACGGVI RNATTGRIVSPGFPNGYNNLTCHWLLEAPEGQRLHLHFKEVSLAEDDDRLLIRNGDNVE APPVYDSYVEYLPFIEGLSSGKHFFVEPRPRPRPYNRITIESAFDNPTYETGSLSLAGD ERI		
	SEQ ID NO: 175	1591 bp	
NOV33j, CG52919-09 DNA Sequence	CACCAGATCTCTCTCTTTAGAGGCCCAACCGTGGGGAAGGACAAGCCCCAGGCATCGA GGAGACAGATGGCGAGCTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCA CTTTGTCAACAGCCCCACCTTGAAGCTGCTCAACCACCACCCGCTGCTTGAGGAATT		

	CCTACAAGAGGGGCTGGAAAAGGGAGATGAGGAGCTGAGGCCAGCACTGCCCTTCCAGCC TGACCCACCTGCACCCCTTCAACCCCAAGTCCCCTTCCCGCCTGGCCAACCAGGACAGCCG CCCTGTCTTTACCAGCCCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAA GGAGGGACCCTGGAGTCCGGAGTCAGAGTCCCCTATGCTTCGAATCACAGCTCCCCTACC TCCAGGGCCCAGCATGGCAGTGCCCCACCCTAGGCCAGGGGAGATAGCCAGCACTACACC CCCCAGCAGAGCCTGGACACCAACCCAAGAGGGTCTGGAGACATGGGAAGGCCGTGGGT TGCAGAGGTTGTGTCCAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCCTCCAC AGCTTCAGGAGATGATGAGGAGACCACCACTACCACCACCATCATCACCACCACCATCAC CACAGTCCAGACACCAGGCCCTTGTAGCTGGAATTTCTCAGGCCAGAGGGTTCTCTGGA CTCCCTACAGACCTCAGTCCCCCACTGATGTTGGCCTGGACTGCTTCTTCTACATCTC TGTCTACCCTGGCTATGGCGTGGAATCAAGGTCCAGAATATCAGCCTCCGGGAAGGGGA GACAGTGACTGTGGAAGGCCTGGGGGGCCTGACCACTGCCCTGGCCAACCAGTCTTT CCTGCTGCGGGGCCAAGTCATCCGCAGCCCCACCAAGCGGCCCTGAGGTTCCAGAG CCTCCCGCCACCGGCTGGCCCTGGCACCTTCCATTTCATTACCAAGCCTATCTCCTGAG CTGCCACTTTCCCGTCTGTCAGCTTATGGAGATGTGACTGTACCAGCCTCCACCCAGG GGGTAGTGCCCGCTTCCATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCATCTCAC CTGTCTCAATGTCAACCCAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTG CGGCGGAGTGATCCGCAATGCCACCACCGGCCGTCATCGTCTCAGGCTTCCCGGGCAA CTACAGCAACAACCTCACCTGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGGCTACA CCTGCACTTTGAGAAGGTTTCCCTGGCAGAGGATGATGACAGGCTCATCATTGCAATGG GGACAACGTGGAGGCCCCACAGTGTATGATTCTTATGAGGTGGAATACCTGCCATTGA GGGCCTGCTCAGCTCTGGCAAACACTTCTTTGTTGAGCCCCGCCCCCGCCCCGCCCCA CAACCGCATTACCATAGAGTCAGCGTTTGACAATCCAATTACGAGACTGGATCTCTTTT CCTTGCAGGAGACGAGAGAATACTCGAGGGC		
	ORF Start: at 2		ORF Stop: at 1583
	SEQ ID NO: 176	527 aa	MW at 56714.8kD
NOV33j, CG52919-09 Protein Sequence	TRSLSEAPTVGKGQAPGIEETDGLTAAPTPEQPERGVHFVTTAPTLLKLLNHHPLEEF LQEGLEKGDDEELRPALPFQPDPPAPFTPSPLPRLANQDSRPVFTSPTPMAAAVPTQPQSK EGPWSPESESPMLRITAPLPPGPSMAVPTLGPGEIASTTPPSRAWPTQEGPGDMGRPWW AEVVSQAGIGIQGTITSSTASGDDEETTTTTTIIITTTITTVQTPGPCSWNFSGPEGLD SPTDLSSPTDVLDCFFYISVYPGYGVEIKVQNISLREGETVTVEGLGGPDPLPLANQSF LLRGQVIRSPTHQAALRFQSLPPAGPGTFHFHYQAYLLSCHFPRRPAYGDVTVTSLHPG GSARFHCATGYQLKGARHLTCLNVTQPFWDSKEPVCIAACGGVIRNATTGRIVSPGFPGN YSNNLTCHWLLEAPEGQRLHLHFKEVSLAEDDDRLLIIRNGDNVEAPPVYDSYEVEYLP GLSSGKHFFVEPRPRPRPNRITIESAFDNPTYETGSLSLAGDERI		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 33B.

Table 33B. Comparison of NOV33a against NOV33b through NOV33j.		
Protein Sequence	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV33b	1..242 1..242	166/242 (68%) 166/242 (68%)
NOV33c	1..242 1..242	166/242 (68%) 166/242 (68%)
NOV33d	1..242 1..242	166/242 (68%) 166/242 (68%)
NOV33e	1..242 1..242	166/242 (68%) 166/242 (68%)
NOV33f	1..242 1..242	166/242 (68%) 166/242 (68%)

NOV33g	1..261 1..261	185/261 (70%) 185/261 (70%)
NOV33h	1..261 1..261	184/261 (70%) 184/261 (70%)
NOV33i	1..242 1..242	166/242 (68%) 166/242 (68%)
NOV33j	20..242 4..226	167/223 (74%) 167/223 (74%)

Further analysis of the NOV33a protein yielded the following properties shown in Table 33C.

Table 33C. Protein Sequence Properties NOV33a	
PSort analysis:	0.8200 probability located in outside; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Cleavage site between residues 20 and 21

- A search of the NOV33a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 33D.

Table 33D. Geneseq Results for NOV33a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB70543	Human PRO13 protein sequence SEQ ID NO:26 - <i>Homo sapiens</i> , 261 aa. [WO200110902-A2, 15-FEB-2001]	1..261 1..261	261/261 (100%) 261/261 (100%)	e-154
AAE15853	Human SEZ6 protein - <i>Homo sapiens</i> , 853 aa. [WO200183552-A2, 08-NOV-2001]	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140
AAU81976	Human secreted protein SECP2 - <i>Homo sapiens</i> , 994 aa. [WO200198353-A2, 27-DEC-2001]	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140

AAB70542	Human PRO12 protein sequence SEQ ID NO:24 - <i>Homo sapiens</i> , 526 aa. [WO200110902-A2, 15- FEB-2001]	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140
AAB70541	Human PRO11 protein sequence SEQ ID NO:22 - <i>Homo sapiens</i> , 525 aa. [WO200110902-A2, 15- FEB-2001]	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140

In a BLAST search of public sequence databases, the NOV33a protein was found to have homology to the proteins shown in the BLASTP data in Table 33E.

Table 33E. Public BLASTP Results for NOV33a				
Protein Accession Number	Protein/Organism/Length	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC33421	Sequence 25 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 261 aa.	1..261 1..261	261/261 (100%) 261/261 (100%)	e-154
CAC33420	Sequence 23 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 526 aa.	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140
CAC33418	Sequence 19 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 525 aa.	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140
CAC33417	Sequence 17 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 525 aa.	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140
CAC33416	Sequence 15 from Patent WO0110902 - <i>Homo sapiens</i> (Human), 994 aa.	1..242 1..242	242/242 (100%) 242/242 (100%)	e-140

PFam analysis predicts that the NOV33a protein contains the domains shown in

5 Table 33F.

Table 33F. Domain Analysis of NOV33a			
Pfam Domain	NOV33a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 34.

The NOV34 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 34A.

Table 34A. NOV34 Sequence Analysis			
	SEQ ID NO: 177	368 bp	
NOV34a, CG55698-01 DNA Sequence	CTGTCCCCTCACCATGGAGAAGATCCTGATCCTCCTGCTTGTGCGCCCTCTCTGTGGCCT ATGCAGCTCCTGGCCCCCGGGGGATCATTATCAACCTGGAGAACGGTGAGCTCTGCATGA ATAGTGCCAGTGTAAGAGCAATTGCTGCCAGCATTCAAGTGCGCTGGGCCTGGCCCGCT GCACATCCATGGCCAGCGAGAACAGCGAGTGCTCTGTCAAGACGCTCTATGGGATTTACT ACAAGTGTCCTGTGAGCGTGGCCTGACCTGTGAGGGAGACAAGACCATCGTGGGCTCCA TCACCAACCAACTTTGGCATCTGCCATGACGCTGGACGCTCCAAGCAGTGAGACTGCC CACCCACT		
	ORF Start: ATG at 15		ORF Stop: TGA at 351
	SEQ ID NO: 178	112 aa	MW at 11953.7kD
NOV34a, CG55698-01 Protein Sequence	MEKILILLVALSVAYAAPGPRGIIINLENGELCMNSAQCKSNCCQHSSALGLARCTSMAS SENSECSVKTLTYGIYKPCERGLTCEGDKTIVGSITNTNFGICHDAGRSKQ		
	SEQ ID NO: 179	394 bp	
NOV34b, CG55698-02 DNA Sequence	AGCTGTCCCCTCGCCATGGAGAAGATCCTGATCCTCCTGCTTGTGCGCCCTCTCTGTGGC CTATGCAGCTCCTGGCCCCCGGGGGATCATTATCAACCTGACGCTCTATGGGATTTACTA CAAGTGTCCCTGTGAGCGTGGCCTGACCTGTGAGGGAGACAAGACCATCGTGGGCTCCAT CACCAACCAACTTTGGCATCTGCCATGACGCTGGACGCTCCAAGCAGTGAGACTGCC ACCCACTCCCAACCTAGCCCAAGATGCTGTAGGCCACTAGGCGCAGGGGCATCTCTCCC CTGCTCCAGCGCATCTCCGGGCTGGCCACCTCCTTGACCAGCATATCTGTTTTCTGATT GCGCTCTTCACAATTAAAGGCCTCTGCAAACCT		
	ORF Start: ATG at 17		ORF Stop: TGA at 230
	SEQ ID NO: 180	71 aa	MW at 7658.9kD
NOV34b, CG55698-02 Protein Sequence	MEKILILLVALSVAYAAPGPRGIIINLTLYGIYKPCERGLTCEGDKTIVGSITNTNF GICHDAGRSKQ		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 34B.

Table 34B. Comparison of NOV34a against NOV34b.		
Protein Sequence	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV34b	1..112	56/112 (50%)
	1..71	56/112 (50%)

Four polymorphic variants of NOV34b have been identified and are shown in Table 41M.

Further analysis of the NOV34a protein yielded the following properties shown in Table 34C.

Table 34C. Protein Sequence Properties NOV34a	
PSort analysis:	0.8200 probability located in outside; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Cleavage site between residues 18 and 19

A search of the NOV34a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 34D.

Table 34D. Geneseq Results for NOV34a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB54163	Human pancreatic cancer antigen protein sequence SEQ ID NO:615 - <i>Homo sapiens</i> , 131 aa. [WO200055320-A1, 21-SEP-2000]	1..112 20..131	112/112 (100%) 112/112 (100%)	3e-62
AAY91513	Human secreted protein sequence encoded by gene 63 SEQ ID NO:186 - <i>Homo sapiens</i> , 122 aa. [WO200006698-A1, 10-FEB-2000]	28..111 33..114	28/84 (33%) 38/84 (44%)	1e-07
AAY35930	Extended human secreted protein sequence, SEQ ID NO. 179 - <i>Homo sapiens</i> , 121 aa. [WO9931236-A2, 24-JUN-1999]	28..111 33..114	28/84 (33%) 38/84 (44%)	1e-07
AAB62640	Human colipase-like protein-1 (Zclps1) - <i>Homo sapiens</i> , 118 aa. [WO200136466-A2, 25-MAY-2001]	32..111 34..111	26/80 (32%) 36/80 (44%)	3e-07
AAB62648	Human colipase-like protein-1 (Zclps1) fragment - <i>Homo sapiens</i> , 97 aa. [WO200136466-A2, 25-MAY-2001]	32..109 22..97	25/78 (32%) 35/78 (44%)	1e-06

In a BLAST search of public sequence databases, the NOV34a protein was found to have homology to the proteins shown in the BLASTP data in Table 34E.

Table 34E. Public BLASTP Results for NOV34a				
Protein Accession Number	Protein/Organism/Length	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P04118	Colipase precursor - <i>Homo sapiens</i> (Human), 112 aa.	1..112 1..112	112/112 (100%) 112/112 (100%)	9e-62
P19090	Colipase precursor - <i>Canis familiaris</i> (Dog), 112 aa.	1..112 1..112	88/112 (78%) 99/112 (87%)	6e-50
P42890	Colipase precursor - <i>Oryctolagus cuniculus</i> (Rabbit), 107 aa.	1..106 1..106	88/106 (83%) 97/106 (91%)	1e-49
Q91XL7	Pancreatic colipase - <i>Spermophilus tridecemlineatus</i> (Thirteen-lined ground squirrel), 111 aa.	3..112 2..111	87/110 (79%) 100/110 (90%)	2e-49
Q9N1T6	Colipase - <i>Sus scrofa</i> (Pig), 112 aa.	1..110 1..110	86/110 (78%) 95/110 (86%)	1e-48

PFam analysis predicts that the NOV34a protein contains the domains shown in

5 Table 34F.

Table 34F. Domain Analysis of NOV34a			
Pfam Domain	NOV34a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Colipase	21..60	32/40 (80%) 40/40 (100%)	5.5e-24
Colipase_C	62..106	41/47 (87%) 45/47 (96%)	3.2e-34

Pancreatic lipase catalyzes the hydrolysis triacylglycerol to fatty acids. These triacylglycerides are present predominantly as an emulsified micelle stabilized by bile acids. Since lipase hydrolyzes the ester linkage of triacylglyceride, the active site must be
 10 positioned at the bile salt-coated water-lipid interface of this micelle. Since the bile salts can

inhibit lipase, colipase is secreted to anchor the lipase to the water-lipid interface so that hydrolysis can occur.

Table 34G shows an alignment of the porcine pancreatic colipase (Q9N1T6; SEQ ID NO:797) with the splice variant NOV34b (CG55698-02; SEQ ID NO:180). The arrow indicates the signal sequence cleavage site. Since the homology between the porcine and human lipases is high, the x-ray crystal structure of the porcine lipase is a suitable comparison for the effects of NOV34b (CG55698-02).

Table 34G. Multiple Alignment of Q9N1T6 and NOV34b (CG55698-02)

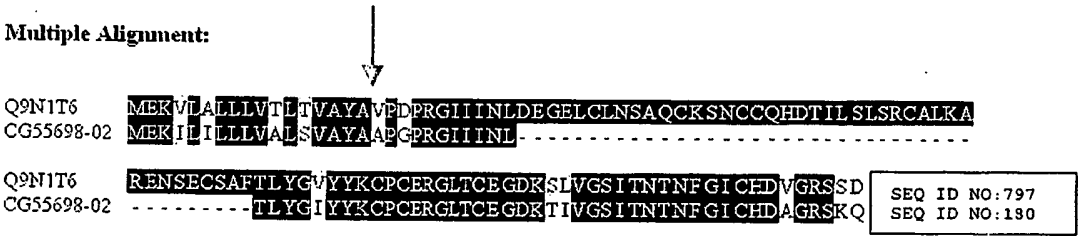


Figure 2 shows the x-ray crystal structure (1ETH) at a 2.84 Å resolution of porcine lipase (right) with colipase (left)(Hermoso, *et. al*, J. Biol. Chem., 2001, 271:1807-18016). The tetra ethylene glycol mono-octyl ether inhibitor is shown in the active site of lipase. The deleted sequence found in NOV34b is indicated with hatch marks.

The amino-terminal domain of lipase contains the active site whereas the carboxy-terminal domain binds to colipase. Likewise, colipase possesses a lipase binding domain and a micelle interfacial binding site. The catalytic site of lipase is inaccessible in solution since there is an N-terminal flap which covers the active site, preventing substrate from entering. The colipase additionally serves to stabilize the active form of lipase by binding to the N-terminal flap and thus keeping it in an open, active conformation which allows substrate to enter the lipase active site.

The interfacial binding site of colipase is composed of four hydrophobic fingers (finger1:14-24, finger2:27-39, finger3:47-64, and finger4: 68-90 numbered according to the colipase sequence in Figure 3). In NOV34b, Fingers1, 2 and a portion of 3 are missing suggesting that the splice variant would be less adept at binding the micelle interface.

- Of the 8 polar interactions (includes hydrogen bonds and salt bridges) between lipase and colipase, 5 of bind to the C-terminal region of lipase and the remainder bind to the N-terminal flap. Of these, only one of the 5 bonds NOV34b:C-terminal bonds is missing, but all three of the NOV34b:N-terminal flap bonds missing. Of the 17
- 5 colipase:lipase van der Waals contacts, 4 of these contact the N-terminal flap and the remainder bond to the C-terminal domain. For NOV34b, 11 of the 13 van der Waals contacts to the lipase C-terminal domain and none of the N-terminal flap contacts are present. Of the 4 bridging water contacts at the colipase:lipase C-terminal binding site, 2 are lost in NOV34b.
- 10 The splice variant NOV34b retains most of the binding sites to the C-terminal of lipase, but are missing half of the micelle interfacial binding domain and the entire N-terminal flap binding site. NOV34b may still bind to lipase, but may not anchor it to the micelle interface very well and would not be able to stabilize the open, active formation of lipase (since it cannot bind the N-terminal flap). Thus, it is possible that NOV34b may
- 15 compete for binding with the normal, lipase-activating form of colipase to lipase. Since the NOV34b lipase complex fails to position the N-terminal flap away from the active site of lipase and thus prevents substrate binding, NOV34b may be considered to be a competitive inhibitor of the lipase enzymatic activity.

Example 35.

- 20 The NOV35 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 35A.

Table 35A. NOV35 Sequence Analysis			
	SEQ ID NO: 181	7286 bp	
NOV35a, CG55832-01 DNA Sequence	GAATTCGCTAGAGCCCTAGAGCCCCAGCAGCACCCAGCCAAACCCACCTCCACCATGGGG GCCATGACTCAGCTGTTGGCAGGTGTCTTCTTGCTTTCCTTGCCCTCGCTACCGAAGGT GGGGTCCTCAAGAAAGTCATCCGGCACAAGCGACAGAGTGGGGTGAACGCCACCCTGCCA GAAGAGAACCAGCCAGTGGTGTTTAACCACGTTTACAACATCAAGCTGCCAGTGGGATCC CAGTGTTCGGTGGATCTGGAGTCAGCCAGTGGGGAGAAAGACCTGGCACCGCCTTCAGAG CCCAGCGAAAGCTTTCAGGAGCACACAGTAGATGGGGAAAACAGATTGTCTTCACACAT CGCATCAACATCCCCGCCGGCCTGTGGCTGTGCCGACGCCCTGATGTTAAGGAGCTG CTGAGCAGACTGGAGGAGCTGGAGAACCTGGTGTCTTCCCTGAGGGAGCAATGTACTGCA GGAGCAGGCTGCTGTCTCCAGCCTGCCACAGGCCGCTTGGACACCAGGCCCTTCTGTAGC GGTGGGGCAACTTCAGCACTGAAGGATGTGGCTGTGTCTGCGAACCTGGCTGGAAAGGC CCCAACTGCTCTGAGCCCCGAATGTCCAGGCAACTGTACCTTCGAGGCCGGTGCATTGAT GGGCAGTGCATCTGTGACGACGGCTTCACGGGCGAGGACTGCAGCCAGCTGGCTTGCCCC AGCGACTGCAATGACCAGGGCAAGTGCGTGAATGGAGTCTGCATCTGTTTCGAAGGCTAC GCGGCTGACTGCAGCCGTGAAATCTGCCAGTGGCCCTGCAGTGAGGAGCACGGCACATGT GTAGATGGCTTGTGTGTGCCACGATGGCTTTCAGGCGATGACTGCAACAAGCCTCTG GTCTCAACAATTGCTACAACCGTGGACGATGCGTGGAGAATGAGTGCCTGTGTGATGAG GGTTCACGGGCGAAGACTGCAGTGAGCTCATCTGCCCAATGACTGCTTCGACCGGGGC		

	CGCTGCATCAATGGCACCTGCTACTGCGAAGAAGGCTTCACAGGTGAAGACTGCGGGAAA CCCACCTGCCACATGCCTGCCACACCCAGGGCCGGTGTGAGGAGGGGAGTGTGTATGT GATGAGGGCTTTGCCGGTGTGGACTGCAGCGAGAAGAGGTGTCTGTGCTGACTGTCACAAT CGTGGCCGCTGTGTAGACGGGCGGTGTGAGTGTATGATGATGGTTTCACTGGAGCTGACTGT GGGGAGCTCAAGTGTCCCAATGGCTGCAGTGGCCATGGCCGCTGTGTCAATGGGCAGTGT GTGTGTGATGAGGGCTATACTGGGGAGGACTGCAGCCAGCTACGGTGCCCAATGACTGT CACAGTCGGGGCCGCTGTGTGAGGGCAAATGTGTATGTGAGCAAGGCTTCAAGGGCTAT GACTGCAGTGACATGAGCTGCCCTAATGACTGTCACCAGCACGGCCGCTGTGTGAATGGC ATGTGTGTTTGTGATGACGGCTACACAGGGGAAGACTGCCGGGATCGCCAATGCCCCAGG GACTGCAGCAACAGGGGCCCTCTGTGTGGACGGACAGTGCCTCTGTGAGGACGGCTTCAAC GGCCCTGACTGTGCAGAACTCTCTGTCCAAATGACTGCCATGGCCAGGGTCTGTGTG AATGGGCAGTGCCTGTGCCATGAAGGATTTATGGGCAAAGACTGCAAGGAGCAAAGATGT CCCAGTGAATGTGATGGCCAGGGCCGCTGCGTGGACGGCCAGTGCATCTGCCACGAGGGC TTCACAGGCCTGGACTGTGGCCAGCACTCCTGCCCACTGACTGCAACAACTTAGGACAA TGCGTCTCGGGCCGCTGCATCTGCAACGAGGGCTACAGCGGAGAAGACTGCTCAGAGGTG TCTCCTCCCAAAGACCTCGTTGTGACAGAAGTGACGGAAGAGACGGTCAACCTGGCCTGG GACAATGAGATGCGGGTCACAGAGTACCTTGTGTGTACACGCCCCACACGAGGGTGGT CTGGAATGCAGTTCCGTGTGCCTGGGGACCAGACGTCCACCATCATCCGGGAGCTGGAG CCTGGTGTGGAGTACTTTATCCGTGTATTTGCCATCCTGGAGAAACAAGAGAGCATTCCT GTCAGCGCCAGGGTGGCCACGTACTTACCTGCACCTGAAGGCCTGAAATTCAAGTCCATC AAGGAGACATCTGTGGAAGTGGAGTGGGATCCTTAGACATTGCTTTTGAACACTGGGAG ATCATCTTCCGGAATATGAATAAAGAGATGAGGGAGAGATCACCAAAAGCCTGAGGAGG CCAGAGACCTCTTACCGGCAAACCTGGTCTAGCTCCTGGGCAAGAGTATGAGATATCTCTG CACATAGTGA AAAACAATAACCGGGGCCCTGGCCTGAAGAGGGTGACCACCACACGCTTG GATGCCCCCAGCCAGATCGAGGTGAAAGATGTACAGACACCACTGCCTTGATCACTGGG TTCAAGCCCTGGCTGAGATCGATGGCATTGAGCTGACCTACGGCATCAAAGACGTGCCA GGAGACCGTACCACCATCGATCTCACAGAGGACGAGAACCAGTACTCCATCGGGAACCTG AAGCCTGACACTGAGTACGAGGTGTCCCTCATCTCCCGCAGAGGTGACATGTCAAGCAAC CCAGCCAAAGAGACCTTCACAACAGGCCTCGATGCTCCAGGAATCTTCGACGTGTTTCC CAGACAGATAACAGCATCACCTTGGAAATGGAGGAATGGCAAGGCAGCTATTGACAGTTAC AGAATTAAGTATGCCCCCATCTCTGGAGGGGACCACGCTGAGGTTGATGTTCAAAGAGC CAACAAGCCACAACCAAAACCACTCACAGGTCTGAGGCCGGAACTGAACATGGGAGT GGAGTTTCTGCTGTGAAGGAAGACAAGGAGAGCAATCCAGCGACCATCAACGCAGCCACA GAGTTGACACGCCCAAGGACCTTCAGGTTTCTGAAACTGCAGAGACCAGCCTGACCCTG CTCTGGAAGACACCGTTGGCCAAATTTGACCGCTACCGCCTCAATTACAGTCTCCCCACA GGCCAGTGGGTGGGAGTGCAGCTTCAAAGAAACACCACTTCCTATGCTCTGAGAGGCCTG GAACCAGGACAGGAGTACAATGTCCTCCTGACAGCCGAGAAAGGCAGACACAAGAGCAAG CCCGCAGCTGTGAAGGCATCCACTGAACAAGCCCCTGAGCTGGAAAACCTCACCGTGACT GAGGTTGGCTGGGATGGCCCTCAGACTCAACTGGACCGCGGCTGACCAGGCCTATGAGCAC TTTATCATTCAGGTGCAGGAGGCCAACAAGGTGGAGGCAGCTCGGAACCTCACCGTGCT GGCAGCCTTCGGGCTGTGGACATACCGGGCCTCAAGGCTGTACGCCTTATACAGTCTCC ATCTATGGGGTGATCCAGGGCTATAGAACACCAAGTGCTCTCTGCTGAGGCCCTCCACAGGG GAAACTCCCAATTTGGGAGAGGTGCTGGTGGCCGAGGTGGGCTGGGATGCCCTCAAACCTC AACTGGACTGCTCCAGAAGGGGCTATGAGTACTTTTTTATTAGGTGCAGGAGGCTGAC ACAGTAGAGGCAGCCAGAACCTCACCGTCCAGGAGGACTGAGGTCCACAGACCTGCCT GGGCTCAAAGCAGCCACTCATTATACCATCACCATCCGCGGGGTCACTCAGGACTTCAGC ACAACCCCTCTCTCTGTTGAAGTCTTGACAGAGGAGGTTCCAGATATGGGAAACCTCACA GTGACCGAGGTTAGCTGGGATGCTCTCAGACTGAACTGGACCACGCCAGATGGAACCTAT GACCAGTTTACTATTAGGTCCAGGAGGCTGACCAGGTGGAAGAGGCTCACAATCTCACG GTTCTTGGCAGCCTGCGTTCCATGGAAATCCAGGCCTCAGGGCTGGCACTCCTTACACA GTCACCTTGCACGGCAGGTGAGGGGCCACAGCACTCGACCCCTTGCTGTAGAGGTGCTC ACAGAGGATCTCCACAGCTGGGAGATTTAGCCGTGTCTGAGGTTGGCTGGGATGGCCCTC AGACTCAACTGGACCGCAGCTGACAATGCCTATGAGCACTTTGTCACTTGGAGTGAGGAG GTCAACAAGTGGAGGCAGCCAGAACCTCACGTTGCCTGGCAGCCTCAGGGCTGTGGAC ATCCGGGGCCTCGAGGCTGCCACGCCTTATAGAGTCTCATCTATGGGGTGATCCGGGGC TATAGAACACCAGTACTCTCTGCTGAGGCCTCCACAGCCAAAGAACTGAAATTGGAAC TTAAATGTTTCTGACATAACTCCCGAGAGCTTCAATCTCTCTGGATGGCTACCGATGGG ATCTTCGAGACCTTACCATTGAAATTATGATTCCAATAGGTTGCTGGAGACTGTGGAA TATAATATCTCTGGTGTGACGAAGTCCCATATCTCAGGGCTACCCCTAGTACTGAT TTTATTGTCTACCTCTCTGGACTTGCTCCAGCATCCGGACCAAAACCATCAGTGCCACA
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GCCACGACAGAGGCCCTGCCCTTCTGGAAAACCTAACCATTTCCGACATTAATCCCTAC GGGTTACAGTTTCTGGATGGCATCGGAGAATGCCTTTGACAGCTTCTAGTAACGGTG GTGGATTCTGGGAAGCTGCTGGACCCCAGGAATTCACACTTTCAGGAACCCAGAGGAAG CTGGAGCTTAGAGGCCCTATAACTGGCATTGGCTATGAGGTTATGGTCTCTGGCTTACC CAAGGGCATCAAACCAAGCCCTTGAGGGCTGAGATTGTTACAGAAGCCGAACCGAAGTT GACAACCTTCTGGTTTCAGATGCCACCCCAGACGGTTTCCGTCTGTCTGGACAGCTGAT GAAGGGGTCTTCGACAATTTTGTCTCAAATCAGAGATACAAAAAGCAGTCTGAGCCA CTGGAAATAACCTACTTGCCCCGAACGTACCAGGGACATAACAGGTCTCAGAGAGGCT ACTGAATACGAAATTGAACTCTATGGAATAAGCAAAGGAAGGCGATCCCAGACAGTCAGT GCTATAGCAACAACAGCCATGGGCTCCCCAAGGAAGTCATTTTCTCAGACATCACTGAA AATTCGGCTACTGTCACTGGAGGGCACCCACGGCCCAAGTGGAGAGCTTCCGGATTACC TATGTGCCCATACAGGAGGTACACCTCCATGGTAAGTGTGGACGGAACCAAGACTCAG ACCAGGCTGGTGAACTCATACCTGGCGTGGAGTACCTTGTGAGCATCATCGCCATGAAG GGCTTTGAGGAAAGTGAACTGTCTCAGGGTCATTACCCACAGCTCTGGATGGCCCATCT GGCCTGGTGACAGCCAACATCACTGACTCAGAAGCCTTGGCCAGGTGGCAGCCAGCCATT GCCACTGTGGACAGTTATGTCTCTCTACACAGGCGAGAAAGTGCCAGAAATTACACGC ACGGTGTCCGGGAACACAGTGGAGTATGCTCTGACCGACCTCGAGCCTGCCACGGAATAC ACACTGAGAATCTTTCAGAGAAAGGGCCCGAGAAGAGCTCAACCATCACTGCCAAGTTC ACAACAGACCTCGATTCTCCAAGAGACTTGACTGCTACTGAGGTTCACTCGGAAACTGCC CTCCTTACCTGGCGACCCCCCGGGCATCAGTCACCGGTTACCTGCTGGTCTATGAATCA GTGGATGGCAGTCAGGAAGTCAATTGTGGGTCCAGATACCACTCTACAGCTGGCA GACCTGAGCCCATCCACCCACTACACAGCCAAGATCCAGGCACTCAATGGGCCCCTGAGG AGCAATATGATCCAGACCATTTTACCACAATTGGACTCCTGTACCCCTTCCCCAAGGAC TGCTCCCAAGCAATGCTGAATGGAGACACGACCTCTGGCCTCTACACCATTATCTGAAT GGTGATAAGGCTCAGGCGCTGGAAGTCTTCTGTGACATGACCTCTGATGGGGGTGGATGG ATTGTGTTCTTGAGACGCAAAAACGGACGCGAGAAGTCTACCAAACTGGAAGGCATAT GCTGCTGGATTGTTGGGGACCGCAGAGAAGAATTCTGGCTTGGGCTGGACAACCTGAACAAA ATCACAGCCCAGGGGCAGTACGAGCTCCGGGTGGACCTGCGGGACCATGGGGAGACAGCC TTTGCTGTCTATGACAAGTTCAGCGTGGGAGATGCCAAGACTCGCTACAAGCTGAAGGTG GAGGGGTACAGTGGGACAGCAGGTGACTCCATGGCCTACCACAATGGCAGATCCTTCTCC ACCTTTGACAAGGACACAGATTGAGCCATCACCACCTGTGCTCTGTCTACAAGGGGCTTC TGGTACAGGAAGTGTACCGTGTCAACCTGATGGGGAGATATGGGGACAATAACACAGT CAGGGCGTTAACTGGTTCCACTGGAAGGGCCACGAACACTCAATCCAGTTTGTGAGATG AAGCTGAGACCAAGCAACTTCAGAAATCTTGAAGGCAGGCGCAACCGGCATAAATTGGA GGGACCACTGGGTGAGAGAGGAATAAGGCGGCCAGAGCGAGGAAAGGATTTTACCAAG CATCAATACAACAGCCCAACCATCGGTCCACACTGGGCATTGGTGAGAAATCAAGCT GACCATGGATCCCTGGGGCCAACGGCAACAGCATGGGCCTCACTCTCTGTGATTTCTT TCTTTGCACCAAGACATCAGTCTCCAACATGTTTCTGTTTTGTTGTTTATTGATTAGCAAA AATCTCCAGTGACAACATCGCAATAGTTTTTACTTCTCTTAGGTGGCTCTGGGATGGG AGAGGGGTAGGATGTACAGGGGTAGTTGTTTTAGAACAGCCGTATTTTACATGAAGCT GTATAATTAATTGTCATTATTTTGTAGCAAGATTAAATGTGTCATTGGAAGCCATCC CTTTTTTACATTTTATACAACAGAAACAGAAAGCAATACTGTTTCCATTTTAAGGAT ATGATTAATATTATTAATATAATAATGATGATGATGATGATGAAAACTAAGGATTTTCA AGAGATCTTTCTTTCCAAACATTTCTGGACAGTACCTGATTGATTTTTTTTTTAAATA AAAGCACAGTACTTTTGAAAAAAA			
ORF Start: ATG at 55		ORF Stop: TAA at 6652	
SEQ ID NO: 182		2199 aa	MW at 240715.6kD
NOV35a, CG55832-01 Protein Sequence	MGAMTQLLAGVFLAFLALATEGGVLKKVIRHKRQSGVNATLPEENQPVVFNHVYNIKL PVGSQCSVDLESASGEKDLAPPSEPSFQEHVTDGENQIVFTHRINIPRRACGCAAPDV KELLSRLEELLENLVSSLRBQCTAGAGCCLQPATGRDLTRPFCSGRGNFSTEGCGCV CEPGWKGPNCSEPECPGNCHLRGRCIDGQCI CDDGFTGEDCSQLACPSDCNDQKCV NVCICFEGYAADCSREICPVPCSEEHGTCDVGLCVCHDGFAGDDCNKPLCLNNCYNR GRVCVENECVCDEGFTGEDCSELICPNDCFDRGRINGTCYCEEGFTGEDCGKPTCPH ACHTQGRCEEGQCVCDEGFAGVDCSEKRCPADCHNRGRCDVGRCEDDGFTGADCGEL KCPNGCSGHGRVCVNGQCVCDEGYTGEDCSQLRCPNDCHSRGRCEVEGKVCVEQGF KYDCSDMSPNDCHQHGRVCVNGMCMVCDDGYTGEDCDRQCPDRCSNRGLCVDGQC VEDGFTGPDCAELSCPNDCGQGRVCVNGQCVCHEGFMGDKCEQRCPSDCHGQGR CVDGQCICHEGFTGLDCGQHSCLPDCNNLQGCVSGRCICNEGYSGEDCSEVSP PKDLVVTEVTEETVNLAWDNEMRVTEYLVVYTPTHE		

	<p>GGLEMQFRVPGDQTSTIIRELEPGVEYFIRVFAILNKKSI PV SARVATYLPAP EGLKFK SIKETSVEVEWDPLDI AFETWEI IFRNMNKEDEGEITKSLRRPETS YRQTGLAPGQEY EI SLHIVKNNTRGPGLKRVTTTRLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKD VPGDRTTIDLTEDENQYSIGNLKPDT EYEVSLISRRGDMSSNPAKETFTTGLDAPRNLR VSQTDNSITILEWRNGKAAIDSYRIKYAPISGGDHA EVDVPKSSQQA TTKTTLTGLRPGTEY GIGVSAVKEDKESNPATINAATELDT PKDLQVSETAETSLTLWKTP LAKFDRYRLNYSL PTGQWVGVLPRNTTSYVLRGLEPGQEYNVLLTAEKGRHKS KPARVKASTEQAPELENLT VTEVGWDGLRLNWTAA DQAYEHFIIQVQEANKVEAARNLTVP GSLRAVDIPGLKAATPYT VSIYGVIOGYRTPVLSAEASTGETPNLGEVVVAE VGDALKLNWTAPEGAYEYFFIQVQE ADTVEAAQNLTVPGLRSTDL PGLKAATHYTTIRGVTQDFSTT PLSVEVLTEEV PDMGN LTVTEVSWDALRLNWTTPDGT YDQFTIQVQEADQVEEAHNLTVPGSLRSM EIPGLRAGTP YTVTLHGEVRGHSTRPLAVEVVTEDLPQLGDLAVSEV GWDGLRLNWTAA DNAYEHFVIQV QEVNKVEAAQNLTLP GSLRAVDIPGLEAATPYRVS IYGVIRGYRTPVLSAEASTAKEPEI GNLNVSDITPESFNLSW MATDGIFETFTIEIIDS NRLLTVEYNTSGAERTAHISGLPPS TDFIVYLSGLAPSIRTKTISATATTEALPLENLTISDINPYGFTVSWMA SENAFDSFLV TVVDSGKLLDPQEFTLSGTQRKLELRGLITGIGYEV MVSGFTQGHQTKPLRAEYITEAEP EVDNLLVSDATPDGFR LSWTADEGVFDNFVLKIRD TKKQSEPLEITLLAPERTRDITGLR EATEYEIELYGISKRRSQT VSAIATTAMGSPKEVIFSDITENSATVSWRAPTAQVESFR ITYVPITGGT PSMVTV DGTKTQRLVKLIPGVEYLVSI IAMKGFESEPVSGSFTTALD G PSGLVTANITDSEALARWQPAIATVDSYVISYTG EKVP EITRTVSGNTVEYALTDLEPAT EYTLRIFA EKGPKSSITAKFTTDLDSPRDLTATEVQSE TALLTWRRPPRASVTGYLLVY ESVDGTVKEVIVGPD TTSYSLADLSPSTHYTAKIQA L NGPLRSNM IQTIFTTIGLLYPPF KDCSQAM L NGDTTSGLYTIYLN GDKAQALEVFCDM TSDGGGWIVFLRRKNGRENFYQNWK AYAAGFGDRREEFWL GDLN LNKITAQQQYELRV DLRDHGETAFAYVDKFSVGDAKTRYKL KVEGYSGTAGDSMAYHNGRS FSTFDKDTSAITNCALSTRGF WYRNCHRVNL MGRYGDNN HSQGVNWFHWKGHEHSIQFAEMKLRPSNFRNLEGR RKRA</p>
	<p>SEQ ID NO: 183 7013 bp</p>
NOV35b. CG55832-03 DNA Sequence	<p>GAATTCGCTAGAGCCCTAGAGCCCCAGCAGCACCCAGCCAAACCCACCTCCACCATGGGG GCCATGACTCAGCTGTTGGCAGGTGCTTCTTGCTTCCTTGCCCTCGCTACCGAAGGT GGGGTCCTCAAGAAAGTCATCCGGCACAAGCGACAGAGTGGGGTGAACGCCACCTGCCA GAAGAGAACCAGCCAGTGGTGTTAACCACGTTTACAACATCAAGCTGCCAGTGGGATCC CAGTGTTTCGGTGGATCTGGAGTCAGCCAGTGGGGAGAAAGACCTGGCACCGCCTTCAGAG CCCAGCGAAAGCTTTCAGGAGCACACAGTAGATGGGGAAAACAGATTGCTTTCACACAT CGCATCAACATCCCCCGCCGGCCTGTGGCTGTGCCGAGCCCTGATGTTAAGGAGCTG CTGAGCAGACTGGAGGAGCTGGAGAACCCTGGTGTCTTCCCTGAGGGAGCAATGTACTGCA GGAGCAGGCTGCTGTCTCCAGCCTGCCACAGGCCGCTTGGACACCAGGCCCTTCTGTAGC GGTCGGGGCAACTTCAGCACTGAAGGATGTGGCTGTGTCTGCGAACCTGGCTGGAAAGGC CCCAACTGCTCTGAGCCCCAATGTCCAGGCAACTGTACCTTCGAGGCCGCTGTCATTGAT GGGCAGTGCATCTGTGACGACGGCTTCACGGGCGAGGACTGCAGCCAGCTGGCTTGCCTC AGCGACTGCAATGACCAGGGCAAGTGCCTGAATGGAGTCTGCATCTGTTTCGAAGGCTAC GCGGCTGACTGCAGCCGTGAAATCTGCCAGTGCCTGCACTGAGGAGCACGGCACATGT GTAGATGGCTTGTGTGTGCCACGATGGCTTTGCAGGCGATGACTGCAACAAGCCTCTG TGTCTCAACAATTGCTACAACCGTGGACGATGCGTGGAGAATGAGTGCCTGTGTGATGAG GGTTTCAGGGCGAAGACTGCAGTGAGCTCATCTGCCCCAATGACTGCTTCGACCGGGGC CGCTGCATCAATGGCACCTGCTACTGCGAAGAAGGCTTCACAGGTGAAGACTGCGGGAAA CCCACCTGCCACATGCCTGCCACACCCAGGGCCGCTGTGAGGAGGGGAGTGTGTATGT GATGAGGGCTTGCCTGGTGTGGACTGCAGCGAGAAGAGGTGTCTGTGCTGACTGTCACAAT CGTGGCCGCTGTGTAGACGGGCGGTGTGAGTGTGATGATGGTTTCACTGGAGCTGACTGT GGGGAGCTCAAGTGTCCCAATGGCTGCAGTGGCCATGGCCGCTGTGTCAATGGGAGTGT GTGTGTGATGAGGGCTATACTGGGGAGGACTGCAGCCAGCTACGGTGCCCAATGACTGT CACAGTGGGGCCGCTGTGTGCGAGGGCAAATGTGTATGTGAGCAAGGCTTCAAGGGCTAT GACTGCAGTGACATGAGCTGCCCTAATGACTGTACCAGCACGGCCGCTGTGTGAATGGC ATGTGTGTTTGTGATGACGGCTACACAGGGGAAGACTGCCGGGATCGCCAATGCCCCAGG GACTGCAGCAACAGGGGCTCTGTGTGGACGGACAGTGCCTGTGTGAGGACGGCTTCACC GGCCCTGACTGTGCAGAACTCTCCTGTCCAAATGACTGCCATGGCCAGGGTGCCTGTGTG AATGGGCAGTGCCTGTGCCATGAAGGATTTATGGGCAAAGACTGCAAGGAGCAAAGATGT CCCAGTGA CTGT CATGGCCAGGGCCGCTGCGTGGACGGCCAGTGCATCTGCCACGAGGGC TTCACAGGCTGGACTGTGGCCAGCACTCCTGCCCCAGTGA CTGCAACA ACTTAGGACAA TGCGTCTCGGGCCGCTGCATCTGCAACGAGGGCTACAGCGGAGAAGACTGCTCAGAGGTG</p>

TCTCCTCCCAAAGACCTCGTTGTGACAGAAGTGACGGAAGAGACGGTCAACCTGGCCTGG
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 GAAACTCCCAATTTGGGAGAGGTGCTGGTGGCCGAGGTGGGCTGGGATGCCCTCAAACCTC
 AACTGGACTGCTCCAGAAGGGGCTATGAGTACTTTTTCATTGAGGTGCAGGAGGCTGAC
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 GACCAGTTTACTATTGAGGTCCAGGAGGCTGACCAGGTGGAAGAGGCTCACAATCTCAGC
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 ACAGAGGATCTCCACAGCTGGGAGATTTAGCCGTGTCTGAGGTTGGCTGGGATGGCCTC
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 AAGAGCTCAACCATCACTGCCAAGTTCAACAACAGACCTCGATTCTCCAAGAGACTTGACT
 GCTACTGAGGTTCACTCGGAACTGCCCTCCTTACCTGGCGACCCCCCGGCATCAGTC

	<p>ACCGTTACCTGCTGGTCTATGAATCAGTGGATGGCACAGTCAAGGAAGTCATTGTGGGT CCAGATACCACCTCTACAGCCTGGCAGACCTGAGCCCATCCACCCACTACACAGCCAAG ATCCAGGCACTCAATGGGCCCCCTGAGGAGCAATATGATCCAGACCATCTTCACCACAATT GGACTCCTGTACCCCTTCCCCAAGGACTGCTCCCAAGCAATGCTGAATGGAGACACGACC TCTGGCCTCTACACCATTATCTGAATGGTGATAAGGCTCAGGCGCTGGAAGTCTTCTGT GACATGACCTCTGATGGGGGTGGATGGATTGTGTTCTGAGACGCAAAAACGGACGCGAG AACTTCTACCAAACTGGAAGGCATATGCTGCTGGATTGTTGGGACCGCAGAGAAGAATTC TGGCTTGGGCTGGACAACCTGAACAAAATCACAGCCCAGGGGACGTACGAGCTCCGGGTG GACCTGCGGGACCATGGGGAGACAGCCTTTGCTGTCTATGACAAGTTCAGCGTGGGAGAT GCCAAGACTCGCTACAAGCTGAAGGTGGAGGGGTACAGTGGGACAGCAGGTGACTCCATG GCCTACCACAATGGCAGATCCTTCTCCACCTTTGACAAGGACACAGATTGACCTCACC AACTGTGCTCTGTCTACAAGGGGCTTCTGGTACAGGAAGTGTCAACCTGTCAACCTGATG GGGAGATATGGGGACAATAACCAAGTCAAGGCGTTAACTGGTTCCACTGGAAGGGCCAC GAACACTCAATCCAGTTTGTCTGAGATGAAGCTGAGACCAAGCAACTTCAGAAATCTTGAA GGCAGGCGCAAACGGGCATAAATTGGAGGGACCACTGGGTGAGAGAGGAATAAGGCGGCC CAGAGCGAGGAAAGGATTTTACCAAAGCATCAATACAACAGCCCAACCATCGGTCCACA CCTGGGCATTGTTGGTGAGAATCAAAGCTGACCATGGATCCCTGGGGCCAACGGCAACAGCA TGGGCCTCACCTCCTCTGTGATTCTTTCTTGCACCAAGACATCAGTCTCCAACATGT TTCTGTTTGTGTTGTTGATTGAGCAAAAATCTCCAGTGACAACATCGCAATAGTTTTTT ACTTCTCTTAGGTGGCTCTGGGATGGGAGAGGGGTAGGATGTACAGGGGTAGTTGTTTT AGAACCAGCCGTATTTTACATGAAGCTGTATAATTAATTGTCATTATTTTGTAGCAAA GATTAAATGTGTCTATTGGAAGCCATCCCTTTTTTACATTTATACAACAGAAACAGAA AAGCAATACTGTTTCCATTTTAAGGATATGATTAATATTATTAATATAATAATGATGATG ATGATGATGAAACTAAGGATTTTCAAGAGATCTTTCTTCCAAACATTTCTGGACAG TACCTGATTGTATTTTTTTTTTAAATAAAAGCACAAAGTACTTTTTGAAAAAAA</p>
	<p>ORF Start: ATG at 55</p>
	<p>ORF Stop: TAA at 6379</p>
	<p>SEQ ID NO: 184</p>
	<p>2108 aa</p>
	<p>MW at 230729.3kD</p>
<p>NOV35b, CG55832-03 Protein Sequence</p>	<p>MGAMTQLLAGVFLAFLALATEGGVLKKVIRHKRQSGVNATLPEENQPVVFNHVYNIKLPV GSQCSVDLESASGEKDLAPPSESPSESPQHEITVDGENQIVFTHRINIPRRACGCAAAPDVK ELLSRLEELLENLVSSLREQCTAGAGCCLOPATGRDLTRPFCSGRGNFSTEGCGVCVCEPGW KGPNCSEPECPCGNCHLRGRCIDGQCICDDGFTGEDCSQLACPSDCNDQKCVNGVCI CFE GYAADCSREICPVPCSEEHGTCDVGLCVCHDGFAGDDCNKPLCLNNCYNRGRVCVENECVC DEGFTGEDCSELICPNDCDFRGRINGTCYCEEGFTGEDCGKPTCPHACHTQGRCEEGQC VCDEGFAGVDCSEKRCPCADCHNRGRCDVGRCEDDGFTGADCGELKCPNGCSGHGRVCNG QCVDEGYTGEDCSQLRCPNDCHSRGRVCEGKVCVEQGFQGYDCSDMSCPNDCQHGRVC NGMCVDDGYTGEDCDRQRCPRDCSNRGLCVDGQCVCEGFTGPDCAELSCPNDCHGQGR CVNGQCVCHGFMGKDCKEQRCPSDCHGQGRCDVGGQCI CHEGFTGLDCGQHSCPSDCNNL GQCVSGRCICNEGYSGEDCSEVSPPKDLVVTEVTEETVNLAWDNEMRVTEYLVVYTPTHE GGLEMQFRVPGDQTSTIIRELEPGVEYFIRVFAILENKKSI PV SARVATYLPAPGLKFK SIKETSVEVEWDPLDIAFETWEII FRNMNKEDEGEITKSLRRPETSRYQTGLAPGQYEYI SLHIVKNNTRGPGLKRVTTTRLDAPSQIEVKDVTDTALITWFKPLAEIDGIELTYGIKD VPGDRTTIDLTEDENQYSIGNLKPDTYEYVSLISRRGDMSSNPAKETFTTGLDAPRNLRR VSQTDNSITLEWRNGKAAIDSYRIKYAPISGGDHAEVDVPSQQAATTKTTLTGLRPGTEY GIGVSAVKEDKESNPATINAATELDTPKDLQVSETAETSLTLLWKTPLAKFDRYRLNYSL PTGQWVGVLPRNTTSYVLRGLEPGQYENVLLTAEKGRHKS KPARVKASTEQAPELENLT VTEVGWDGLRLNNTAADQAYEHFIIQVQEAANKVEAARNLTVPGLRAVDIPGLKAATPYT VSIYGVIIQGYRTPVLSAEASTGETPNLGEVVVAEVGWDALKLNWTAPEGAYEYFFIQVQE ADTVEAAQNLTVPGLRSTDLPLGLKAATHYITIRGVTQDFSTPLSVEVLTEVPDMGN LTVTEVSWDALRLNWTTPDGYDQFTIQVQEAQVVEAHNLTVPGLSRSMIEI PGLRAGTP YTVTLHGEVRGHSTRPLAVEVVTEDLPQLGDLAVSEVGWDGLRLNNTAADNAYEHFVIQV QEVNKVEAAQNLTLPGLRAVDIPGLEAATPYRVSIYGVIRGYRTPVLSAEASTAKEPEI GNLNVSDITPESFNLSWMATDGI FETFTIEIIDSRLLETVEYNISGAERTAHISGLPPS TDFIVYLSGLAPSIRTKTISATATTEAPEVDNLLVSDATPDGFRLSWTADEGVDFDNFVL KIRDTKKQSEPLEITLLAPERTRDITGLREATEYEI ELYGISKRRRSQTVSAIATTAMGS PKEVIFSDITENSATVSWRAPTAQVESFRITYVPTITGGTSPSMVTVDGTKTQTRLVKLI PG VEYLVSI IAMKGFESEFPVSGSF TTDALDGPSGLVTANITDSEALARWQPAIATVDSYVIS YTGEKVPEITRTVSGNTVEYALTDLEPATEYTLRIFAEGKPKSSITITAKFTTDLDSPRD LTATEVQSETALLTWRPPRASVTGYLLVYESVDGTVEVIVGPDTSYSLSADLSPSTHYT</p>

	AKIQALNGPLRSNMIQTIFTTIGLLYPFPKDCSQAMLNQDTSGLYTIYLNQDKAQALEV FCDMTSDGGGWIVFLRRKNGRENFYQNWKAYAAGFGDRREEFWLGLDNLNKITAQGGYEL RVDLRDHGETAFAYDKFSVGDATRYKLKVEGYSGTAGDSMAYHNGRSFSTFDKDTDSA ITNCALSTRGFWRNCHRVNLMGRYGDNNHSQGVNWFHWKGHEHSIQFAEMKLRSNFRN LEGRRKRA
	SEQ ID NO: 185 5375 bp
NOV35c, CG55832-02 DNA Sequence	GAATTCGCTAGAGCCCTAGAGCCCCAGCAGCACCCAGCCAAACCCACCTCCACCATGGGG GCCATGACTCAGCTGTTGGCAGGTGTCTTTCTTGCTTCCTTGCCCTCGCTACCGAAGGT GGGGTCCTCAAGAAAGTCATCCGGCACAAGCGACAGAGTGGGGTGAACGCCACCTGCCA GAAGAGAACCAGCCAGTGGTGTTTAACCACGTTTACAACATCAAGCTGCCAGTGGGATCC CAGTGTTCGGTGGATCTGGAGTCAGCCAGTGGGGAGAAAGACCTGGCACCGCCTTCAGAG CCCAGCGAAAGCTTTCAGGAGCACACAGTAGATGGGGAAAACAGATTGTCTTCACACAT CGCATCAACATCCCCCGCGGGCCTGTGGCTGTGCGCAGCCCTGATGTTAAGGAGCTG CTGAGCAGACTGGAGGAGCTGGAGAACCCTGGTGTCTTCCTGAGGGAGCAATGTACTGCA GGAGCAGGCTGCTGTCTCCAGCCTGCCACAGGCCGCTGGACACCAGGCCCTTCTGTAGC GGTCGGGGCAACTTCAGCACTGAAGGATGTGGCTGTCTGCGAACCTGGCTGGAAAGGC CCCAACTGCTCTGAGCCCCGAATGTCCAGGCAACTGTACCTTCGAGGCCGGTGCATTGAT GGGCAGTGCATCTGTGACGACGGCTTCACGGGCGAGGACTGCAGCCAGCTGGCTGGCCCC AGCGACTGCAATGACCAAGGCAAGTGCCTGAATGGAGTCTGCATCTGTTTCGAAGGCTAC GCGGCTGACTGCAGCCGTGAATCTGCCAGTGCCTGCAGTGAGGAGCACGGCACATGT GTAGATGGCTTGTGTGTGTGCACGATGGCTTGCAGCGCATGACTGCAACAAGCCTCTG TGTCTCAACAATTGCTACAACCGTGGACGATGCGTGGAGAATGAGTGCCTGTGTGATGAG GGTTTCACGGGCGAAGACTGCAGTGAGCTCATCTGCCCAATGACTGCTTCGACCGGGGC CGCTGCATCAATGGCACCTGCTACTGCGAAGAAGGCTTCACAGGTGAAGACTCGGGGAAA CCCACCTGCCACATGCCTGCCACACCCAGGGCCGGTGTGAGGAGGGGCAGTGTGTATGT GATGAGGGCTTTGCGGGTGTGGACTGCAGCGAGAAGAGGTGTCTGCTGACTGTCACAAT CGTGGCCGCTGTGTAGACGGGCGGTGTGAGTGTGATGATGGTTTCACTGGAGCTGACTGT GGGGAGCTCAAGTGTCCCAATGGCTGCAGTGGCCATGGCCGCTGTGTCAATGGGCAGTGT GTGTGTGATGAGGGCTATACTGGGGAGGACTGCAGCCAGCTACGGTGCCTCAATGACTGT CACAGTCGGGGCCGCTGTGTGAGGGCAAATGTGTATGTGAGCAAGGCTTCAAGGGCTAT GACTGCAGTGACATGAGCTGCCCTAATGACTGTACCAGCACGGCCGCTGTGTGAATGGC ATGTGTGTTTTGTGATGACGGCTACACAGGGGAAGACTGCCGGGATCGCCAATGCCCCAGG GACTGCAGCAACAGGGGCCCTCTGTGTGGACGGACAGTGCCTGTGTGAGGACGGCTTCACC GGCCCTGACTGTGCAGAACTCTCTGTCCAAATGACTGCCATGGCCAGGGTCTGCTGTGTG AATGGGCAGTGCCTGTGCCATGAAGGATTTATGGGCAAAGACTGCAAGGAGCAAAGATGT CCCAGTGAATGTGATGGCCAGGGCCGCTGCGTGGACGGCCAGTGCATCTGCCACGAGGGC TTCACAGGCCTGGACTGTGGCCAGCACTCCTGCCCCAGTGAATGCAACAATTAGGACAA TGCGTCTCGGGCCGCTGCATCTGCAACGAGGGCTACAGCGGAGAAGACTGCTCAGAGGTG TCTCTCCCAAAGACTCGTTGTGACAGAAGTGACGGAAGAGACGGTCAACCTGGCTGG GACAATGAGATGCGGGTCACAGAGTACCTTGTCTGTACACGCCCCACCCACGAGGGTGGT CTGGAATGCAGTTCCGTGTGCTGGGGACAGAGCTCCACCATCATCCGGGAGCTGGAG CCTGGTGTGGAGTACTTTATCCGTGTATTTGCCATCCTGGAGAACAAGAAGAGCATTCCCT GTCAGCGCCAGGGTGGCCACGTACTTACCTGCACCTGAAGGCCTGAAATTCAGTCCATC AAGGAGACATCTGTGGAAGTGGAGTGGATCCTTAGACATTGCTTTTGAAACCTGGGAG ATCATCTTCCGAATATGAATAAAGAAGATGAGGGAGAGATCACCAAAGCCTGAGGAGG CCAGAGACCTCTTACCGGCAAACCTGGTCTAGCTCCTGGGCAAGAGTATGAGATATCTCTG CACATAGTGAAAAACAATACCCGGGGCCCTGGCCTGAAGAGGGTGACCACCACACGCTTG GATGCCCCAGCCAGATCGAGGTGAAGATGTACAGACACCACTGCCTTGATCACCTGG TTCAAGCCCCCTGGCTGAGATCGATGGCATTGAGCTGACCTACGGCATCAAAGACGTGCCA GGAGACCGTACCACCATCGATCTCACAGAGGACGAGAACCAGTACTCCATCGGGAACCTG AAGCCTGACACTGAGTACGAGGTGTCCCTCATCTCCCGCAGAGGTGACATGTCAAGCAAC CCAGCCAAAGAGACCTTCAACACAGGCCTCGATGCTCCAGGAATCTTCGACGTGTTTCC CAGACAGATAACAGCATCACCTGGAATGGAGGAATGGCAAGGCAGCTATTGACAGTTAC AGAATTAAGTATGCCCCATCTCTGGAGGGGACCAAGCTGAGGTTGATGTTCCAAAGAGC CAACAAGCCACAACCAAAACCACTCACAGGTCTGAGGCGGGAACTGAATATGGGATT GGAGTTTCTGCTGTGAAGGAAGACAAGGAGAGCAATCCAGCGACCATCAACGCAGCCACA GAGTTGGACACGCCCCAAGGACCTTCAGGTTTCTGAAACTGCAGAGACCAGCCTGACCCTG CTCTGGAAGACACCGTTGGCCAAATTTGACCGCTACCGCCTCAATTACAGTCTCCCCACA GGCCAGTGGGTGGGAGTGCAGCTTCCAAGAAACACCACTTCTATGTCTGAGAGGCCCTG

	GAACCAGGACAGGAGTACAATGTCTCTGACAGCCGAGAAAGGCAGACACAAGAGCAAG CCCGCACGTGTGAAGGCATCCACTGCCATGGGCTCCCCAAAGGAAGTCATTTTCTCAGAC ATCACTGAAAATTTCGGCTACTGTCTAGCTGGAGGGCACCCACAGCCCAAGTGGAGAGCTTC CGGATTACCTATGTGCCCATTACAGGAGGTACACCCTCCATGGTAACTGTGGACGGAACC AAGACTCAGACCAGGCTGGTGAAACTCATACCTGGCGTGGAGTACCTTGTTCAGCATCATC GCCATGAAGGGCTTTGAGGAAAGTGAACCTGTCTCAGGGTCATTACCACAGCTCTGGAT GGCCCATCTGGCCTGGTGACAGCCAACATCACTGACTCAGAAGCCTTGGCCAGGTGGCAG CCAGCCATTGCCACTGTGGACAGTTATGTCTCTCTACACAGGCGAGAAAGTGGCAGAA ATTACACGCACGGTGTCCGGGAACACAGTGGAGTATGCTCTGACCGACCTCGAGCCTGCC ACGGAATACACACTGAGAATCTTTGCAGAGAAAGGGCCCCAGAAGAGCTCAACCATCACT GCCAAGTTCACAACAGACCTCGATTCTCCAAGAGACTTGACTGCTACTGAGGTTTCAGTCG GAAACTGCCCTCTTACCTGGCGACCCCCCGGGCATCAGTCACCGGTTACCTGTCTGGTC TATGAATCAGTGGATGGCACAGTCAAGGAAGTCATTGTGGGTCCAGATACCACCTCCTAC AGCCTGGCAGACCTGAGCCCATCCACCCACTACACAGCCAAGATCCAGGCACTCAATGGG CCCCTGAGGAGCAATATGATCCAGACCATCTTACCACAATTGGACTCCTGTACCCTTTC CCCAAGGACTGCTCCCAAGCAATGCTGAATGGAGACACGACCTCTGGCCTCTACACCATT TATCTGAATGGTGATAAGGCTCAGGCGCTGGAAGTCTTCTGTGACATGACCTCTGATGGG GGTGGATGGATTGTGTCTCTGAGACGCAAAAACGGACGCGAGAACTTTACAAAACTGG AAGGCATATGCTGCTGGATTGTTGGGGACCGCAGAGAAGAAATCTGGCTTGGGCTGGACAAC CTGAACAAAATCACAGCCAGGGGCAGTACGAGCTCCGGGTGGACCTGCGGGACCATGGG GAGACAGCCTTTGCTGTCTATGACAAGTTTCAGCGTGGGAGATGCCAAGACTCGCTACAAG CTGAAGGTGGAGGGGTACAGTGGGACAGCAGGTGACTCCATGGCCTACCACAATGGCAGA TCCTTCTCCACCTTTGACAAGGACACAGATTACGCCATCACCACCTGTCTGTCTACA AGGGGCTTCTGGTACAGGAAGTGTACCGTGTCAACCTGATGGGGAGATATGGGGACAAT AACCACAGTCAGGGCGTTAACTGGTTCCTGGAAGGGCCACGAACACTCAATCCAGTTT GCTGAGATGAAGCTGAGACCAAGCAACTTCAGAAATCTTGAAGGCAGGCGCAAAACGGCA TAAATTGGAGGGACCACTGGGTGAGAGAGGAATAAGGCGGCCAGAGCGAGGAAAGGATT TTACCAAAGCATCAATACAACCAGCCCAACCATCGGTCCACACCTGGGCATTTGGTGAGA ATCAAAGCTGACCATGGATCCCTGGGGCCAAACGGCAACAGCATGGGCTCACCTCCTCTG TGATTTCTTTCTTTGACCAAAGACATCAGTCTCCAACATGTTTCTGTTTGTGTTTGA TTCAGCAAAAATCTCCAGTGACAACATCGCAATAGTTTTTACTTCTCTTAGGTGCTC TGGGATGGGAGAGGGGTAGGATGTACAGGGGTAGTTTGTGTTTAGAACCAGCCGATTTT CATGAAGCTGTATAATTAATTGTCATTATTTTGTGTTAGCAAAGATTAAATGTGTCTATTG AAGCCATCCCTTTTTTACATTTATACAAACAGAAACCAGAAAAGCAATACTGTTTCCAT TTTAAGGATATGATTAATATTATTAATAATAATGATGATGATGATGATGAAAACTAAG GATTTTTCAAGAGATCTTTCTTTCCAAAACATTTCTGGACAGTACCTGATTGTATTTTT TTTTAAATAAAAGCACAGTACTTTTGAAAAAAA		
	ORF Start: ATG at 55		ORF Stop: TAA at 4741
	SEQ ID NO: 186	1562 aa	MW at 171222.6kD
NOV35c, CG55832-02 Protein Sequence	MGAMTQLLAGVFLAFLALATEGGVLKKVIRHKRQSGVNATLPEENQPVVFNHVNLIKLPV GSQCSVDLESASGEKDLAPPSEPSFQEHTVDGENQIVFTHRINIPRRACGCAAPDVK ELLSRLEELLENLVSSLREQCTAGAGCCLQPATGRLDTRPFCSGRGNFSTEGCGVCEPGW KGPNCSEPECNCHLRGRCIDGQCICDDGFTGEDCSQLACPSDCNDQGKCVNGVCICFE GYAADCSREICPVPCSEEHGTCVDGLCVCHDGFAGDDCNKPLCLNNCYNRGRVCVENECVC DEGFTGEDCSELICPNDFDRGRINGTCYCEGFTGEDCGKPTCPHACHTQGRCEBEGQC VCDEGFAGVDCSEKRCPADCHNRGRCDVGRCEDDGFTGADCGELKCPNGCSGHGRVNG QCVCEGYTGEDCSQLRCPNDCHSRGRVCVEGKCVCEQGFKGYDCSDMSCPNDCHQHGRV NGMCVDDGYTGEDCRDRQCPRDCSNRGLCVDGQCVCEDGFTGPDCAELSCPNDCHGQGR CVNGQCVCHGFMGDKCEQRCPDCHGQGRCDGQCICHEGFTGLDCGQHSCPSDCNNL GQCVSGRICNEGYSGEDCSEVSPKDLVVTEVTEETVNLAWDNEMRVTEYLVTPTHE GGLEMQFRVPGDQTSTIIRELEPGVEYFIRVFAILENKKSIPIVSARVATYLPAGEGLKFK SIKETSVEVEWDPLDIAFETWEIIFRNMNKEDEGEITKSLRRPETSRYQTGLAPGQYEI SLHIVKNNTRGPGLKRVTTTTRLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKD VPGDRTTIDLTEDENQYSIGNLKPDTYEVSLSRRGDMSSNPAKETFTTGLDAPRNLRR VSQTDNSITLEWRNGKAAIDSYRIKYAPISGGDHAEDVPKSSQATTKTTLTGLRPGTEY GIGVSAVKEDKESNPATINAATELDTPKDLQVSETAETSLTLWLKTPAKFDYRLNYSL PTGQWVGVLPRNTTSYVLRGLEPGQEYNVLLTAEKGRHKSPPARVKASTAMGSPKEVIF SDITENSATVSWRAPTAQVESFRITYVPITGGTPSMVTVDGKTQTRLVKLIPGEYVLVS		

IIAMKGFEESEPVSGSFTTALDGPSGLVTANITDSEALARWQPAIATVDSYVISYTGEKV PEITRTVSGNTVEYALTDLEPATEYTLRIFAEGPKQSSTITAKFTTDLSPDLTATEV QSETALLTWRPPRASVTGYLLVYESVDGTVKEVIVGPDTTSSYSLADLSPSTHYTAKIQAL NGPLRSNMIQTIFTTIGLLYPFPKDCSQAMLNDDTSSGLYTIYLNKDKAQALEVFCDMTS DGGGWIVFLRRKNGRENFYQNWKAYAAGFGDRREEFWLGLDNLNKITAQQQYELRVDLRD HGETAFAYVDKFSVGDATRYKLKVEGYSGTAGDSMAYHNGRSFSTFDKDTDSAITNCAL STRGFWYRNCHRVNLMGRYGDNNHSQGVNWFHWKGHEHSIQFAEMKLRPSNFRNLEGRRK RA

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 35B.

Table 35B. Comparison of NOV35a against NOV35b and NOV35c.		
Protein Sequence	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV35b	1..1884 1..1881	1595/1886 (84%) 1660/1886 (87%)
NOV35c	1..1332 1..1327	1079/1335 (80%) 1120/1335 (83%)

Twelve polymorphic variants of NOV35c have been identified and are shown in Table 41N.

- 5 Further analysis of the NOV35a protein yielded the following properties shown in Table 35C.

Table 35C. Protein Sequence Properties NOV35a	
PSort analysis:	0.8200 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in plasma membrane; 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Cleavage site between residues 23 and 24

A search of the NOV35a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 35D.

10

Table 35D. Geneseq Results for NOV35a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAR94562	Human cytotactin - <i>Homo sapiens</i> , 2199 aa. [WO9608513-A1, 21-MAR-1996]	1..2199 1..2199	2199/2199 (100%) 2199/2199 (100%)	0.0
AAB36935	Human tenascin-C - <i>Homo sapiens</i> , 2201 aa. [WO200066628-A1, 09-NOV-2000]	1..2199 1..2201	2194/2201 (99%) 2198/2201 (99%)	0.0
AAR94563	Chicken cytotactin - <i>Gallus</i> sp, 1810 aa. [WO9608513-A1, 21-MAR-1996]	1..1602 1..1581	848/1620 (52%) 1121/1620 (68%)	0.0
AAM39043	Human polypeptide SEQ ID NO 2188 - <i>Homo sapiens</i> , 4618 aa. [WO200153312-A1, 26-JUL-2001]	627..2194 2901..4616	544/1741 (31%) 834/1741 (47%)	0.0
AAW18824	Human restrictin - <i>Homo sapiens</i> , 1358 aa. [US5635360-A, 03-JUN-1997]	484..1414 188..1107	338/935 (36%) 528/935 (56%)	0.0

In a BLAST search of public sequence databases, the NOV35a protein was found to have homology to the proteins shown in the BLASTP data in Table 35E.

Table 35E. Public BLASTP Results for NOV35a

Protein Accession Number	Protein/Organism/Length	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P24821	Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Miotendinous antigen) (Glioma-associated-extracellular matrix antigen) (GP 150-225) (Tenascin-C) (TN-C) - <i>Homo sapiens</i> (Human), 2201 aa.	1..2199 1..2201	2194/2201 (99%) 2198/2201 (99%)	0.0
JQ1322	tenascin precursor - mouse, 2019 aa.	1..1796 1..1791	1282/1807 (70%) 1453/1807 (79%)	0.0
Q64706	Tenascin C precursor - <i>Mus musculus</i> (Mouse), 2019 aa.	1..1796 1..1791	1277/1807 (70%) 1449/1807 (79%)	0.0

Q29116	Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Miotendinous antigen) (Glioma-associated- extracellular matrix antigen) (GP 150-225) (Tenascin-C) (TN-C) (P230) - <i>Sus scrofa</i> (Pig), 1746 aa.	1..1528 1..1521	1050/1532 (68%) 1213/1532 (78%)	0.0
P10039	Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Miotendinous antigen) (Glioma-associated- extracellular matrix antigen) (GP 150-225) - <i>Gallus gallus</i> (Chicken), 1808 aa.	1..1602 1..1579	849/1618 (52%) 1123/1618 (68%)	0.0

PFam analysis predicts that the NOV35a protein contains the domains shown in Table 35F.

Table 35F. Domain Analysis of NOV35a			
Pfam Domain	NOV35a Match Region	Identities/ Similarities for the Matched Region	Expect Value
EGF	185..216	10/48 (21%) 27/48 (56%)	0.34
EGF	251..278	13/47 (28%) 24/47 (51%)	0.51
EGF	283..309	12/47 (26%) 22/47 (47%)	0.0055
EGF	314..340	12/47 (26%) 21/47 (45%)	0.076
EGF	345..371	9/47 (19%) 20/47 (43%)	0.93
EGF	376..402	13/47 (28%) 22/47 (47%)	0.0026
EGF	407..433	14/47 (30%) 25/47 (53%)	0.0014
EGF	469..495	13/47 (28%) 22/47 (47%)	0.0049
EGF	500..526	13/47 (28%) 22/47 (47%)	0.0023
EGF	531..557	12/47 (26%) 23/47 (49%)	0.007

EGF	562..588	11/47 (23%) 24/47 (51%)	0.0033
EGF	593..619	12/47 (26%) 24/47 (51%)	0.023
fn3	622..700	29/85 (34%) 58/85 (68%)	5.5e-15
fn3	711..794	24/87 (28%) 65/87 (75%)	2.6e-13
fn3	802..881	26/85 (31%) 66/85 (78%)	1.9e-15
fn3	892..973	35/87 (40%) 65/87 (75%)	4.1e-19
fn3	984..1061	30/84 (36%) 65/84 (77%)	4.3e-16
fn3	1073..1156	26/87 (30%) 65/87 (75%)	2.8e-14
fn3	1164..1242	23/85 (27%) 58/85 (68%)	3.4e-13
fn3	1255..1334	26/85 (31%) 65/85 (76%)	3.4e-15
fn3	1346..1429	21/87 (24%) 64/87 (74%)	3.6e-13
fn3	1437..1513	20/85 (24%) 56/85 (66%)	8e-08
fn3	1528..1607	22/85 (26%) 58/85 (68%)	3.2e-11
fn3	1619..1698	21/85 (25%) 61/85 (72%)	2e-12
fn3	1709..1787	29/84 (35%) 58/84 (69%)	4.4e-17
fn3	1798..1875	23/84 (27%) 60/84 (71%)	8.5e-14
fn3	1886..1963	31/84 (37%) 60/84 (71%)	3.3e-19
fibrinogen_C	1979..2187	121/272 (44%) 208/272 (76%)	2.1e-134

Example 36.

The NOV36 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 36A.

Table 36A. NOV36 Sequence Analysis		
	SEQ ID NO: 187	4077 bp
NOV36a, CG56054-01 DNA Sequence	GGAGCGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGTCTGGGAGACGTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCTGCGAGA TTTCCTTGCATTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCTTGGGGGGCCTCCGGGATTTGCTACCTTTTGGCTCCCTGCTCGTGAAGTGC TCTTCTCAGGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGGCGAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCCTGGGCAGCAGGCGAATC GCACTGGAGGCCTCTTCGCTTGGCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTTCCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATATGAGGCAA GGCAGCAGTGGACAGATCCTGGAGACGCGGGATATGATTGGTGGCTGCTTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGAAGTTCTGTGAGGGAC GCCCCAAGGCCATGAACAATTTGGGTCTGCCAGCAGGGCACAGCTGCCGCCCTTCTCCC CTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTTGCTTT TTGTGACCAACATTGATAGCTCAGACCCCGACAGCTGGTGTATAAACTTTGAGACCCTG CTGACCGGCTCCCAGGACCAGCCGGAGACTTGGCCCTCAATAGCTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCGTGCAGAAGAGCTGAGCTTTGTGGTGGAGCCCCC GCGCCAACCACAAGGGTGTGTGGTTATCCTGCGCAAGGACAGCGCCAGTCGCTGGTGC CCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCCCCCTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGTCACTGGGCTG GGATCTCCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCTGGCTG TCCTGGGGACCTCAACCAAGATGGCTTTCAGATATTGCAGTGGGTGCCCCCTTTGATG GTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTGTGCGCAAACTTCAC AGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTGAGGCAGCT TGGATATGGATGGGAACCAATACCCTGACCTGTGGTGGGCTCCCTGGCTGACACCGCAG TGCTCTTCAGGGCCAGACCCTCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAA GCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCAAGGG TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATG TGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCGTGTGACGTTCCCTGA GCCGTAACCTGGAAGAACCACAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGC ATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTC GGGCCATTGTAGTGACCTTGTCTTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTC CTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCCTCAATGCCCCACAGCCAGCACCAGC GGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATC TGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATCCAACCTCTGC CCATGGATGTGGATGGAACAACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTGGCC TGGAGCTGATGGTACCAACCTGCCATCGGACCCAGCCAGCCAGCCAGGCTGATGGGATG ATGCCCATGAAGCCAGCTCCTGGTCATGCTTCTGACTCACTGCACTACTCAGGGGTCC GGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTG AGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACCTCATCCTTA GCACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGA TCAGTGAGCAGGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCAATTGAGCTGCCAC TGTCATTGCAGGAATGGCCATTCCCCAGCAACTCTTCTTCTCTGGTGTGGTGAGGGCG AGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGTCAAGTATGAGGTACAGGTTT CCAACCAAGGCCAGTCGCTCAGAACCTGGGCTCTGCCTTCTCAACATCATGTGGCCTC ATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGC AGGGGCTGGGCAGAAAGGGCTTGTCTCTCCAGGCCAACATCCTCCACCTGGATGTGG ACAGTAGGGATAGGAGGCGGGAGCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGC GGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAGAAGAAGAAAACATCA CCCTGGACTGCGCCCGGGCACGGCAACTGTGTGGTGTTCAGCTGCCACTCTACAGCT TTGACCGCGCGGCTGTGCTGCATGTCTGGGGCGTCTCTGGAACAGCACCTTTCTGGAGG AGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCAGTGAAAGTCTCT CCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATGGTATACTTGG ACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGTGATCCTCCTGGCTGTACTGG CTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTTCAAAC GGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAG	

	ACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCC CCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG GCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCCAGCCTGGCCTGT GGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCT GCTGGTGTGCGATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCAC CCACAAGAACTCCTCCCAACCACTTCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAA TCAGGGACAGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGCTCTGATGCAAAGGTGGG GAGAAGGGATCCTAATCCCTTCTCTCCCATCACCCTGTGTAAACAGGACCCCAAGGACC TGCTCCCCGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAG GCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTG GTTTCGTGGTTTCGTCTATTATTAAAAAATATTGAGAACAAAAA
	ORF Start: ATG at 162 ORF Stop: TAG at 3573 SEQ ID NO: 188 1137 aa MW at 124286.2kD
NOV36a, CG56054-01 Protein Sequence	MAGARSRDPWASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQADMQKESKE NQWLGVSVRSQGPQGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELGGGE WKFCBGRPQGHQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGLLFTVNISSDPDQLV YKTLDPADRLPGPAGDLALNSYLGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKD SASRLVPEVMSGERLTSGFGYS LAVADLNSDGWPD LIVGAPYFFERQEELGGAVVYVYN QGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDKVFIYHGSSLG VVAKPSQVLEGEAVGIKSFYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHE VSIAPRSIDLEQPNACAGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDADTDRRLRGQV PRVTFLSRNLLEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTP RLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQGGEDKIQSNLQLVHARFCTRVSD TEFQPLPMDVDGTTALFALSQGPVIGLELMVTNLPSDPAQPDADGDDAHEAQLLVMLPDS LHYSGVRLDPAEKPLCLSNENASHVECELGNPMKRGAVTFYLILSTSGIS IETTELEV ELLLATISEQLHPVSARARVFIELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKV KYEVTVSNQGSRLTLGSAFLNIMWPHEIANGKWL LYPMQVELEGGQGPQKGLCSRPNN ILHLDVDSRDRRRRELEPPEQEPGERQEPSMSWWPVSSAEKKKNITLDCARGTANCVVF SCPLYSFDRAAVLHVWGLWNSTFLEEYS AVKSLEIVRANITVKSSIKNMLLRDASTVI PVMVYLDPMVVAEAGVPWWVILLAVLAGLLVALLVLLWKMGGFFKRAKHPEATVPQYHA VKIPREDRQQFKEEKTGTILRNNWGS PRREGPD AHPILAADGHP ELGPDGHPGPGTA
	SEQ ID NO: 189 2564 bp
NOV36b, CG56054-03 DNA Sequence	GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGCTGGGAGACGCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGACCTGGGGCTTGGGGCGTGCAGAGA TTTCCCTTGCATTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCTTGGGGGGCTCCGGGATTTGCTACCTTTTGGCTCCCTGCTCGTGAAGTGC TCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTTGGCAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTGTGGCCCTGCACCGGCAGTTGCGACCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGCCTCTCGCTTGCCCGTTGAGCCTGGAGGAGACTGACTGTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGTTGGGAGTCA GTGTTTCGGAGCCAGGGCCTGGGGGCAAGATTGTTACCTGTGCACACCGATATGAGGCAA GGCAGCGAGTGGACCATCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGAC GCCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCC CTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTTGCTTT TTGTGACCAACATTGATAGCTCAGACCCGACAGCTGGTGTATAAACTTTGGACCTGT CTGACCGGCTCCCAAGGACAGCGGAGACTTGGCCCTCAATAGCTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCC GCGCCAACCACAAGGGTGTGTGGTTATCTGCGCAAGGACAGCGCCAGTGCCTGGTGC CCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCCCCCTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGTGCTGTGTATGTGTAAGTGAACAGGGGGTCACTGGGCTG GGATCTCCCTCTCCGGCTCTGCAACTCCCGCACTCCATGTTCCGGGATCAGCCTGGCTG TCCTGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATG GTGATGGGAAAGTCTTCACTACCATGGGAGCAGCCTGGGGGTTGTGCGCAACCTTCAC AGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTAGGCAGCT

	<p>TGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACCGCAG TGCTCTTCAGGGCCAGACCCATCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAA GCATCGACCTGGAGCAGCCCACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG TCTGTTTCAGCTACATTGCACTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATG TGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCTCTGA GCCGTAACTGGAAGAACCACAGCACCAGGCCCTCGGGCACCCTGTGGCTGAAGCACCAGC ATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAATGTCAAAGACAAGCTTC GGGCCATTGTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGGGAGGGCC CGGATGCACACCCCATCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATC CAGGGCCAGGCACCGCCTAGGTTCCCATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCC CTTCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTCCGATCA AGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAACTCTC CCACCCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCA TGGGGTAGGGTGAGAAGGGCAGGGGTGTCTGTATGCAAAGGTGGGGAGAAGGGATCCTAA TCCCTTCTCTCCATTACCCCTGTGTAACAGGACCCCAAGGACCTGCTCCCGGGAAGT GCCTTAACCTAGAGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCTTCTCTA GTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGT CTATTTATTAAAAATATTGAGAACAAAAA</p>
	<p>ORF Start: ATG at 162</p>
	<p>ORF Stop: TAG at 2058</p>
	<p>SEQ ID NO: 190</p>
	<p>632 aa</p>
	<p>MW at 68332.4kD</p>
NOV36b, CG56054-03 Protein Sequence	<p>MAGARSRDPWGASGICYLFGSLVLLFSLRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVIDIQGADMQKESKE NQWLGVSVRSQPGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDLDGGE WKFCEGRPQGHQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGLLFTNIDSSDPQLV YKTLDPADRLPGPAGDLALNSYLGSIDSGLVRAEELS FVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSGFGYSLAVADLNSDGNPDLLVIGAPYFFERQBELGGAVVYLN QGGHWAGISPLRLCNSPHSMFGISLAVLGDLDNQDGFDPDIAVGAPFDGDKVFIYHGSSLG VVAKPSQVLEGEAVGIKSGYSLSGSLMDGNQYPDLLVGLADTAVLFRARPILHVSHE VSIAPRSIDLEQPNACAGHSVCVDLRVCFYSIAVPSSYSPTVALDYLDADTDRLRGQV PRVTFLSRNLEBPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLTSLYSLQTP RLRREGPDAPHPILAADGHPDLGPDGHPGPGTA</p>
	<p>SEQ ID NO: 191</p>
	<p>2017 bp</p>
NOV36c, CG56054-04 DNA Sequence	<p>GGAGCGGCGGGCGGGCGGAGGGCTGGCGGGCGGAACGCTGGGAGACGCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTGGGGCGTGCAGAGA TTTCCCTTGCACTTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCTTGGGGGGCTCCGGGATTTGCTACCTTTTGGCTCCCTGCTCGTCAACTGC TCTTCTCAGGGGCTGTCGCCTTCAATCTGGACGTGATGGGTGCCTTGCAGCAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCAGGCCCTGGCTCTTCTGGGACAGGCGAATC GCACTGGAGGCCTCTTCGCTTGGCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATATGAGGCAA GGCAGCGAGTGGACCAGATCTGGAGACGCGGGATATGATTGGTTCGCTGCTTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGAAGTTCTGTGAGGGAC GCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCC CTGATAGCCACTACCTCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTGCTTT TTGTGACCAACATTGATAGCTCAGACCCGACAGCTGGTGTATAAACTTTGACCCCTG CTGACCGGCTCCCAGGACAGCCGAGACTTGGCCCTCAATAGCTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCC GCGCAACCAAGGGTGTGTGGTCACTCTGCGCAAGGACAGCGCAGTCCGCTGGTGC CCGAGGTTATGCTGTCTGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCCCTTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGTGCTGTGTATGTGTACTTGAACAGGGGGTCACTGGGCTG GGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTCCGGATCAGCCTGGCTG TCTGGGGGACCTCAACCAAGATGGCTTCCAGATATGCAGTGGGTGCCCTTTGATG GTGATGGGAAAGTCTTCACTACCATGGGAGCAGCCTGGGGGTGTGCGCAAGCCTTAC AGGTGCTGGAGGGCGAGGCTGTGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCC AGGACCCGCTAGGTTCCCATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCC</p>

	AGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGATTG GCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAACTCTCCACCCA ACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTA GGGTGAGAAGGGCAGGGGTGTCTGTATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTC CTCTCCCATTACCCCTGTGTAAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAA CCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCTAGTTTCCC CTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTCTATTTA TTAAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAA		
	ORF Start: ATG at 162		ORF Stop: TGA at 1764
	SEQ ID NO: 192	534 aa	MW at 57440.7kD
NOV36c, CG56054-04 Protein Sequence	MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVDIDQADMQKESKE NQWLGVSVRSQGPQGGKIVTCAHRYEARQVVDQILETRDMIGRCFVLSQDLAIRDELDDGGE WKFCBGRPQGHQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSSDPDQLV YKTLDPADRLPGPAGDLALNSYLFGSIDSCKGLVRAEELSFAVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSFGYSLAVADLNSDGWPDILVGPYFFERQEEELGGAVVYVLN QGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGLPDIAGVAPFDGDKVFIYHGSSLG VVAKPSQVLEGEAVGIPSWAPMGIQQAAPPFPCLACGCPPSLPQRWLLGMKRVEWAA GVASRFGRIGFLRGTDLSHPQELLPPNFPLECCMRVKGSGTGPNWGRVRRAGVS		
	SEQ ID NO: 193	999 bp	
NOV36d, CG56054-05 DNA Sequence	ATGGCCCGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTGTCTACCTTTTGGC TCCCTGCTCGTCAAGTCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGT GCCTTGGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGG CAGTTGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTT CCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGGCCGTGAGCCTGGAGGAG ACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAAGGAG AACCAGTGGTTGGGAGTCACTGTTCCGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGT GCACACCCCATCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGCATCCAGGG CCAGGCACCGCCTAGGTTCCCATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCC CCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGATT TGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAACTCTCCACCC CAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGG TAGGGTGAGAAGGGCAGGGGTGTCTGTATGCAAAGGTGGGGAGAAGGGATCCTAATCCCT TCCTCTCCCATTACCCTGTGTAAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTT AACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCTAGTTTC CCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTCTATT TATTAATAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAA		
	ORF Start: ATG at 1		ORF Stop: TAG at 493
	SEQ ID NO: 194	164 aa	MW at 17332.5kD
NOV36d, CG56054-05 Protein Sequence	MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGF SVAL HRQLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVDIDQGA DMQK ESKENQWLGVSVRSQGPQGGKIVTCAHPILAADGHPELPGDPGHPGPGTA		
	SEQ ID NO: 195	2701 bp	
NOV36e, CG56054-06 DNA Sequence	GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGTCTGGGAGACGTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCGTCCGAGA TTTCCTTGCATTGCTGAGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGCTCGGAGCC GCGACCCCTTGGGGGGCTCCGGGATTTGCTACCTTTTGGCTCCCTGCTCGTCAAGTGC TCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCAGCAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCTGGACTA TGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCGTGTGACGTTCTCT GAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACCCTGTGGCTGAAGCACA GCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAATGTCAAAGACAAGCT TCGGGCCATTGTAGTGACCTTGTCTACAGTCTCAGACCCCTCGGCTCCGGCGACAGGC TCCTGGCCAGGGGCTGCCTCCAGTGGCCCCATCTCAATGCCACCAGCCAGCCAGCACC		

	<p>GCGGGCAGAGATCCACTTCTCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAA TCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCACCTCT GCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTCTGAGTGGGCAGCCAGTCATTGG CCTGGAGCTGATGGTCACCAACCTGCCATCGGACCCAGCCAGCCAGCCAGGCTGATGGGGA TGATGCCCATGAAGCCAGCTCCTGGTCATGCTTCTGACTCACTGCTACTAGGGGT CCGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAATGAGAATGCCCTCCCATGT TGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCATCCT TAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTGGCCAC GATCAGTGAGCAGGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCC ACTGTCCATTGCAGGAATGGCCATTCCCAGCAACTTCTTCTCTGGTGTGGTGAGGGG CGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGTCAAGTATGAGGTCACGGT TTCCAACCAAGGCCAGTCTGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTGGCC TCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGG GCAGGGGCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGT GGACAGTAGGGATAGGAGCGCGGGAGCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGA GCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAGAAGAAGAAAAACAT CACCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCACTCTACAG CTTTGACCGCGCGGTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTCTGGA GGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTC CTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATGGTATACTT GGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTATCCTCTGGCTGTACT GGCTGGGCTGCTGGTGCTAGCACTGCTGGTGCTGCTCCTGTGGAAGATGGGATTCTTCAA ACGGGCGAAGCACCCCGAGGCCACCGTGCCCACTACCATGCGGTGAAGATTCTCGGGA AGACCAGCAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAG CCCCCGGCGGAGGGCCCCGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCT GGGCCCGATGGGCATCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCAGCTGCGCT GTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGG CTGCTGGTGTGCGATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCC ACCCACAAGAACTCCTCCACCCAACTTCCCTTAGAGTGCTGTGAGATGAGAGTGGGTA AATCAGGGACAGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCTGATGCAAAGGTG GGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGTGTAACAGGACCCCAAGGA CCTGCTCCCGGAAGTGCTTAACCTAGAGGGTCCGGGAGGAGGTTGTGTCACTGACTC AGGCTGCTCCTTCTTAGTTCCTCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAG TGGTTTCGTGGTTTCGTCTATTTATTAATAAATATTGAGAACAAAAAATAAAAAA A</p>		
	ORF Start: ATG at 162		ORF Stop: TAG at 366
	SEQ ID NO: 196	68 aa	MW at 7433.6kD
NOV36e, CG56054-06 Protein Sequence	MAGARSRDPWAGSGICYLFGSLLVELLPSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPWTMC		
	SEQ ID NO: 197	1131 bp	
NOV36f, CG56054-07 DNA Sequence	<p>GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGCGAACGTCTGGGAGACGCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGCGTGCGAGA TTTCCCTTGCACTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCCTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCCTGCTGCTCGAAGTGC TCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTTGGCGAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCGAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGGCTCCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAG CAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCGGCGG GAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGAT GGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCAGCCTGGCCTGTGGCTGCCC TCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTGGTGT CGCATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAGA ACTCCTCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAATCAGGGAC AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCTGATGCAAAGTGGGGAGAAGGG ATCCTAATCCCTTCTCTCCCATTCACCCCTGTGTAACAGGACCCCAAGGACCTGCCTCCC</p>		

	CGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCC TTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTG GTTTCGTCTATTTATTAATAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAA		
	ORF Start: ATG at 162		ORF Stop: TGA at 573
	SEQ ID NO: 198	137 aa	MW at 14203.9kD
NOV36f, CG56054-07 Protein Sequence	MAGARSRDPWGASGICYLFGSLLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLRAPVPCGEDSSGRPTAVQGGEDGHHPEEQ LGQPPAGGPGCTPHPGC		
	SEQ ID NO: 199	2175 bp	
NOV36g, CG56054-08 DNA Sequence	GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGCTCTGGGAGACGCTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCGTGCAGAGA TTTCCCTTGCAATTCTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCTTGGGGGGCTCCGGGATTGCTACCTTTTGGGCTCCCTGCTCGTCAAGTGC TCTTCTCACGGGCTGTCGCCTTCAATCTGGACGTGATGGGTGCCTTGCAGCAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATATGAGGCAA GGCAGCGAGTGGACCAGATCTCGAGACGCGGGATATGATTGGTCTGCTCTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGAAGTTCTGTGAGGGAC GCCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCC CTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTTGCTTT TTGTGACCAACATTGATAGCTCAGACCCGACCCAGCTGGTGTATAAACTTTGGACCCTG CTGACCGGCTCCCAGGACCAGCCGAGACTTGGCCCTCAATAGCTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCC GCGCCAACCAAGGGTGTGTGGTTCATCTGCGCAAGGACAGCGCCAGTCCGCTGGTGC CCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGTGGCTGGCCAGACCTGATAGTGGGTGCCCTTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGTGTGTGTATGTGTAAGTGAACAGGGGGGTCACTGGGCTG GGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTG TCCTGGGGGACCTCAACCAAGATGGCTGTGGTGGCAGAGGAGTGCCCTGGTGGGTGATC CTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCTGTGGAAG ATGGGATTCCTTCAACGGGCGAAGCACCCTGAGGCCACCGTGCCCCAGTACCATCGGGTG AAGATTCTCGGGAAGACCGACAGAGTTCAAGGAGGAGAAGACGGGCACCATCTGAGG AACAATGGGGCAGCCCCCGGGCGGGAGGGCCCGGATGCACACCCCATCTGGCTGCTGAC GGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCTAGGTTCCCATG TCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAA GAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGATTTGGCAGGATCGGCTTCTCAGGGG CACAGACCTCTCCCAACCCCAAGAACTCTCCCAACCAACTTCCCCTTAGAGTGTGTGA GATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTC CTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGTGTAA CAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGT TGTGTCACTGACTCAGGCTGCTCCTTCTCTAGTTTCCCCTCTCATCTGACCTTAGTTTGC TGCCATCAGTCTAGTGGTTTCGTGGTTTCGTCTATTTATTAATAAATATTTGAGAACAA AAAAAAAAAAAAAAAA		
	ORF Start: ATG at 162		ORF Stop: TGA at 1617
	SEQ ID NO: 200	485 aa	MW at 51430.2kD
NOV36g, CG56054-08 Protein Sequence	MAGARSRDPWGASGICYLFGSLLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVRSQPGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDELDDGGE WKFCBGRPQGHQGFQCQGTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSDPDQLV YKTLDPADRLPGPAGDLALNSYLGFSDSGKGLVRAEELS FVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSFGYS LAVADLNSDGWPD LIGAPYFFERQEELGGA VVYVLN QGGHWAGISPLRLCGSPDSMFGISLAVLGD LNDGCGRRSALVGHPPPGCTGWAAGASTA		

	GAAPVEDGILOTGEAPRGHRAVPFCGEDSSGRPTAVQGGEDGHHHPBEQLGQPPAGGPGCT PHPGC
	SEQ ID NO: 201 1458 bp
NOV36h, CG56054-09 DNA Sequence	TTGGGGCGTGCAGATTTCCTTGCATTTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCTTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCC TGCTCGTGAAGTCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCT TGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGT TGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTCTCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCAC ACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTC GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGCACAG CTGCCGCTTCTCCCTGATAGCCACTACCTCTCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGG ACGACGGTCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCGCTCATCCCGGTCC CTGCGAACAGCACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTATTGTCC GGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAG TGATCCAGTGATGTTACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGT GGGTATCTCTCTGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCTC TGTGGAAGATGGGATTCTTCAAACGGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACC ATGCGGTGAAGATTCTTCGGGAAGACCGACAGCAGTTCAGGAGGAGAAGACGGGCACCA TCCTGAGGAACAATGGGGCAGCCCCCGGGAGGGCCCGGATGCACACCCCATCCTGG CTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGG TTCCCATGTCCCAGCCTGGCTGTGGCTGCCCTCCATCCCTTCCCAGAGATGGCTCCTT GGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGATTGGCAGGATCGGCTTC CTCATGGGCACAGACCTC
	ORF Start: ATG at 57 ORF Stop: TAG at 1317
	SEQ ID NO: 202 420 aa MW at 45990.1kD
NOV36h, CG56054-09 Protein Sequence	MAGARSRDPWASGICYLFGSLLEVLLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVRSQGPGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDELDDGE WKFCEGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGARVELCAQGSADLAH LDDGPYEAGGEKEQDPRLPVPANSTFLEEYSAVKSLEIVIRANITVKSXIKNMLLRDAS TVIPVMVYLDPMVAEVPWWVILLAVLAGLLVLLALLVLLWKMGGFFKRAKHPEATVPQ YHAVKI PREDRQQFKEEKTGTILRNWGS PRREGPD AHPILAADGHP ELGPDGHPGP GTA
	SEQ ID NO: 203 3595 bp
NOV36i, CG56054-10 DNA Sequence	TTGGGGCGTGCAGATTTCCTTGCATTTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCTTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCC TGCTCGTGAAGTCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCT TGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGT TGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTCTCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCAC ACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTC GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGCACAG CTGCCGCTTCTCCCTGATAGCCACTACCTCTCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGG ACGACGGTCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCGCTCATCCCGGTCC CTGCCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAG AGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCACAAGGGTGTGTGGTCATCCTGC GCAAGGACAGCGCAGTCCGCTGGTGGCCGAGGTTATGCTGTCTGGGAGCGCTGACCT CCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGCTGGCCAGACCTGA TAGTGGGTGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTCTGTGTATGTGT

	<p> ACTTGAACCAGGGGGGTCACTGGGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCTG ACTCCATGTTGCGGATCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCCAG ATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCATGGGAGCA GCCTGGGGTTGTGCGCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGA GCTTCGGCTACTCCCTGTCAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGC TGGTGGGCTCCCTGGTGACACCGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCT CCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCG GCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCCCAGCAGCT ATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGG GCCAGGTTCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCGCT CGGGCACCCTGTGGCTGAAGCACCAGCATGACCGAGTCTGTGGAGACGCCATGTCTCCAGC TCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGTAGTGACCTGTCTACAGTCTCC AGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCC TCAATGCCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTG GTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGG TCAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTG CACTGAGTGGGCAGCCAGTCAATTGGCCTGGAGCTGATGGTCACCAACCTGCCATCGGACC CAGCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGTCATGCTTC CTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTCTGCC TGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTG CCCAGGTCACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACCAGCGAAC TGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTCTGCAC GAGCCCGTGTCTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATCCCCAGCAAC TCTTCTTCTCTGGTGTGGTGGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCA GCAAGGTCAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCT CTGCCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTGTCTGTACC CAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCCTGGGCAGAAAGGGCTTTGCTCTCCCA GGCCCAACATCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGGAGCTGGAGC CACCTGAGCAGCAGGAGCCTGGTGGAGCGGCAGGAGCCAGCATGTCTGTTGGCCAGTGT CCTCTGCTGAGAAGAAGAAAAACATCACCCTGGACTGCGCCCGGGGACCGGCCAACTGTG TGGTGTTCAGCTGCCCACTCTACAGCTTTGACCGCGGGCTGTGCTGCATGTCTGGGGCC GTCTCTGGAACAGCACCTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTG TCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCA CAGTGATCCCAGTGATGTTACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCT GGTGGGTATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTCTGC TCCTGTGGAAGTGTGGCTTCTTCCATCGGAGCAGCCAGAGCTCATTTTTCCCACT ATCACCGGGCTGTCTGGCTGTGCAGCCTTCAGCCATGGAAGTTGGGGGTCCAGGGACTG TGGGATGGGATTCTTCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGC GGTGAAGATTCTCGGGAAGACCGCAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCT GAGGAACAACCTGGGGCAGCCCCCGCGGGAGGGCCCGGATGCACACCCCATCTGGCTGC TGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAG </p>
	<p> ORF Start: ATG at 57 ORF Stop: TGA at 3423 </p>
	<p> SEQ ID NO: 204 1122 aa MW at 122352.9kD </p>
<p> NOV36i, CG56054-10 Protein Sequence </p>	<p> MAGARSRDPWGASGICYLFGSLLEVLLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDDIDQADMQKESKE NQWLGVSVRSQGPGGKIIVTCAHYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGE WKFCGRPGQHEQGFQCGQGTAAAFSPDSHYLLFGAPGTYNWKGARVELCAQGSADLAH LDDGPYEAGGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQEBELGGAVY VYLNQGGHWAGISPLRLCGSPDSMFGISLAVLGLDNLQDGPDIAGVAPFDGDKVFIYHG SSLGVVAKPSQVLEGEAVGIKSPGYSLSGSLMDGNQYPDLLVGLADTAVLFRARPILH VSHEVSIAPRSIDLEQPNACAGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLADTDRLR RGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYS LQTPRLRRQAPGQLPPVAPILNAHQPSQRAEIHFLKQCGEDKICQSNLQLVHARFCT RVSDTEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVM LPDSLHYSQVRLDPAEKPLCLSNENASHVECELGNPMKRGAVTFYILISTSGISIIET ELEVEILLATISEQELHPVSARARVFIELPLSIAGMAIPQLLFFSGVVRGERAMQSERDV GSKVKYEVTVSNQGSRLTLGSAFLNIMWPHEIANGKWLLYPMQVELEGGQGPQKGLCS </p>

	PRPNILHLDVDSRDRRRRELEPPEQQEPGERQEPSMSWWPVSSAEKKKNTLDCARGTAN CVVFSCPLYSFDRRAVLHVWGRLLWNSTFLEEYSVKSLVIVRANITVKSSIKNLMRLDA STVIPVMVYLDPMVVAEGVPWWVILLAVLAGLLVLALLVLLLLWKCGFPHRSSQSSSFPT NYHRACLAVQPSAMEVGGPGTVGWDSSNGRSTPRPPCPSTMR
	SEQ ID NO: 205 1034 bp
NOV36j, CG56054-11 DNA Sequence	GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGTCTGGGAGACGTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCGTGCGAGA TTTCCCTTGCATTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCCTTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCCTGCTCGTGAAGTGC TCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCACAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTCTCTGTCTGAGAAGAAGAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAAC TGTGTGGTGTTCAGCTGCCCACTCTACAGCTTTGACCGCGCGCTGTGTGTCATGTCTGG GGCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTG ATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTGATGCTCCGAGATGCC TCCACAGTGATCCCACTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTG CCCTGGTGGTCATCCTCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTG CTGCTCCTGTGAAGTGTGGCTTCTTCCATCGGAGCAGCCAGAGCTCATCTTTCCACC AACTATCACCGGCCTGTCTGGCTGTGCAGCCTTCAGCCATGGAAGTTGGGGGTCCAGGG ACTGTGGGGTAACT
	ORF Start: ATG at 162 ORF Stop: TGA at 552
	SEQ ID NO: 206 130 aa MW at 14098.0kD
NOV36j, CG56054-11 Protein Sequence	MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKBEPEGSLFGFSVALHR QLQRPQSWLLVGAPQALALPQQANRTGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVLC
	SEQ ID NO: 207 3972 bp
NOV36k, CG56054-12 DNA Sequence	GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGGCGAACGTCTGGGAGACGTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCGTGCGAGA TTTCCCTTGCATTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCCTTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCCTGCTCGTGAAGTGC TCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCACAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTTGCGAGCCAGGGGCCTGGGGGCAAGATTGTTACCTGTGCACACCGATATGAGGCAA GGCAGCGAGTGGACCAGATCTGGAGACGCGGGATATGATTGGTGTGCTGCTTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGAC GCCCCAAGGCCATGAACAATTGGGTTCTGCCAGAGGGCACAGCTGCCGCCTTCTCCC CTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTGCTTT TTGTGACCAACATTGATAGCTCAGACCCCGACAGCTGGTGTATAAACTTTGGACCCTG CTGACCGGCTCCAGGACCAGCCGAGACTTGGCCCTCAATAGTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCC GCGCCAACCACAAGGGTGTGTGGTTATCCTGCGCAAGGACAGCGCCAGTGCCTGGTGC CCGAGGTTATGCTGTCTGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCCCTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGTCACTGGGCTG GGATCTCCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCTGGCTG TCCTGGGGGACCTCAACCAAGATGGCTTCCAGATATTGCAGTGGGTGCCCTTTGATG GTGATGGGAAAGTCTTCACTACCATGGGAGCAGCCTGGGGTTGTGCGCAACCTTCAC AGGTGCTGGAGGGCAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAAGCAGCT TGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACCGCAG TGCTCTTCAGGGCCAGACCATCCTCCATGTCTCCATGAGGTCTTATTGCTCCACGAA

	GCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATG TGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCTCTGA GCCGTAACCTGGAAGAACCCAAGCACCAGGCCCTCGGGCACCCTGTGGCTGAAGCACCAGC ATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTC GGGCCATTGTAGTGACCTTGTCCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTC CTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCCTCAATGCCACCAGCCAGCACCAGC GGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATC TGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCACCTCTGCG CCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGAAGTGGGAGCAGCAGTCAATTGGCC TGGAGCTGATGGTCACCAACCTGCCATCGGACCCAGCCAGCCAGCCAGCTGATGGGGATG ATGCCCATGAAGCCCAGCTCCTGGTCATGCTTCTGACTCACTGCACTACTCAGGGGTCC GGGCCCTGACCCCTGCGGAGAAGCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTG AGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCATCTTA GCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTTGGCCACGA TCAGTGAGCAGGAGCTGCATCCAGTCTCTGACGAGCCCGTGTCTTCAATTGAGCTGCCAC TGTCCATTGCAGGAATGGCCATTCCCCAGCAACTCTTCTTCTGTTGTGGTGAAGGGCG AGAGAGCCATGCAGTCTGAGCGGATGTGGGCAGCAAGGTCAAGTATGAGGTACCGTTT CCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTGGCCTC ATGAGATTGCCAATGGGAAGTGGTGTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGC AGGGGCTGGGCAGAAAGGGCTTGTCTCTCCAGGCCAACATCCTCACCTGGATGTGG ACAGTAGGGATAGGAGGCGGGGAGCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAAGC GGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAGAAGAAGAAAAACATCA CCCTGGACTGCGCCCCGGGACGCGCAACTGTGTGGTGTTCAGCTGCCCACTCTACAGCT TTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGG AGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCAGAGTGAAGTCCCT CCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTATCCCAAGTATGGTATACTTGG ACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGTATCCTCTGGCTGTACTGG CTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTTCAAAC GGGCGAAGCACCCCCCGGGGAGGGGCGGGATGCACACCCATCCTGGCTGCTGACGGG CATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGACCGCCTGCTCCCATGTCTCC CAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAG GGTAGAGTGGGCTGCTGGTGTGCGCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCAC AGACCTCTCCACCCACAAGAACTCCTCCACCCAACTTCCCTTAGAGTGCTGTGAGAT GAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGGTGAAGAAGGCAGGGGTGTCTG ATGCAAAGGTGGGAGAAAGGATCCTAATCCCTTCTCTCCATTACCCTGTGTAACAG GACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTGGGGAGGAGGTTGT GTCACTGACTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTG CATCAGTCTAGTGGTTTCGTGGTTTCGTCTATTTATTAATAAATATTGAGAACAAAAA AAAAA		
	ORF Start: ATG at 162		ORF Stop: TGA at 3414
	SEQ ID NO: 208	1084 aa	MW at 118234.7kD
NOV36k, CG56054-12 Protein Sequence	MAGARSRD PWGASGI CYLFGSLV LELF SRAVAFNL DVMGALRKEGEPGSLFGF SVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVIDQGADMQKESKE NQWLGVSVRSQPGGKIVTCAHRYEARQVRVDQILETRDMIGRCFVLSQDLAIRDEL DGGE WKFCEGRPQGHEQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSSDPDQLV YKTLDPADRLPGPAGDLALNSYLGFSDSGKGLVRAEELS FVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVVYVLN QGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGVAPFDGDKVFIYHGSSLG VVAKPSQVLEGEAVGIKSGFYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHE VSIAPRSIDLEQPN CAGGHSVCVDLRVCF SYIAVPSSYSPTVALDYVLDADTDRRLRGQV PRVTFLSRNLEEPKHQASGT VMLKHQHDRVC GDMFQLQENVKDKLRAIVVTL SYSLQTP RLRRQAPGQGLPPVAPILNAHQ PSTQRABIHFLKQCGEDKICQSNLQLVHARFCTRVSD TEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDS LHYSGVRALDPAEKPLCLSNENASHVECELGNPMKRAQVTFYLLISTSGIS IETTELEV ELLLATISEQELHPVSARARVFIELPLSIAGMAIPQLFFSGVVRGERAMQSERDVGSKV KYEVTVSNQGSRLRTLGS AFLNIMWPHEIANGKWLLYPMQVELEGQGPQGKGLCSRPN ILHLDVDSRDRRRRELEPPEQEPGERQEPSMSWWPVSSAEKKKNITLDCARGTANCVVF		

	SCPLYSFDRRAVLHVWGRWNSTFLEBYSVAVKSLEIVIVRANITVKSSIKNLMRLDASTVI PVMVYLDPMVVAEGVPWWVILLAVLAGLLVLLVLLWKMGGFFKRAKHPPAGGPGCTP HPGC
	SEQ ID NO: 209 3583 bp
NOV361, CG56054-13 DNA Sequence	TTGGGGCGTGCAGATTTCCTTGCATTGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCCTTGGGGGGCTCCGGGATTGTACCTTTTGGCTCCC TGCTCGTCGAAGTCTCTCTCACGGGCTGTCGCCTCAATCTGGACGTGATGGGTGCCT TGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGT TGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGGCTGGGGGCAAGATTGTACCTGTGCAC ACCGATATGAGGCAAGGCAGAGTGGACCATCTGGAGACGCGGGATGAGTTGGATGGTGAATGGA GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGGCACAG CTGCCGCTTCTCCCTGATAGCCACTACCTCCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGGTTGCTTTTTGTGACCAACATTGATAGCTCAGACCCCGACAGCTGGTGTATA AAACTTTGACCCTGCTGACCGGCTCCAGGACCAGCCGGAGACTTGGCCCTCAATAGCT ACTTAGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTG TGGCTGGAGCCCCCGCGCAACCACAAGGGTGTGTGGTATCCTGCCAAGGACAGCG CCAGTGCCTGGTGCCTGAGGTTATGCTGTCTGGGAGCGCCTGACCTCCGGCTTTGGCT ACTCACTGGCTGTGGCTGACCTCAACAGTGTGCTGGCCAGACCTGATAGTGGGTGCCC CCTACTTCTTTGAGCGCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGG GGGTCACTGGGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCTG GGATCAGCCTGGCTGTCTGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCACTGG GTGCCCCCTTTGATGGTGTATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGTTG TCGCCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGTACT CCCTGTGAGGAGCTTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCC TGGCTGACACCGCAGTCTCTTCAGGGCCAGACCCATCTCCATGTCTCCATGAGGTCT CTATTGCTCCACGAAGCATCGACCTGGAGCAGCCCACTGTGCTGGCGGCCACTCGGTCT GTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTG TGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCC GTGTGACGTTCTGAGCCGTAACCTGGAAGAACCACAGCAGGCTCCGGGACCGGTGT GGCTGAAGCACCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATG TCAAAGACAAGCTTCGGGCCATTGTAGTGACCTTGTCTTACAGTCTCCAGACCCCTCGGC TCCGGGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCTCAATGCCACC AGCCAGCAGCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGACAAGA TCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGGACACGG AATTCCAACCTCTGCCATGATGTGGATGGAACAACAGCCCTGTTTGCAGTGTGGG AGCCAGTCATTGGCTGGAGCTGATGGTCACCAACCTGCCATCGAGCCAGCCAGCCCC AGGCTGATGGGGATGATGCCATGAAGCCCAGCTCCTGGTCATGCTTCTGACTCACTGC ACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTTGCCTGTCCAATGAGA ATGCCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCT TCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGC TGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCT TCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGCAACTCTTCTCTCTG GTGTGGTGAAGGGCGAGAGACCATGCACTCTGAGCGGATGTGGGCAGCAAGGTCAAGT ATGAGGTACAGGTTTCCAACCAAGGCCAGTGCCTCAGAACCCTGGGCTCTGCCTTCTCA ACATCATGTGGCTCATGAGATTGCCAATGGGAAGTGGTGTACCCAATGCAGGTTG AGCTGGAGGGCGGGCAGGGCCCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCC TCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGAGCTGGAGCCACTGAGCAGC AGGAGCCTGGTGAAGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAGA AGAAGAAAAACATCACCTGGACTGCGCCCGGGGACGGCCAACTGTGTGGTGTTCAGCT GCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACA GCACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACA TCACAGTGAAGTCTTCCATAAAGAACTTGATGCTCCGAGATGCTCCACAGTATCCAG TGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTCTCC TCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGT GTGGCTTCTTCCATCGGAGCAGCCAGAGCTCATTTTTCCCACTATCACCGGGCCT

	GTCTGGCTGTGCAGCCTTCAGCCATGGAAGTTGGGGTCCAGGGACTGTGGGATGGGATT CTTCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCC TCGGGAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTG GGGCAGCCCCCGGCGGGAGGGCCCCGATGCACACCCCATCTTGCTGCTGACGGGCATCC CGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAG		
	ORF Start: ATG at 57		ORF Stop: TGA at 3411
	SEQ ID NO: 210	1118 aa	MW at 121969.6kD
NOV36l, CG56054-13 Protein Sequence	MAGARSRDPWAGSGICYLFGSLLEVLLFSRAVAFNLDVMGALRKEGEPGSLFGFVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGE WKFCEGRFPQGHQGFQCGQTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSSDPDQLV YKTLDPADRLPGPAGDLALNSYLGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQEEELGGAVVYVYN QGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDGKVFYIHGSSSLG VVAKPSQVLEGEAVGKISFGYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHE VSIAPRSIDLEQPNACAGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDADTDRLRGQV PRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTP RLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQGGCEDKIQSNLQVLHARFCTRVSD TEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPSPDPAQPPQADGDDAHEAQLLMLPDS LHYSGVRALDPAEKPLCLSNENASHVECELGNPMKRGAVTFYILISTSGISIEETLELV ELLLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKV KYEVTVSNQGSRLTLGSAFLNIMWPHEIANGKWLlyPMQVELEGGQGPQKGLCSRPFN ILHLDVDSRDRRRRELEPPEQQEPGERQEPSMSWWPVSSAEKKKNITLDCARGTANCVF SCPLYSFDRAAVLHVWGRLLWNSTFLEEYSAVKSLVIVRANITVKSSIKNLMRLDASTVI PVMVYLDPMVAEVPWWVILLAVLAGLLVALLVLLWKGFFHRSSQSSSFPTNYHR ACLAVQPSAMEVGGPGTGVWDSSNGRSTPRPPCPSTMR		
	SEQ ID NO: 211	3938 bp	
NOV36m, CG56054-14 DNA Sequence	TTGGGGCGTGCGAGATTTCCTTGCAATTCGTGGGAGCTCGCGCAGGGATCGTCCCATG GCCGGGGCTCGGAGCCGCGACCTTGGGGGGCCTCCGGGATTTGCTACCTTTTGGGCTC CCTGCTCGTGAAGTCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTG CCTTGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGG CAGTTGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCT TCCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGG AGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAAG GAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTAC CTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATA TGATTGGTTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGT GGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTTGGGTTCTGCCA GCAGGGCAGAGCTGCCGCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAG GAACCTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGAC CTTGCCACACCTGGACGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCG CCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTC TGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCAAGGGT GCTGTGGTTATCCTGCGCAAGGACAGCGCCAGTGCCTGGTGCCGAGGTTATGCTGTC TGGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTG ATGGCTGGCCAGACCTGATAGTGGGTGCCCCCTACTTCTTTAGCGCCAAAGAAGAGCTG GGGGGTGCTGTGATGTGTACTTGAACAGGGGGGTCACTGGGCTGGGATCTCCCTCT CCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGACC TCAACCAAGATGGCTTTCCAGATATTGCACTGGGTGCCCCCTTTGATGGTGATGGGAAA GTCTTCTATCTACCATGGGAGCAGCCTGGGGTTGTGCGCAAACCTTCACAGGTGCTGGA GGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTGAGGCAGCTTGGATATGG ATGGGAACCAATACCCTGACCTGTGCTGGTGGGCTCCCTGGTGTGACACCGCAGTGCTCTTC AGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGA CCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTT TCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTA GATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCGGTGTGACGTTCTGTGAGCCG TAACCTGGAAGAAGCAACGACCAGGCCTCGGGCACCCTGTGGCTGTGCTGAAGCACCAGCATG ACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGG		

	<p>GCCATTGTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCC TGGCCAGGGGCTGCCTCCAGTGGCCCCCATCCTCAATGCCCCACGAGCCAGCAGCCAGC GGGCAGAGATCCACTTCTGAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAAT CTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACCTCT GCCCATGGATGTGGATGGAACAACAGCCCTGTTTGAAGTGGGAGCCAGGCTGATGGG GCCTGGAGCTGATGGTCACCAACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGG GATGATGCCCATGAAGCCCAGCTCCTGGTCATGCTTCTGACTCACTGCACTACTCAGG GGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAATGAGAATGCCTCCC ATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTC ATCCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTT GGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTCTGCACGAGCCCGTCTTCTCATTG AGCTGCCACTGTCCATTGACGGAATGGCCATTCCCCAGCAACTCTTCTTCTGTTGTG GTGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGTCAAGTATGA GGTCACGGTTTCCAACCAAGGCCAGTCCGTCAGAACCCCTGGGCTCTGCCTTCTCAACA TCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTGTGTACCCAATGCAGGTTGAG CTGGAGGGCGGGCAGGGGCTGGGCAGAAAGGGCTTGTCTCTCCAGGCCCAACATCCT CCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGAGCTGGAGCCACCTGAGCAGC AGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAG AAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAAGTGTGTGGTGTTCAG CTGCCACTCTACAGCTTACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGA ACAGCACCTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTATTGTCCGGGCC AACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGATGCCCTCCACAGTAT CCCAGTGTGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGG TCATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGTACTGCTGGTGTCTCTCTG TGGAAGATGGGATTCTTCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCA TGCGGTGAAAATTCTCGGGAAGACCGACAGCAGTTCAGGAGGAGAAGACGGGCACCA TCCTGAGGAACAACCTGGGCGAGCCCCCATCCTGGCTGGGCCCCGATGGGCATCCAGGGC CAGGCACCGCCTAGGTTCCTCATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCC CCAGAGATGGCTCCTTGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGAT TTGGCAGGATCGGCTTCTCAGGGCACAGACCTCTCCCCCACAAGAACTCCTCCACC CAACTTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGGACAGGGCCATGGG GTAGGGTGAGAAGGGCAGGGGTGTCTGATGCAAGGTGGGAGAAGGAGTCTTAATCC CTTCTCTCCCATTACCCCTGTGTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGC CTTAACCTAGAGGGTGGGGAGGAGTTGTGTACTGACTCAGGCTGCTCCTTCTCTAG TTTCCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGT CTATTTATTAAAAATATTGAGAACAAAAA</p>		
	ORF Start: ATG at 57		ORF Stop: TGA at 3621
	SEQ ID NO: 212	1188 aa	MW at 130044.2kD
NOV36m, CG56054-14 Protein Sequence	<p>MAGARSRPWGASGICYLFGSLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFVALH RQLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVIDQDADMQKES KENQWLGVSVRSQPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDDEL GGEWKFCEGRPQGHEQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQSSA DLAHLDDGPYEAGGEKEQDPRILIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANH GAVVILRKDSASRLVPEVMSLGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQEE LGGAVYVYLNQGGHWAGISPLRLCGSPDSMFGISLAVLGLDNLQDGFPIAVGAPFDG KVFIYHGSSLGVVAKPSQVLEGEAVGIKSFYSLSGSLDMDGNQYPDLLVGLSADTAVL FRARPILHVSHEVSIAPRSIDLEQPNACAGHSVCVDLRCVFSYIAVPSSYSPTVALDYV LDADTDRLRLRGQVPRVTFLSRNLLEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKL RAIVVTLISYSLQTPRLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQCGEDKICQS NLQLVHARFCTRVSDTEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPSPDPAQPAD GDDAHEAQLLVMPLDLSHYSGVRALDPAEKPLCLSNENASHVECELGNPMKRGAQVTFY LILSTSGISIIETLEVELELLATISEQELHPVSARARVFIPLSIAGMAIPQLFFSG VVRGERAMQSERDVGSKVKYEVTVSNQGQSLRTLGS AFLNIMWPHEIANGKWLIPMQV ELEGGQGPQKGLCSRPNIIHLDVDSDRRRRRELEPPEQEPGERQEPSMSWWPVSSA EKKKNITLDCARGTANCVVFSPLYSFDRAAVLHVWGLWNSTFEEYSKLVLEIVR ANITVKSSIKNMLRDASTVIPVMVYLDPMVVAEGVPWWVILLAVLAGLLVLALLVLL LWKMGGFFKRAKHPEATVPQYHAVKIPREDRQFKEEKTGTILRNNWGSPPHGWAPMGIQ GQAPPRFPCLSLACGCPSSLQORWLLGMKRVEWAAGVASRFGRIQGLRAQTSPPTRTPP</p>		

	TQLPLRLV	
	SEQ ID NO: 213	2471 bp
NOV36n, CG56054-15 DNA Sequence	TTGGGGCGTGCGAGATTCCCTTGCAATTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCTTGGGGGGCCCTCCGGGATTGCTACCTTTTTGGGTCCC TGCTCGTGAAGTCTCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTT TGCAGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGT TGCAGCCCCGACCCAGAGCTGGCTGTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTCCGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCAC ACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTC GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCAGAG CTGCCGCCCTTCTCCCCGTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGG ACGACGGTCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCCGGTCC CTGCCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGTGCGTGCAGAAG AGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCAAGGGTGTGTGGTTATCCTGTC GCAAGGACAGCGCCAGTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT CCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGTGGCCAGACCTGA TAGTGGGTGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGT ACTTGAACAGGGGGGTCACTGGCTGGGATCTCCCTCTCCGGCTCTGCAACTCCCCGC ACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCCAG ATATTGCAGTGGGTGCCCCCTTTGATGGTGTGGGAAAGTCTTCACTTACCATTGGGAGCA GCCTGGGGGTGTGCGCAACCTTCAAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGA GCTTCGGCTACTCCCTGTGAGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGC TGGTGGGTCCCTGGCTGACACCGCAGTGTCTTCAGGGCCAGACCCATCCTCCATGTCT CCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCG GCCACTCGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGACCTCCAGCTGACCT ATAGCCCTACTGTGCCCCGCTGATGTGTAGATGCGGACACAGACCGGAGGCTCCGGG GCCAGGTTCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCT CGGGCACCCTGTGGCTGAAGCACCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGC TCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGTAGTGACCTGTCTTACAGTCTCC AGACCCCTCGGCTCCGGCGGGAGGGCCCGATGCACACCCATCCTGGCTGCTGACGGGC ATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCCCTAGGTTCCCATGTCCC AGCCTGGCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGG GTAGAGTGGGCTGTGGTGTGCGCATCAAGATTGGCAGGATCGGCTTCCTCAGGGGCACA GACCTCTCCACCCACAAGAATCCTCCCAACCAACTTCCCCTTAGAGTGTGTGAGATG AGAGTGGGTAATCAGGGACAGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCTGA TGCAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCCATTCACCTGTGTAAACAGG ACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTG TCACTGACTCAGGCTGCTCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTCTGCC ATCAGTCTAGTGGTTTCGTGGTTTCGTCTATTATTAATAAATATTGAGAACAAAAAA AAAAA	
	ORF Start: ATG at 57	ORF Stop: TAG at 1965
	SEQ ID NO: 214	636 aa
		MW at 68715.7kD
NOV36n, CG56054-15 Protein Sequence	MAGARSRDPWGASGICYLFGSLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPQQANRTGGLFACPLSLEETDCYRVDIDQADMQKESKE NQWLGVSVRSQPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDLDGGE WKFCGRPQGHEQFGFCQGGTAAAFSPDSHYLLFGAPGTYNWKGATARVLCAGGSADLAH LDDGPEYAGGEKEQDPRILPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVI LRKDSASRLVPEVMSGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQELGGAVY VYLNQGGHWAGISPLRLCNSPHSMFGISLAVLGLDNLQDGFDPDIAGVAPFDGDKVFIYHG SSLGVVAKPSQVLEGEAVGKISFGYSLSGSLMDGNQYPDLLVGLSLADTAVLFRARPILH VSHEVSIAPRSIDLEQPNACGHSVCVLRVCFSYIAPSSYSPTVALDYVLADTDRLR RGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYS LQTPRLRREGPDAPHPIAADGHPGLPDGHPGPGTA	

	SEQ ID NO: 215	1924 bp	
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	ORF Start: ATG at 57		ORF Stop: TGA at 1671
	SEQ ID NO: 216	538 aa	MW at 57824.0kD
NOV360, CG56054-16 Protein Sequence	MAGARSRDPWAGSGICYLFGSLLELLEFRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVIDDQADMQKESKE NQWLGVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELGGGE WKFCBGRPQGHEQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAH LDDGPYEAGGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVY VYLNQGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGLPDIAVGAPFDGDGVFIYHG SSLGVVAKPSQVLEGEAVGIPSWAPMGIQQAAPPFRPCPSLACGCPPSLPQRWLLGMKRV EWAAGVASRFGRIGFLRGTDLSHPQELLPPNFPLECCEMRVGKSGTGPWGRVRRAGVS		
	SEQ ID NO: 217	2082 bp	
NOV36p, CG56054-17 DNA Sequence	TTGGGGCGTGCGAGATTTCCTTGCATTTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTGCTACCTTTTGGCTCCC TGCTCGTGAAGTCTCTTCTCACGGGCTGTGCCTTCAATCTGGACGTGATGGGTGCCT TGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGCCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTTCGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCAC ACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTC GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGCACAG		

	<p>CTGCCGCCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGG ACGACGGTCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCCGGTCC CTGCCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAG AGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCAAGGGTGTGTGGTCACTCTGTC GCAAGGACAGCGCCAGTCGCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCT CCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGA TAGTGGGTGCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTCTGTGTATGTGT ACTTGAACAGGGGGGTCACTGGGTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTG ACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTGTGGTG GCAGAAGGAGTGCCCTGGTGGGTATCCTCCTGGCTGTACTGGCTGGCTGTGGTGCTA GCACTGCTGGTGTCTCCTGTGGAAGATGGGATTCTTCAAACGGGCGAAGCACCCCGAG GCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCAGTTCAAG GAGGAGAAGACGGGCACCATCCTGAGGAACAAGTGGGGCAGCCCCCGCGGGAGGGCCCG GATGCACACCCCATCCTGGCTGTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCA GGGCCAGGCACCGCCTAGGTTCCCATGTCCAGCCTGGCTGTGGCTGCCCTCCATCCCT TCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGTGTGTGCGATCAAG ATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCACCCACAAGAAGTCTCCC ACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGTAAATCAGGGACAGGGCCATG GGGTAGGGTGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCTTAATC CCTTCTCTCCCATTCACCTGTGTAACAGGACCCCAAGGACCTGCCCTCCCGGAAGTGC CTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCTAGT TTCCCCTCTCATCTGACCTTAGTTTGTGTCATCAGTCTAGTGGTTTCGTGGTTTCGTCT ATTTATTAATAAATATTGAGAACAAAAA</p>
	<p>ORF Start: ATG at 57</p> <p>ORF Stop: TGA at 1524</p>
	<p>SEQ ID NO: 218</p> <p>489 aa</p> <p>MW at 51813.5kD</p>
NOV36p, CG56054-17 Protein Sequence	<p>MAGARSRDPWASGICYLFGSLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFVSVALHR QLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVDIDQADMQKESKE NQWLGVSVRSQPGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRBELDGGE WKFCGRFPQGEHQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGSTARVELCAQGSADLAH LDDGPYEAGGEKEQDRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI LRKDSASRLVPEVMLSGERLTSFGYSLAVADLNSDGPDLIVGAPYFFERQEBLGGAVY VYLNQGGHWAGISPLRLCGSPDSMFGISLAVLGLDNLQDGCGRRSALVGHPPGCTGWAAG ASTAGAAPVEDGILQTEAPRGRHAPVPCGEDSSGRPTAVQGGEDGHHPEQLGQPPAGG PGCTPHPGC</p>
	<p>SEQ ID NO: 219</p> <p>13879 bp</p>
NOV36q, CG56054-18 DNA Sequence	<p>TTGGGGCGTGCGAGATTTCCCTTGCACTCGCTGGGAGCTCGCGCAGGGATCGTCCCATGG CCGGGGCTCGGAGCCGCGACCTTGGGGGGCTCCGGGATTTGCTACCTTTTGGCTCCC TGCTCGTCGAAGTCTCTTCTCAGGGCTGTGCGCTTCAATCTGGAGCTGAGGTGCGCT TGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTGGCTTCTCTGTGGCCCTGCACCGGCAGT TGCAGCCCCGACCCAGAGCTGGCTGTGTGGTGGTGTCCCCAGGCCCTGGCTCTTCCTG GGCAGCAGGCGAATCGCACTGGAGGCCTCTTGGCTTGGCCGTTGAGCCTGGAGGAGACTG ACTGCTACAGAGTGGACATCGACAGGGAGCTGATATGCAAAGGAAAGCAAGGAGAACC AGTGGTTGGGAGTCAGTGTTGCGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCAC ACCGATATGAGGCAAGGCAGCGAGTGGACAGATCCTGGAGACGCGGATATGATTGGTC GCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGA AGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCACAG CTGCCGCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATT GGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGG ACGACGGTCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCCGGTCC CTGCCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAG AGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCAAGGGTGTGTGGTTATCCTGC GCAAGGACAGCGCCAGTCGCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCT CCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGCCAGACCTGA TAGTGGGTGCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGT ACTTGAACAGGGGGGTCACTGGGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTG ACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCCAG ATATTGCACTGGGTGCCCCCTTGTAGTGTGATGGGAAAGTCTTCATCTACCATGGGAGCA</p>

	<p>GCCTGGGGTGTGCGCCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGA GCTTCGGCTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGC TGGTGGGCTCCCTGGCTGACACCGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCT CCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCTGGAGCAGCCCAACTGTGTGGCG GCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCCCAGCAGCT ATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGG GCCAGGTTCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCT CGGGCACCGTGTGGCTGAAGCACCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGC TCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGTAGTGACCTTGTCTACAGTCTCC AGACCCCTCGGCTCCGGCGCAGAGCTCCTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCC TCAATGCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTG GTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCGCTTCTGTACCCGGG TCAGCGACACGGAATTCCAACCTCTGCCATGGATGTGGATGGAACAACAGCCCTGTTTG CACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGATGGTCACCAACTGCCATCGGACC CAGCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGTCATGCTTC CTGACTCACTGCACACTCTCAGGGTTCGGGCCCTGGACCTGCGGAGAAGCCACTTGCC TGTCCAATGAGAATGCCCTCCCATGTTGAGTGTGAGCTGGGAACCCATGAAGAGAGGTG CCCAGGTCACCTTCTACCTCATCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAC TGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTCTGCAC GAGCCCCTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATCCCCAGCAAC TCTTCTCTCTGGTGTGGTGAGGGCGAGAGAGCCATGAGTCTGAGCGGGATGTGGCA GCAAGGTCAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCT CTGCCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACC CAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGGGCAGAAAGGCTTTGCTCTCCCA GGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGGAGCTGGAGC CACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCCTGGTGGCCAGTGT CCTCTGCTGAGAAGAAGAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACTGTG TGGTGTTCAGCTGCCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGCC GTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTG TCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAAGTTGATGCTCCGAGATGCCTCCA CAGTGATCCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCT GGTGGGTCATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTG TCCTGTGGAAGATGGGATTCTTCAAACGGGCGAAGCACCCCCGGCGGGAGGGCCCGGAT GCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGGATGGGCATCCAGGG CCAGGCACCGCCTAGGTTCCCATGTCCAGCTGGCCTGTGGCTGCCTCCATCCCTTCC CCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTGGTGTGCGATCAAGATT TGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAACTCCTCCACCC CAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGGACAGGGCCATGGGG TAGGGTGAGAAGGGCAGGGGTGCTCTGATGCAAAGGTGGGAGAAGGGATCCTAATCCCT TCCTCTCCCATTCACCTGTGTAAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTT AACCTAGAGGGTCCGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCTAGTTTC CCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTCTATT TATTAATAAATATTGAGAACAAAAA</p>
	<p>ORF Start: ATG at 57</p>
	<p>ORF Stop: TGA at 3321</p>
	<p>SEQ ID NO: 220</p>
	<p>1088 aa</p>
	<p>MW at 118618.0kD</p>
<p>NOV36q, CG56054-18 Protein Sequence</p>	<p>MAGARSRDPWGASGICYLFGSLVLELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPOALALPGQANRTGGLFACPLSLEETDCYRVIDQGDAMQKESKE NWLVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELGGGE WKFCEGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAH LDDGPEYAGGEKEQDPRILIPVANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI LRKDSASRLVPEVMSGERLTSFGYSLAVADLNSDGNPDIVGAPYFFERQEELGGAVY VYLNQGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDKVFIYHG SSLGVVAKPSQVLEGEAVGIKSFYSLSGSLDMDGNQYPDLLVGSGLADTAVLFRARPILH VSHEVSIAPRSIDLEQPNACGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDADTDRL RGQVPRVTFLSRNLEBPKHQASGTVWLKHQHDVCGDAMFQLQENVKDKLRAIVVTLSSYS LQTPRLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQGGCEDKIQSNLQLVHARFCT RVSDFEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPSPDAQPDAGDDAHEAQLLVM LPDSLHYSQVRLDPAEKPLCLSNENASHVECELGNPMKRGAVTFYILSTSGISIETT</p>

	ELEVELLLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFSGVVRGERAMQSERDV GSKVKYEVTVSNQGSRLTLGSAFLNIMWPHEIANGKWLlyPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRELEPPEQQEPGERQEPMSWVPVSSAEKKKNITLDCARGTAN CVVFSCPLYSFDRRAVLHVWGRLLWNSTFLEEYSVKSLEIVIRANITVKSSIKNMLLRDA STVIVPMVYLDPMVAEVPWWVILLAVLAGLLVLALLVLLLWKMGGFFKRAKHPPAGGP GCTPHPGC		
	SEQ ID NO: 221	2709 bp	
NOV36r, CG56054-19 DNA Sequence	GGGCTTGGGGCGTGCAGATTTCCTTGCAATTCGCTGGGAGCTCGCGCAGGGATCGTCCC ATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCTCCGGGATTGCTACCTTTTGGC TCCCTGCTCGTGAAGTCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGT GCCTTGCAGAGGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGG CAGTTGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGTGTCTCCCGAGGCCCTGGCTCTT CCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGGCCGTTGAGCCTGGAGGAG ACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAAGGAG AACCAGTGGTTGGGAGTCACTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTACCTGT GCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGATATGATT GGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAA TGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTGGGTTCTGCCAGCAGGGC ACAGCTGCCGCCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCAGGAACCTAT AATTGGAAGGGGTGCTTTTGTGACCAACATTGATAGCTCAGACCCCGACCACTGGT TATAAACTTTGGACCCTGCTGACCGGCTCCAGGACCAGCCGAGACTTGGCCCTCAAT AGCTACTTAGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGC TTTGTGGCTGGAGCCCCCGCGCAACCACAAGGGTGTGTGGTTCATCTGCGCAAGGAC AGCGCCAGTCGCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCTGACCTCGGCTTT GGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGCTGGCCAGACCTGATAGTGGGT GCCCCCTACTTCTTTGAGCGCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAAC CAGGGGGGTCACTGGGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATG TTCGGGATCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCAGATATTGCA GTGGGTGCCCCCTTTGATGGTGTATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGG GTTGTGCGCCAAACCTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGC TACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGC TCCCTGGCTGACACCGCAGTCTCTTCAGGGCCAGACCCATCCTCATGTCTCCCATGAG GTCTCTATTGCTCCACGAAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCG GTCTGTGTGGACCTAAGGGTCTGTTTCACTACATTGCAGTCCCAGCAGCTATAGCCCT ACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTT CCCCGTGTGACGTTCTTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACC GTGTGGCTGAAGCACCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGTCCAGGAA AATGTCAAAGACAAGCTTCGGGCCATTGTAGTGACCTTGTCTACAGTCTCCAGACCCCT CGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGGGCCTGGGCAGAAAGGGCTT TGCTCTCCAGGCCCAACATCTCCACCTGGATGTGGACAGTAGGAGTAGGAGCGCGG GAGCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGG TGGCCAGTGTCTCTGCTGAGAAGAAGAAAACATACCCTGGACTGCGCCCGGGGCACG GCCAACTGTGTGGTGTTCAGCTGCCACTCTACAGCTTGTACCGCGCGGCTGTGCTGCAT GTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTG GAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGA GATGCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCATGGCTGTGGTGGCAGAA GGAGTGCCCTGGTGGGTATCCTCCTGGCTGTACTGGCTGGGCTGTGGTGTAGCACTG CTGGTGTGCTCCTGTGGAAGATGGGATCTTCAAACGGGCGAAGCACCCTGAGGCCACC GTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCAGTTCAAGGAGGAG AAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCGGCGGGAGGGCCCGGATGCA CACCCTCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCTCCAGGGCCA GGCACCCTAGGTTCCCATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCA GAGATGGCT		
	ORF Start: ATG at 61		ORF Stop: TAG at 2650
	SEQ ID NO: 222	863 aa	MW at 94348.4kD
NOV36r, CG56054-19	MAGARSRDWPAGSGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVRSQGPGGKIVTCAHRYEARQVRVDQILETRDMIGRCFVLSQDLAIRDELDDGGE		

Protein Sequence	<p>WKFCGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSSDPDQLV YKTLDPADRLPGPAGDLALNSYLGSIDSGLVRAEELSFVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQEEELGGAVVYVLN QGGHWAGISPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDKGVFIYHGSSLG VVAKPSQVLEGEAVGIKSGYSLSGSLMDGNQYPDLLVGLADTAVLFRARPIILHVSHE VSIAPRSIDLEQPNACAGHSVCVDLRVCFYIAVPSSYSPTVALDYVLADTDRLRLRGQV PRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSTLSLQTP RLRRQAPGQGLPPGPQKGLCSRPNILHLDVDSRDRRRRELEPPEQQEPGERQEPSMSW WPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRRAVLHVWGRNLWNSTFLEEYSAVKSL EVIVRANITVKSSIKNMLRDASTVIPVMVYLDPMVAEVPWWVILLAVLAGLLVLAL LVLLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNWGSPPREGPDA HPILAADGHPGLGPDGHPGPSTA</p>
	<p>SEQ ID NO: 223 4031 bp</p>
NOV36s, CG56054-02 DNA Sequence	<p>GGAGCGGCGGGCGGGCGGGAGGGCTGGCGGGCGGAACGCTCTGGGAGACGCTCTGAAAGACC AACGAGACTTTGGAGACCAGAGACGCGCCTGGGGGGACCTGGGGCTTGGGGCGTGCAGAG TTTCCCTTGCATTCTGCTGGGAGCTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCC GCGACCCCTTGGGGGGCTCCGGGATTTGCTACCTTTTTGGCTCCCTGCTCGTCGAAGTGC TCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAAGGAGGGCG AGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCC AGAGCTGGCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATC GCACTGGAGGCTCTTCGCTTGGCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGG ACATCGACCAAGGAGCTGATATCAAAAGGAAAGCAAGGAGAACCAGTGGTTGGGAGTCA GTGTTCCGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACCCGATATGAGGCAA GGCAGCGAGTGGACCAAGATCCTGGAGACGCGGGATATGATTGGTCTGCTTTGTGCTCA GCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGAC GCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCC CTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAATTGGAAGGGGTGCTTTT TTGTGACCAACATTGATAGCTCAGACCCCGACAGCTGGTGTATAAACTTTGGACCCCTG CTGACCGGCTCCAGGACCAAGCGGAGACTTGGCCCTCAATAGCTACTTAGGCTTCTCTA TTGACTCGGGGAAAGGTCTGGTGCCTGCAGAGAGCTGAGCTTTGTGGCTGGAGCCCCC GCGCCAACCACAAGGGTGTGTGGTTATCCTGCGCAAGGACAGCGCCAGTGCCTGGTGC CCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGG CTGACCTCAACAGTGTGGTGGCCAGACCTGATAGTGGGTGCCCCCTACTTCTTTGAGC GCCAAGAAGAGCTGGGGGTGCTGTGTATGTGTAATTGAACAGGGGGCTCACTGGGCTG GGATCTCCCTCTCCGGCTCTCGGGCTCCCTGACTCCATGTTCCGGATCAGCTGGGCTG TCCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATG GTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTGTGCGCAACCTTCAC AGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAGGCAGCT TGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACCGCAG TGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAA GCATCGACCTGGAGCAGCCCACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATG TGTTAGATGCGGACACAGACCGAGGCTCCGGGGCCAGGTTCCCGGTGTGACGTTCTCTGA GCCGTAACCTGGAAGAACCACAGCAGGCTCGGGCACCCTGTGGCTGAAGCACCAGC ATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTC GGGCCATTGTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTC CTGGCCAGGGGCTGCCTCCAGTGGCCCCCATCCTCAATGCCACCAGCCCAGCACCAGC GGGCAGAGATCCACTTCCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATC TGCAGCTGGTCCACGCGCGCTTCTGTACCCGGGTGAGCGACACGGAATCCAACCTCTGC CCATGGATGTGGATGGAACAACAGCCCTGTTGCACTGAGTGGGCAGCAGTCACTGGCC TGGAGCTGATGGTCACCAACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATG ATGCCCATGAAGCCCAGCTCCTGGTCATGCTTCTGACTCACTGCACTACTCAGGGGTCC GGGCCCTGGACCTGCGGAGAAGCCACTTGCCTGTCCAATGAGAATGCCTCCCATGTTG AGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCATCCTTA GCACCTCCGGGATCAGCAATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGA TCAGTGAGCAGGAGTGCATCCAGTCTCTGCACGAGCCGCTGTCTTCACTGAGCTGCCAC TGTCCATTGCAGGAATGGCCATTCCCCAGCAACTCTTCTCTGTGGTGTGGTGGGGGCG AGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGTCAAGTATGAGGTCACGGTTT CCAACCAAGGCCAGTCTGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTGGCCTC</p>

	ATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGC AGGGGCTTGGGCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGG ACAGTAGGGATAGGAGGCGGCGGAGCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGC GGCAGGAGCCCAGCATGTCTGGTGGCCAGTGTCTCTGCTGAGAAGAAGAAAAACATCA CCCTGGAGCTGCGCCCGGGGACGGCCAACTGTGTGGTGTTTCAGCTGCCCACTCTACAGCT TTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGG AGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCT CCATAAAGAAGTGTATGCTCCGAGATGCTCCACAGTGATCCAGTGATGGTATACCTTGG ACCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTCTATCCTCTGGCTGTACTGG CTGGGCTGTGGTGCTAGCACTGTGGTGTCTCTGTGGAAGATGGGATCTTCAAAC GGGCGAAGCACCCCGAGGCCACCGTGCCCGAGTACCATGCGGTGAAAATTCTCGGGAAG ACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCTGAGGAACAAGTGGGGCAGCC CCCATCCTGGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCTATGTC CCAGCCTGGCCTGTGGCTGCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGA GGGTAGAGTGGGCTGTGGTGTGCGATCAAGATTGGCAGGATCGGCTTCTCAGGGCAC AGACCTCTCCCCCACAAGAACTCTCCCAACCACTTCCCTTAGAGTGGTGTGAGATG AGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCTGA TGCAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGTGTAACAGG ACCCAAGGACCTGCCTCCCGGAAGTGCTTAACCTAGAGGGTCGGGGAGGAGGTTGTG TCACTGACTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGCTGCC ATCAGTCTAGTGGTTTCGTGGTTTCGTCTATTTATTAATAAATATTGAGAACAAAAAA AAAAAAAAAA		
	ORF Start: ATG at 162		ORF Stop: TGA at 3714
	SEQ ID NO: 224	1184 aa	MW at 129660.8kD
NOV36s, CG56054-02 Protein Sequence:	MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHR QLQPRPQSWLLVGAPQALALPGQQANRTGGGLFACPLSLEETDCYRVIDIDQADMQKESKE NQWLGVSVRSQGPGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDELDDGGE WKFCGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGLLFVTNIDSSDPDQLV YKTLDPADRLPGPAGDLALNSYLGFSDSGKGLVRAEELSFFVAGAPRANHKGAVVILRKD SASRLVPEVMLSGERLTSFGYSLAVADLNSDGWPDIVGAPYFFERQEELGGAVVYVLN QGGHWAGISPLRLCGSPDSMPGISLAVLGDNLQDGFDDIAGVAPFDGDGKVFYIHGSSLG VVAKPSQVLEGEAVGIKSGYSLSGSLDMDGNQYPDLLVGSLLADTAVLFRARPILHVSHE VSIAPRSIDLEQPNACGGHVCVDLRLVCFYSYIAVPSSYSPTVALDYVLDADTDRRLRGQV PRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTP RLRRQAPQGGLPPVAPILNAHQSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSD TEFQPLPMDVDGTTALFALSGQPVIGLELMVTNLPDPAQPPQADGDDAHEAQLLVMLPDS LHYSGVRLDPAEKPLCLSNENASHVECELGNPMKRGAQVTFYLILSTSGISIIETTELEV ELLLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKV KYEVTVSNQGSRLTLGS AFLNIMWPHEIANGKWLlyPMQVELEGGQGPQGKGLCSRP ILHLDVDSRDRRRRELEPPEQEPGERQEPMSWVPVSSAEKKKNITLDCARGTANCVVF SCPLYSFDRAAVLHVWGRNLNSTFLEEYSAVKSLEIVVRANITVKSSIKNMLRDASTVI PVMVYLDPMVAEVGPWWVILLAVLAGLLVLALLVLLWKMGGFFKRAKHPEATVPQYHA VKIPREDRQQFKEEKTGTILRNWGSPPHGWAPMGIQQAAPPFPFPCPSLACGCPPSLPQR WLLGMKRVEWAAGVASRFGRIGFLRAQTSPPTRTPPTQLPLRVL		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 36B.

Table 36B. Comparison of NOV36a against NOV36b through NOV36s.		
Protein Sequence	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV36b	1..607 1..607	590/607 (97%) 591/607 (97%)

NOV36c	1..439 1..439	423/439 (96%) 424/439 (96%)
NOV36d	1..142 1..142	129/142 (90%) 129/142 (90%)
NOV36e	1..64 1..64	64/64 (100%) 64/64 (100%)
NOV36f	1..113 1..112	84/113 (74%) 86/113 (75%)
NOV36g	1..395 1..395	382/395 (96%) 382/395 (96%)
NOV36h	1..276 1..283	225/286 (78%) 233/286 (80%)
NOV36i	1..1079 1..1083	963/1089 (88%) 969/1089 (88%)
NOV36j	1..128 1..128	115/128 (89%) 115/128 (89%)
NOV36k	1..1076 1..1076	997/1076 (92%) 997/1076 (92%)
NOV36l	1..1079 1..1079	991/1079 (91%) 993/1079 (91%)
NOV36m	1..1137 1..1134	1011/1147 (88%) 1015/1147 (88%)
NOV36n	1..607 1..611	562/617 (91%) 567/617 (91%)
NOV36o	1..439 1..443	395/449 (87%) 400/449 (88%)
NOV36p	1..395 1..399	354/405 (87%) 358/405 (87%)
NOV36q	1..1076 1..1080	969/1086 (89%) 973/1086 (89%)
NOV36r	1..606 1..606	593/606 (97%) 593/606 (97%)
NOV36s	1..1137 1..1130	1039/1137 (91%) 1039/1137 (91%)

Further analysis of the NOV36a protein yielded the following properties shown in Table 36C.

Table 36C. Protein Sequence Properties NOV36a	
PSort analysis:	0.4600 probability located in plasma membrane; 0.1363 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)

SignalP analysis:	Cleavage site between residues 34 and 35
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A search of the NOV36a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 36D.

Table 36D. Geneseq Results for NOV36a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB36936	Integrin alpha chain 7 - <i>Homo sapiens</i> , 1137 aa. [WO200066628-A1, 09- NOV-2000]	1..1137 1..1137	1137/1137 (100%) 1137/1137 (100%)	0.0
AAU29083	Human PRO polypeptide sequence #60 - <i>Homo sapiens</i> , 1141 aa. [WO200168848-A2, 20- SEP-2001]	1..1137 1..1141	1109/1147 (96%) 1113/1147 (96%)	0.0
AAB44308	Human PRO768 (UNQ406) protein sequence SEQ ID NO:437 - <i>Homo sapiens</i> , 1141 aa. [WO200053756- A2, 14-SEP-2000]	1..1137 1..1141	1109/1147 (96%) 1113/1147 (96%)	0.0
AAY41752	Human PRO768 protein sequence - <i>Homo sapiens</i> , 1141 aa. [WO9946281-A2, 16-SEP-1999]	1..1137 1..1141	1109/1147 (96%) 1113/1147 (96%)	0.0
AAB94058	Human protein sequence SEQ ID NO:14232 - <i>Homo sapiens</i> , 973 aa. [EP1074617-A2, 07-FEB- 2001]	159..1137 1..973	970/979 (99%) 971/979 (99%)	0.0

In a BLAST search of public sequence databases, the NOV36a protein was found to
5 have homology to the proteins shown in the BLASTP data in Table 36E.

Table 36E. Public BLASTP Results for NOV36a				
Protein Accession Number	Protein/Organism/Length	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
JCS950	integrin alpha-7 chain precursor - human, 1137 aa.	1..1137 1..1137	1137/1137 (100%) 1137/1137 (100%)	0.0

Q13683	Integrin alpha-7 precursor - <i>Homo sapiens</i> (Human), 1181 aa.	1..1137 1..1181	1137/1181 (96%) 1137/1181 (96%)	0.0
I61186	alpha-7 integrin - mouse, 1135 aa.	14..1137 14..1135	985/1124 (87%) 1046/1124 (92%)	0.0
Q61738	Integrin alpha-7 precursor - <i>Mus musculus</i> (Mouse), 1179 aa.	14..1137 14..1179	985/1168 (84%) 1046/1168 (89%)	0.0
Q63258	Integrin alpha-7 (H36-alpha7) - <i>Rattus norvegicus</i> (Rat), 1106 aa.	34..1137 1..1106	922/1110 (83%) 981/1110 (88%)	0.0

PFam analysis predicts that the NOV36a protein contains the domains shown in Table 36F.

Table 36F. Domain Analysis of NOV36a			
Pfam Domain	NOV36a Match Region	Identities/ Similarities for the Matched Region	Expect Value
FG-GAP	49..114	20/67 (30%) 48/67 (72%)	6.1e-11
FG-GAP	260..317	20/66 (30%) 42/66 (64%)	5.4e-06
FG-GAP	318..377	26/65 (40%) 49/65 (75%)	1.3e-14
FG-GAP	378..435	30/67 (45%) 51/67 (76%)	2.2e-18
FG-GAP	436..489	20/66 (30%) 42/66 (64%)	6.1e-08
integrin_A	1061..1075	7/15 (47%) 14/15 (93%)	0.0074

Example 37.

The NOV37 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 37A.

Table 37A. NOV37 Sequence Analysis		
	SEQ ID NO: 225	4096 bp
NOV37a, CG88634-01 DNA Sequence	ATCTGTTTATTTATTCTGTTAATTTCCAATAGTATAATTTGACATGCATTTCTGTTTT GTCTTTTCAGGTGCCATTGGATTGTACTTTAGTGGCAGCATGTACTCTGAGTGGAGGTC ACTGCATTTGGTGATTCAGAATGATCAAGGCCATACCACTGTGCTGCACAGCTATCCAGA GAGCGTTGGACGAGAGGTGGCAAATGCTGTAGTCCGTCCTCTTGGGCAGGTGTTAGGTAC CCCTTCAGTGGCTGGTAGTGAGAATTTGTTAAAACTGACAAAGAAGTAAAATGGACCAT	

GGAGTAATTTGCTATGGACTGACCCTTCCATTGGATGGAGAGACTGTAAATATTGCGT
TGATGTATATACAGACTGGATTATGGCTTTAGTGTGCCAAAAGATTCTATTCCATTGCC
AGTTATTAAAGAGCCTAATCAATATGTTCAAACATACTAAAACACCTACAGAATCTTTT
TGTACCAAGACAGGAACAGGGTCCAGTCAGATTGCGACTATGCTTACAGGTCTTGAGAGC
CATTACAGAACTGGCCCCGTGAGTCATCTCTCATGGCCCGAGAACTTGGGAAGTCTTACT
GTTGTTTTCTTCTGCAGATTAACGACATACTTCTGGCCCCACCACTGTTCAAGGTTTGAT
TGCTGAGAATCTAGCAGAGAAGTTGATTGGTGTCTCTTTGAGGTGTGGTTACTAGCTTG
TACTCGGTGCTTCCCAACACCTCCTTATTGGAAAACAGCCAAGGAGATGGTGGCTAACTG
GAGGCATCACCCAGCAGTGGTGGAGCAGTGGAGCAAGGTCAATTGTGCACTCACTTCCAG
GTTACTACGCTTTACATATGGTCCTTCATTTCCTGCATTTAAAGTTCCTCGATGAAGATGC
CAGTCTGATCCCTCCAGAAATGGATAATGAGTGTGTTGCACAGACATGGTTTCGCTTTTTT
ACACATGTTAAGTAATCCTGTGGATTGAGTAACCCAGCTATTATAAGCTCTACTCCCAA
ATTTACAGGAACAGTTCTTGAATGTGAGCGGAATGCCGCAAGAATTGAATCAGTATCCCTG
CCTTAAACATCTGCCTCAAATATTTTTCGTGCCATGCGTGGAAATCAGCTGTCTGGTGGG
TGCACTCTTAGGTATTTCTAGACCCCGATCAGACAGTGTCTCCCCAACACCCGTGAATAG
ATTAAGTATGCCTCAAAGTGTCTGTGTCAGTACCACCCCCCACATAACCGGAGGCACCG
GGCTGTTACTGTGAATAAGGCCACCATGAAGACAAGCACAGTTAGTACTGCTCATGCCTC
TAAAGTTCAGCACCAGACGTCTCTCACCTCTCCTCTGTCAAGTCCAAATCAGACTAGTTC
AGAACCCCGGCCACTGCCTGCCCTCGGAGACCAAGGTTAACAGCATCTTGAATCTCTT
TGGATCATGGTTATTTGATGCAGCATTGTTATGGAGTTTCGACGGAAAGGGTCACAAAT
GTCCACAGACACCATGGTTTCCAATCCTATGTTTGTGCAAGTGAATTTCTGATAACTA
TGAAGCAGGAAGAGCTGAGGCTTGTGGGACACTGTGTAGGATTTTTGTAGCAAGAAGAC
TGGAGAAGAGATTCTGCCAGCTTATTTATCCAGATTTTACATGCTTTTAAATCAAGGTTT
GCAGATAAATGATTATGTGTGCCATCCTGTCTTGGCCAGCGTTATTCTAAACTCTCCTCC
TTTGTCTGCTGTGACTTGAAAGGGATTGATGTTGTGGTTTCCTTACTTTATTTACAGTCT
TGAACCATTTTGCCTGACAGGAGAGAACTCTCAAATTCAAAAGCTATGTAATCCAAC
AGAATTGCGAAGATCCTCCATTAATATCTGCTTTCTTGTGGCCCTCCCTCATCATTT
TGGCACAGTCAAATCTGAGTCTTATGATAAACCAATACTTTTCTGTCCCTGAAGTTGAG
ACTTGTGAATATATTAATAGGTGCCTTGCAAACCTGAAACGGACCCCAACAACCCCAAT
GATATTAGGTGATTACAGTGTCTGGGCTCCTGATTGCGAGCATTATCTCGTCAACCAAG
ACTCAACTCCAGTGGCGCCAAGACATGAGCATATCACTGGCAGCTCTAGAGCTCCTCTC
TGGCCTTGCAAAGGTGAGGAAGACAGACTCAGGAGACCGGAAGCGAGCATCAGTTCTGT
GTGCACCTACATTGTTTATCAGTGTAGTCTGGCCAGCTCCTTTACACTCCAGGGATCTGCA
CTCCATGATAGTGGCAGCTTTTCACTGTCTCTGTGTCTGGCTGACAGAGCACCTGATAT
GCTTGATGAAAAGGACTGCCTTAAGGAAGTACTGGAGATTGTGGAAGTGGGTATCTCAGG
AAGTAAGTCCAAGAACAATGAGCAAGAGGTCAAGTACAAAGGAGATAAGGAGCCAAACCC
TGCACTATGAGGGTAAGGATGCTGTGAAGCCACCTAACATCCATTCTCCATAGCAT
TGGCGCATTTCTTACCTAGTGGTCTGCTCTCCTTGTAGTCTTGTGAATGAGACCAC
TTTGATTAAATACTCCAGGCTGCCAACCATAAACAAGCATAGTTTCCGGTACTTTGTCTT
GGATAACAGTGTCTCCTGCAATGCTGGAACAACCTCTTGGAAATGAGCAGAATGATTT
TTTCCCTCTGTCACTGTGCTGGTCCGGGAATGTCTGGAAGACTTGCTTGGGCACAACA
GCTTGTCTTTTACCAGAGGAGCAAAGCAAATCAGAAGCTTTTGTACCTGAACCTCG
CCCAGTTCTTAAATGACGTTGGATTAAATATTCTGTGAACATCGGCCATTTCTGTA
AGAGGTGGACAAGATTCTTTTGTGAAAGCAGATCTCAGCATTCAGATTTGCATGAAT
AGTCACTGAAGAATTAGAAGAGAGACACGAAAAATTAAGGAGTGGCATGGCCAGCAGAT
TGCTTATGAAATACACCTTGAGCAACAGAGTGAGGAGGAATTGAGAAGAGAAGTTTTC
TGACCCAGTTACGGATTGCAAGCCCCGCCTCCTGCCAGGAATCCAAACAGCCGCCT
TTTTCTCTCACACTTTGGATTTTTGTCTTGAAGCACTGAAGGAACCTGCAATAGTCG
TCTACCTCTCACCTTATTGCACTTGATTCCACGATACCTGGATTTTTTGTATGACATTGG
GTATCTGGATCTCTTGCCATGTGCTCCTTTTGACACAGTTTTTATTTCTATATGAAGCC
AGGTACAGAAAACGAACCAAGAGATTTTAAAGAATGTGGAGTCTTCCAGAACTGTTACGCC
ACATTTCTAGAAATTTTGTCTTCCCTTGGCTGGTCACTAGATGTGGGCAGACACCTGG
TTGACTGGGCATGTTTCTACAGTTGGTCTATTAAATGTTGTGTGATGGTGAAGGATC
TCAACAAGAAGTGATTTCTCTGAAGATATTGGAGCTAGCATTTTCAATGGACAGAAGAA
GGTGTGTATTATGCTGATGCCCTTACAGAAATTGCTTTTGTGGTTCCTTCTCCTGTGGA
GTCCTTAACTGATTCATTGAAAGTAACATCTCGGACCAAGATAGTGATTCAAATATGGA
TCTTATGCCAGGAATCTGAAACAGCCATCCCTGACACTTGAGCTTTTCCCAATCATAC
AGACAATCTTAATCTCACAGAGGCTCAGTCCAGTTCAGAAATGAGGAAGCTGCCTCA
GGGTGCGCTGTCTCCTCCCTTGGACCTGAGACAAAGAGTTTCTGTAGTCTGGGTGGAACG
CTATGATGATATAGAAAATTTCCCTCTCAGAGCTGATGACAGAGATCAGTACTGGTGT

	GGAAACTACTGCAAATAGTAGCACTTCACTGAGATCTACAACCTTTGAAAAAGAAGTTCC TGTCATCTTCATCCACCCTTTAAACACTGGATTATTCGGATAAAAATTCAAGGAGCCAC TGGAAAATTTAATATGGTCATCCCTCTTGTGGATGGGATGATTGTGAGCAGCGAGCTCT TGGCTTTCTGGTGAGG		
	ORF Start: ATG at 101		ORF Stop: end of sequence
	SEQ ID NO: 226	1332 aa	MW at 149066.8kD
NOV37a, CG88634-01 Protein Sequence	MYSEWRSLHLVIQNDQGHTSVLHSPESVGREVANAVVRPLGQVLGTPSVAGSENLLKTD KEVKWTMEVICYGLTLPDGETVKYCVDTWDIMALVLPKDSIPLPVIKEPNQYVQTIL KHLQNLFPVPRQEQGSSQIRLCLQVLRATQKLARESSLMARETWEVLLLFLQINDILLAP PTVQGLIAENLAEKLGVLFEVWLLACTRCFPTPPYWKTAEMVANWRHHPAVVEQWSKV ICALTSRLLRFTYGPSFPAPKVPDEASLIPEMDNECVAQTWFRFLHMLSNPVDLSNPA IISSTPKFQEQFLNVSGMPQELNQYPCCLKHLPQIFFRAMRGISCLVDAFLGISRPRSDSA PPTPVNRLSMPQSAAVSTTPHNRRHRAVTVNKATMKTSTVSTAHASKVQHTSSTSPLS SPNQTSSEPRPLPAPRRPKVNSILNLFSGSWLFDAAFVMEFRRKGSQMSTDTMVSNNPMFDA SEFPDNYEAGRAEACGTLCRIFCSKKTGEEILPAYLSRFYMLLIQGLQINDYVCHPVLAS VILNSPPLFCCDLKGDVVPYFISALETILPDRRELSKFKSYVNPTELRRSSINILLSL LPLPHHFGTVKSESYDKPITFLSLKRLVNLIGALQTETDPNNTQMILGDSAAGLLIRS IHLVTQRLNSQWRQDMSISLAALLESLGLAKVRKTDGDRKRAISSVCTYIVYQCSRPA LHSRDLHSMIVAFAQCCLCVLTHEPDMLEKDKLKEVLEIVELGISGSKSKNNEQEVKYK GDKEPNPASMVRKDAEATLTSILHSIGAFSPSPGPASPCSLVNETTLIKYSRLPTINKH SFRYPVLDNSVILAMLEQPLGNEQNDFFPSVTVLVRGMSGRLOWAQQLCLPRGAKANQK LFVPEPRPVKNDVGFYKSVKHPFPPEEVDKIIPVKADLSIPDLHEIVTEELEERHEKLR SGMAQQIAYEIHLEQQSEBELQKRSFPDPVTDCKPPPAQEFQTARLFLSHFGFLSLEAL KEPANSRLPPLIALDSTIPGFFDDIGYLDLLPCRPFDTVFIFYMKPGQKTNQEIILNVE SSRTVQPHFLEFLSLGWSVDVGRHPGWTGHVSTWSINCCDDGEGSQQEVISSEDIGAS IFNGQKKVLYYADALTEIAFVVPSPVESLTDLSLESNISDQSDSNMDLMPGILKQPSLTL ELFPNHTDNLNSSQRLSPSSRMKLPQGRPVPLGPETRVSVVWVERYDDIENFPLSELM TEISTGVETTANSSTSLRSTTLEKEVPVIFIHPLNTGLPRIKIQGATGKFNMMVIPLVDGM IVSRRALGFLVR		

Two polymorphic variants of NOV37a have been identified and are shown in Table 410. Further analysis of the NOV37a protein yielded the following properties shown in Table 37B.

Table 37B. Protein Sequence Properties NOV37a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.3500 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.3000 probability located in Golgi body
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV37a protein against the Geneseq database, a proprietary
5 database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 37C.

Table 37C. Geneseq Results for NOV37a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAM39605	Human polypeptide SEQ ID NO 2750 - <i>Homo sapiens</i> , 515 aa. [WO200153312-A1, 26-JUL-2001]	878..1332 1..456	455/456 (99%) 455/456 (99%)	0.0
AAM41391	Human polypeptide SEQ ID NO 6322 - <i>Homo sapiens</i> , 321 aa. [WO200153312-A1, 26-JUL-2001]	1072..1332 1..262	261/262 (99%) 261/262 (99%)	e-147
ABB58732	<i>Drosophila melanogaster</i> polypeptide SEQ ID NO 2988 - <i>Drosophila melanogaster</i> , 1523 aa. [WO200171042-A2, 27-SEP-2001]	1..658 1..660	309/705 (43%) 412/705 (57%)	e-141
AAB43113	Human ORFX ORF2877 polypeptide sequence SEQ ID NO:5754 - <i>Homo sapiens</i> , 221 aa. [WO200058473-A2, 05-OCT-2000]	1171..1332 1..162	162/162 (100%) 162/162 (100%)	3e-87
AAB41768	Human ORFX ORF1532 polypeptide sequence SEQ ID NO:3064 - <i>Homo sapiens</i> , 128 aa. [WO200058473-A2, 05-OCT-2000]	683..801 2..121	115/120 (95%) 116/120 (95%)	6e-59

In a BLAST search of public sequence databases, the NOV37a protein was found to have homology to the proteins shown in the BLASTP data in Table 37D.

Table 37D. Public BLASTP Results for NOV37a				
Protein Accession Number	Protein/Organism/Length	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H3X8	DJ927M24.2 (KIAA1219) - <i>Homo sapiens</i> (Human), 1188 aa (fragment).	1..1169 1..1188	1143/1208 (94%) 1144/1208 (94%)	0.0
BAA86533	KIAA1219 protein - <i>Homo sapiens</i> (Human), 1112 aa (fragment).	651..1332 371..1053	674/683 (98%) 677/683 (98%)	0.0
CAD39096	Hypothetical protein - <i>Homo sapiens</i> (Human), 1333 aa (fragment).	651..1332 591..1274	674/684 (98%) 677/684 (98%)	0.0

Q9ULK1	KIAA1219 protein - <i>Homo sapiens</i> (Human), 532 aa (fragment).	860..1332 1..473	473/473 (100%) 473/473 (100%)	0.0
Q8WWC0	Hypothetical 47.6 kDa protein - <i>Homo sapiens</i> (Human), 423 aa (fragment).	970..1332 2..364	363/363 (100%) 363/363 (100%)	0.0

PFam analysis predicts that the NOV37a protein contains the domains shown in Table 37E.

Table 37E. Domain Analysis of NOV37a			
Pfam Domain	NOV37a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 38.

The NOV38 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 38A.

Table 38A. NOV38 Sequence Analysis	
	SEQ ID NO: 227 3116 bp
NOV38a, CG97012-01 DNA Sequence	ATGCCCGCCGCCCCGCCCCCGCCCGCCGCGCTGCGGGGCATCAGCCTGTTCTGGCCCTG CTGCTGGGCAGCCCCGCGCCGCGCCCTGGAGCGGGACGCCCTGCCCGAGGGCGACGCCAGC CCCCGGGCCCCCTACCTGCTGCCAGCGCGCCCCCGAGCGGGGCAGCCCCGCAAGGAG CACCCCGAGGAGCGGGTGGTGACCGCCCCCCCCAGCAGCAGCCAGAGCGCCGAGGTGCTG GGCGAGCTGGTGTGACGGCACCGCCCCAGCGCCACACGACATCCCCGCCCTGAGC CCCCTGCTGCCCGAGGAGGCCCGGCCAAGCACGCCCTGCCCCCCAAGAAGAGCTGCC AGCCTGAAGCAGGTGAACAGCGCCCCGGAAGCAGCTGCGGGCCCAAGGCCACAGCGCCGCC ACCGTGACGCGGGCCGGCAGCCAGCCCGCCAGCCAGGGCCTGGACCTGCTGAGCAGCAGC ACCGAGAAGCCCCGCCCCCGCGGACCCCGACCCCATCGTGGCCAGCAGGAGGCCAGC GAGGTGCCCTGTGGCTGGACCGGAAGGAGAGCGCCGTGCCACCACCCCGCAGCCCTG CAAATCTCCCCCTCACTTCGAGCCCTATGTGGCCACACACTCCCCAGAGGCCAGAA CCCGGGGAGCCTGGGCCTGACATGGCCAGGAGGCCCCCCAGGAGGACACAGCCCCATG GCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGAG ACCACTACCTCCACCATTATCACCACCACGGTCATCACCACCGAGCAGGCACCGCTCTC TGCACTGTGAGCTTCTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCACTGCTG CCCCTCAACAACTTTCTGGAGTGACATACAACGTGACAGTCTACACTGGCTATGGGGTG GAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGTCTCCATCCGCGGGGTG GACGGCCCTACCTGACCGTCCTGGCCAACAGACACTCCTGGTGGAGGGGCAGGTAATC CGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGCGCTTGGG ACCTTCCAGCTTCACTACCAGGCCTTCATGCTGAGCTGCAACTTTCCCCGCGCGCCTGAC TCTGGGGATGTACGGTGATGGACCTGCACTCAGGTGGGGTGGCCCACTTTCACTGCCAC CTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAATGCCTCCAGCCGCAC TGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGACAATGCCACC ATCGGCCGCGTCTCTCCCAAGTTACCCTGAAAACCAATGGGAGCCAATTCTGCATC TGGACGATTGAAGCTCCAGAGGGCCAGAAGCTGCACCTTGCACTTTGAGAGGCTGTTGCTG CATGACAAGGACAGGATGACGGTTCACAGCGGGCAGACCAACAAGTCAGCTCTTCTCTAC GACTCCCTTCAAACCGAGAGTGTCCCTTTTGGGGCCTGCTGAGCGAAGGCACACCATC CGCATCGAGTTCAGTCCGACAGGCCCGGGCGGCCTCCACCTTCAACATCCGATTTGAA

	<p> GCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTCACTACATCC GACCCGACCTATAACATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTG GAGCAGGGCCCGGCCATCATCGAATGCATCAATGTGCGGGACCCATACTGGAATGACACA GAGCCCCCTGTGCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTG TCCCCAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGTG GGAGAAGAGAAACGGATCTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATC TTGACCATCTACGATGGCGACGAGGTCTATGCCCCACATCTTGGGGCAGTACCTTGGGAAC AGTGGCCCCCAGAAACTGTACTCCTCCAGCCAGACTTAACCATCCAGTTCATTCCGAC CCTGCTGGCCCTCATCTTTGGAAGGGCCAGGGATTTATCATGAACTACATAGAGGTATCA AGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCAC ACGGAGTTGGTGCAGGGGAGCCAGAATCACCTACCAGTGTGACCCCGGCTATGACATCGTG GGGAGTGACACCCTCACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCATTTGT GAGAAAATTATGTACTGCACCGACCCCGAGAGGTGGATCACTCGACCCGCTTAATTTG GATCCTGTGCTGCTGGTGGGGACCCATCCAATACACCTGCAACCCCGGTTTTGTGCTT GAAGGGAGTCTCTTCTGACCTGCTACAGCCGTGAAACAGGGACTCCCATCTGGACGTCT CGCCTGCCCCACTGCGTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAA AATGGATACCAAATCCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATG TGCTACGAAGGCTTTGAGCTCATGGGTGAAGTGACCATCCGCTGCATCCTGGGACAGCCA TCCCACTGGAACGGGGCCCTGCCCGTGTGTAAGTAGCAGAAGCGGCAGCAGAGACGTCG CTGGAAGGGGGGAACATGGCCCTGGCTATCTTCATCCCGGTCTCATCATCTCTTACTG CTGGGAGGAGCCTACATTTACATCACAAGATGTCGCTACTATTCCAACCTCCGCTGCCT CTGATGTACTCCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCATT TACGAGACAGGGGAAACCAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGA AGGGGACTTGTGAACTCAACCACATCTCCTCGAGACATTATCCAGAGACCATGT </p>
	<p> ORF Start: ATG at 1 ORF Stop: TAA at 3040 SEQ ID NO: 228 1013 aa MW at 110509.9kD </p>
NOV38a, CG97012-01 Protein Sequence	<p> MPAARPPAAGLRGISLFLALLLGSFAAALERDALPEGDASPLGPYLLPSGAPERGSPGKE HPEERVVTAPPSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKLP SLKQVNSARKQLRPKATSATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPIVASEEAS EVPLWLDKESAVPTTPAPLQISFPTSQPYVAHTLPORPEPGEPPDMAQEAPQEDTSPM ALMDKGENELTGSASEESQETTTSTIIITTVITTEQAPALCSVSFNPGEYIDSSDYPLL PLNFFLECTYNVTYVYTGYGVELQVKS VNLSDGELLSIRGVDGPTLTVLANQTLLEVGQVI RSPNTNISVYFRFTQDDGLGTFQLHYQAFMLSCNFPFRPDSDGDTVMDLHSGGVANFHCH LGYELQGAKMLTICINASKPHWSSQEPICSA PCGGAVHNATIGRVLSPSYPENTNGSQFCI WTIEAPEGQKLHLHFERLLLHDKDRMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEAFENKHCYEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSL EQGPAIIECINVRDPYWNDEPLCRAMCGGELSAGVGVLSPNWPEPYVEGEDCIWKIHV GEEKRIFLDIQFLNLSNSDILTIYDGDEVMPHILGQYLGNSGPQKLYSSTPDLTIQFHSD PAGLIFGKGQGFIMNYIEVSRNDS CSDLPEIQNGWKTTSHTELVRGARITYQCDDPGYDIV GSDTLTCQWDLSSWSDPPFCEKIMYCTDPGEVDHSTR LISDPVLLVGTTIQYTCNPGFVL EGSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENGYQILYKRLYLPGESLTFM CYEGFELMGVETIRCILGQPSHWNGPLPVCKVAEAAAETSLEGGMALAI FIPVLIISLL LGGAYIYITRCRYYSNLRPLMYSHPYSQITVETEDNPIYETGETREYEVSI </p>
NOV38b, CG97012-02 DNA Sequence	<p> SEQ ID NO: 229 2420 bp CCTGGGCCTGACATGGCCAGGAGGCCCCCAGGAGGACACCAGCCCCATGGCCCTGATG GACAAAGGTGAGATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGAGACCACTACC TCCACCATTATCACCACCACGGTCATCACCACCGAGCAGGCACCACTCTCTGCACTGTG AGCTTCTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAAC AACTTTCTGGAGTGACATACAACGTGACAGTCTACACTGGCTATGGGGTGGAGCTCCAG GTGAAGAGTGTGAACCTGTCCGATGGGGAAGTCTCTCCATCCGCGGGGTGGACGGCCCT ACCCTGACCGTCTGGCCAACAGACACTCCTGGTGGAGGGGCAGGTAATCCGAAGCCCC ACCAACACCATCTCCGTCTACTTCCGACCTTCCAGGACGACGGCCTTGGGACCTTCCAG CTTCACTACCAGGCCTTCATGCTGAGCTGCAACTTCCCCCGCCGGCCTGACTCTGGGGAT GTCACGGTGATGGACCTGCACCTCAGGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTAT GAGCTCCAGGGCGCTAAGATGCTGACATGCATCAATGCCTCCAAGCCACTGGAGCAGC CAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCACCATCGGCCG GTCCTCTCCCAAGTTACCTGAAAACAAATGGGAGCCAATTCTGCATCTGGACGATT GAAGCTCCAGAGGGCCAGAAGCTGCACCTGCACCTTGAGAGGCTGTTGCTGCATGACAAG </p>

	GACAGGATGACGGTTCACAGCGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTT CAAACCGAGAGTGTCCCTTTTGAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAG TTCACGTCGACACGAGCCCGGGCGGCTCCACCTTCAACATCCGATTTGAAGCGTTTGAG AAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTCACTACATCCGACCCGACC TATAACATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGC CCGGCCATCATCGAATGCATCAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTG TGCAGAGCCATGTGTGGTGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAAC TGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGTGGGAGAAGAG AAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATC TACGATGGCGACGAGGTATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCC CAGAACTGTACTCCTCCACGCCAGACTTAACCATCCAGTTCATTTCGGACCTGCTGGC CTCATCTTTGGAAGGGCCAGGGATTTATCATGAACTACATAGAGGTATCAAGGAATGAC TCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAACCACTTCTCACACGGAGTTG GTGCGGGGAGCCAGAATCACTACCAGTGTGACCCCGGCTATGACATCGTGGGGAGTGAC ACCCCTCACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCATTTTGTGAGAAAT ATGTACTGCACCGACCCCGGAGAGGTGGATCACTCGACCCGCTTAATTTTCGGATCTGTG CTGCTGGTGGGACCAACCATCCAATACACCTGCAACCCCGGTTTGTGCTTGAAGGGAGT TCTCTTCTGACCTGCTACAGCCGTGAACAGGGACTCCCATCTGGACGTCTCGCTGCC CACTGCGTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAATGGATAC CAAATCCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTATGTGCTACGAA GGCTTTGAGCTCATGGGTGAAGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGG AACGGGCCCTGCCCCTGTGTAAAGTTAATCAAGACAGTTTTGAACATGCTTTAGAAGTA GCAGAAGCGGCAGCAGAGAGCTCGCTGGAAGGGGGGAACATGGCCCTGGCTATCTTCATC CCGGTCTCATCATCTCCTTACTGCTGGGAGGAGCTACATTACATCACAGATGTCCG TACTATTCCAACCTCCGCCTGCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTG GAAACCGAGTTTGACAACCCATTTACGAGACAGGGGAAACCAGAGAGTATGAGGTTTCT ATCTAAAGAGAGCTACACTT		
	ORF Start: ATG at 13		ORF Stop: TAA at 2404
	SEQ ID NO: 230	797 aa	MW at 88285.1kD
NOV38b, CG97012-02 Protein Sequence	MAQEAPQEDTSPMALMDKGENELTGSASEESQETTTSTIIITTVITTEQAPALCSVSFSN PEGYIDSSDYPLPLNNFLECTYNVTVTGYGVELQVKSNNLSDELLSIRGVDGPTLTV LANQTLLEGGQVIRSPNTISVYFRFTQDDGLGTFQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGAAMLTCTINASKPHWSSQEPICSAPEGAVHNATIGRVLSP SYPENTNGSQFCIWTIEAPEGQKLHLHFERLLHDKDRMTVHSGQTNKSALLYDSLQTES VPFEGLLSEGNTRIEFTSDQARAASTFNIRFEAFEGKHGCEPYIQNGNFTSDPTYNIG TIVEFTCDPGHSLGQPAIEICINVRDPYWNDEPLCRAMCGGELSAGVAVLSPNWPPEP YVEGEDCIWKIHVGBEKRIFLDIQFLNLSNDILTIYDGEVMPHILGQYLNGSGPQKLY SSTPDLTIQFHS DPAGLIFGKGQGFIMNYIEVSRNDSCLDLPEIQNGWKTTSHTELVRGA RITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCEKIMYCTDPGEVDHSTRLLSDPVLLVG TTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSESLACDNPGLPENGYQILY KRLLYLPGESLTFMCEYGFELMGEVTIRICILGQPSHWNGPLPVCKVNQDSFEHALEVAEAA AETSLEGGNMALAIPIPVLIISLLLGAYIYITRCRYSNLRLPLMYSHPYQSITVETEF DNPIYETGETREYEVSI		
	SEQ ID NO: 231	1434 bp	
NOV38c, CG97012-03 DNA Sequence	AGATCTTGCAACTTTCCCGCGCGCCTGACTCTGGGGATGTCACGGTGATGGACCTGCAC TCAGGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATG CTGACATGCATCAATGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCT CCTTGTGGAGGGCAGTGACAATGCCACCATCGGCCGCGTCTCTCCCCAAGTTACCT GAAAACACCAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCAGAAG CTGCACCTGCACCTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCACAGC GGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTT GAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCCGACCAAGGCCGG GCGGCCTCCACCTTCAACATCCGATTTGAAGCGTTTGAGAAAGGCCACTGCTATGAGCCC TACATCCAGAATGGGAACCTCACTACATCCGACCCGACCTATAACATTGGGACTATAGTG GAGTTCACCTGCGACCCCGGCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGCATC AATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGG GAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAACTGGCCGAGCCCTACGTGGAA GGTGAAGATTGTATCTGGAAGATCCACGTGGGAGAAGAGAAACGGATCTTCTTAGATATC		

	CAGTTCTCGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTGTCATG CCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCACG CCAGACTTAACCATCCAGTTCATTTCGGACCTGCTGGCCTCATCTTTGGAAAGGGCCAG GGATTATCATGAACACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTACCCGAG ATCCAGAATGGCTGGAAACCATTCTCACACGGAGTGGTGGCGGGGAGCCAGAATCACC TACCAGTGTGACCCGGCTGTGACATCGTGGGAGTGACACCTCAGCTGCCAGTGGGAC CTCAGCTGGAGCAGCGACCCCCCATTTTGTGAGAAAACGGAGGAGTCCCTGGCATGTGAC AACCAGGGCTGCCTGAAAATGGATACCAAATCCTGTACAAGCGACTCTACCTGCCAGGA GAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGAAGTGACCATCCGC TGCATCCTGGGACAGCCATCCCACTGGAACGGGCCCCCTGCCCGTGTGTGTCGAC		
	ORF Start: at 7		ORF Stop: at 1429
	SEQ ID NO: 232	474 aa	MW at 52744.6kD
NOV38c, CG97012-03 Protein Sequence	CNFPRRPSGDVTVMDLHSGGVAHFHCHLGYELQGAKMMLTCINASKPHWSSQEPICSAPO GGAHVHNATIGRVLSPSPYPTNGSQFCIWTIEAPEGGQKLHLHFRLLLHDKDRMTVHSGP TNKSALLYDSLQTESVFFELLSBENTIRIEFTSDQARAASFNIREFAFEKHGCHYEPIY QNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDEPLCLRAMCGGEL SAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGEVMPH ILGQYLGNSGPKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDCSDLPEIQ NGWKTTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCKEETESLACDNP GLPENGYILYKRLYLPGESLTFMCEYBGFELMGVETIRICLGPSPHWNGLPLVC		
	SEQ ID NO: 233	3116 bp	
NOV38d, CG97012-01 DNA Sequence	ATGCCCGCCGCCGGCCCCCGCCGCCGCTGCGGGGCATCAGCCTGTTCTGCCCCTG CTGCTGGGCAGCCCCGCCGCCGCTTGGAGCGGGACGCCCTGCCCGAGGGCGACGCCAGC CCCCTGGGCCCTACCTGCTGCCAGCGCGCCCCGAGCGGGGCAGCCCCGCAAGGAG CACCCCGAGGAGCGGGTGTGACCGCCCCCAGCAGCAGCCAGAGCGCCGAGGTGCTG GGCAGAGCTGGTGCTGGACGGCACCGCCCCAGCGCCACACGACATCCCCGGCCTGAGC CCCCTGCTGCCGAGGAGGCCCGGCCCAAGCACGCCCTGCCCCCAAGAAGAAGTGCACC AGCCTGAAGCAGGTGAACAGCGCCCGGAAGCAGCTGCGGCCCAAGGCCACAGCGCCGCC ACCGTGCAGCGGGCCGGCAGCCAGCCGCCAGCCAGGGCCTGGACCTGCTGAGCAGCAGC ACCGAGAAGCCCGGCCCCCCCGGCCGACCCCCGACCCCATCGTGCCAGCGAGGAGGCCAGC GAGGTGCCCTCTGGGCTGGACCGGAAGGAGAGCGCCGTCGCCACACCCCGCAGCCCTG CAAATCTCCCCCTTCACTTCGACGCCCTATGTGCCACACACTCCCCAGAGGCCAGAA CCGGGGAGCCTGGGCCCTGACATGGCCCCAGGAGGCCCCCCAGGAGGACACAGCCCCATG GCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGAG ACCACTACCTCACCATTATCACCACCACGGTCATCACCACCGAGCAGGCACCAAGCTCTC TGCAGTGTGAGCTTCTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCACTGCTG CCCCTCAACAACCTTCTGGAGTGCATACAACTGACAGTCTACACTGGCTATGGGGTG GAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGTCTCCATCCGCGGGGTG GACGGCCCTACCCTGACCGTCTTGCCCAACACAGACTCCTGGTGGAGGGGCAGGTAATC CGAAGCCCCACCAACACCATCTCCGTCTACTTCCGACCTTCCAGGACGACGGCCTTGGG ACCTTCCAGCTTCACTACGAGCCCTTCACTGCTGAGCTGCAACTTTCCCCCGGCCCTGAC TCTGGGATGTCAAGGTGACCTGACCTCAGTCAAGTGGGTGGCCCACTTTCATGCCAC CTGGGCTATGAGCTCCAGGGCGCTAAGATGTGACATGCATCAATGCCTCCAAGCCGCAC TGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCACC ATCGGCCGCGTCTCTCCCAAGTTACCCTGAAAAACCAATGGGAGCCAATTCTGCATC TGGACGATTGAAGCTCCAGAGGGCCAGAAGCTGCACCTGCATCTTGAGAGGCTGTTGCTG CATGACAAGGACAGGATGACGGTTCACAGCGGCAGACCAACAAGTCAAGCTCTTCTCTAC GATGCTCCCTTCAAACCGAGAGTGTCCGTTTTGAGGGCCTGCTGAGCGAAGGCAACACCATC CGCATCGAGTTCAGTCCGACAGGCCCGGGCGGCCTCCACCTTCAACATCCGATTTGAA GCGTTTGAGAAAGGCCACTGTCTATGAGCCCTACATCCAGAATGGGAACTTCACTACATCC GACCCGACCTATAACATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTG GAGCAGGCGCCGGCCATCATGCAATGCATCAATGTGCGGACCCATCTGGAATGACACA GAGCCCCGTGTGACAGGCATGTGTGTGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTG TCCCCAAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGTG GGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATC TTGACCATCTACGATGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCTTGGGAAC AGTGGCCCCCAGAACTGTACTCTCCACGCCAGACTTAACCTCAGTTCATCTCGGAC CCTGCTGGCCTCATCTTTGGAAAGGCCAGGAGTTTATCATGAACACTAGAGGTATCA		

	AGGAATGACTCCTGCTCGGATTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCAC ACGGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGCTATGACATCGTG GGGAGTGACACCTCACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCATTGTG GAGAAAATTATGTACTGCACCGACCCGGAGAGGTGGATCACTCGACCCGCTTAATTTG GATCCTGTGCTGCTGGTGGGGACCACCATCCAATACACCTGCAACCCCGGTTTTGTGCTT GAAGGGAGTTCTCTTCTGACCTGCTACAGCCGTGAAACAGGGACTCCCATCTGGAGCTCT CGCCTGCCCACTGCGTTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAA AATGGATACCAAATCCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATG TGCTACGAAGGCTTTGAGCTCATGGGTGAAGTGACCATCCGCTGCATCCTGGGACAGCCA TCCCCTGGAACCGGGCCCTGCCCGTGTGTAAAGTAGCAGAAGCGGCAGCAGACGCTCG CTGGAAGGGGGGAACATGGCCCTGGCTATCTTCATCCCGTCTCATCTCTCTTACTG CTGGGAGGAGCCTACATTTACATCACAAGATGTCGCTACTATTCCAACCTCCGCTGCCT CTGATGTACTCCCACCCCTACAGCCAGATCACCGTGGAACCGAGTTTGACAACCCCAT TACGAGACAGGGGAAACCAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGA AGGGGACTTGTGAACTCAACCACAATCTCCTCGAGACATTATCCAGAGACCATGT		
	ORF Start: ATG at 1		ORF Stop: TAA at 3040
	SEQ ID NO: 234	1013 aa	MW at 110509.9kD
NOV38d, CG97012-01 Protein Sequence	MPAARPPAAGLRGISLFLALLLGSAAALERDALPEGDASPLGPYLLPSGAPERGSPGKE HPEERVVTAPPSSQSAEVLGELVLDGTAPSAHNDIPALSPLPPEARPKHALPPKKLP SLKQVNSARKQLRPKATSAAVQRAGSQPASQGLDLLSSSTEKPGPPGDPDIVASEEAS EVPLWLDRKESAVPTTPAPLQISPFTSQPYVAHTLPQRPPEPGEPPDMAQEAPQEDTSPM ALMDKGENELTGSASEESQETTTSTIIITTVITTEQAPALCSVSFSPNPEGYIDSSDYPLL PLNNFLECTYNVTVTYGYGVELQVKSVDGELLIRGVDPGLTLVLANQTLLEGGQVI RSPNTISVYFRTFQDDGLGTQLHYQAFMLSCNFPRRPDSGDVTVMDLHSGGVAHFHCH LGYELQGAQMILTINASKPHWSSQEPICAPCGGAVHNATIGRVLSPSPYENTNGSQFCI WTIEAPEGQKLHLHFERLLLHDKDRMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEAFEGHCHYEPIQNGNFTTSDPTYNIGTIVEFTCDPGHSL EQGPAIIECINVRDPYWNDEPLCRAMCGGELSAGVAVVLSPNWPEPYVEGEDCIWKIHV GEEKRIFLDIQFLNLSNSDILTIYDGDEVMPHILGQYLGNSSGPQKLYSSTPDLTIQFHSD PAGLIFGKGQGFIMNYIEVSRNDSDDLPEIQNGWKTTSHTELVRGARITYQCDPGYDIV GSDTLTCQWDLWSDDPPFCEKIMYCTDPGEVDHSTRLISDPVLLVGTIQTICNPGFVL EGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENGYQILYKRLYPGESLTFM CYEGFELMGEVTIRCILGQPSHWNGPLPVCKVAEAAEETSLEGGNMAIAIFPVLIIISLL LGGAYIYITRCRYVSNLRLPLMYSHPYSQITVETEFDPNPIYETGETREYEVSI		
	SEQ ID NO: 235		867 bp
NOV38e, 210120300 DNA Sequence	AGATCTTGTGGAGGGGAGTGCACAATGCCACCATCGCCGCGTCTCTCCCCAAGTTAC CCTGAAAACACCAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCAG AAGCTGCACCTGCACTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCAC AGCGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCT TTTGAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCCGACAGGCC CGGGCGGCCTCCACCTTCAACATCCGATTGAAGCGTTTGAGAAAGGCCACTGCTATGAG CCCTACATCCAGAATGGGAACCTCACTACATCCGACCCGACCTATAACATTGGGACTATA GTGGAGTTTCACTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGC ATCAATGTGCGGGAACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGT GGGGAGCTCTCTGCTGTGCTGGGGTGGTATTGTCCCAAACCTGGCCCGAGCCCTACGTG GAAGGTGAAGATTGTATCTGGAAGATCCAGTGGGAGAGAGAAACGGATCTTCTTAGAT ATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTC ATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCC ACGCCAGACTTAACCATCCAGTTCATTCCGACCCTGCTGGCCTCATCTTTGGAAGGGC CAGGGATTTATCATGAACACGTCGAC		
	ORF Start: at 1		ORF Stop: end of sequence
	SEQ ID NO: 236	289 aa	MW at 32172.6kD
NOV38e, 210120300 Protein Sequence	RSCGAVHNATIGRVLSPSPYENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKDRMTVH SGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEGHCHYE PYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLAQGPAIIECINVRDPYWNDEPLCRAMCG GELSAGVAVVLSPNWPEPYVEGEDCIWKIHVGEKRIFLDIQFLNLSNSDILTIYDGDEV MPHILGQYLGNSSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYVD		

	SEQ ID NO: 237	867 bp
NOV38f, 210120376 DNA Sequence	AGATCTTGTGGAGGGGCGAGTGACACAATGCCACCATCGGCCGCGTCTCTCCCCAAGTTAC CCTGAAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCAG AAGCTGCACCTGCACCTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCAC AGCGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCT TTTGAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCGACAGGCC CGGGCGGCCTCCACCTTCAACATCCGATTGAAGCGTTTGAGAAAGGCCACTGCTATGAG CCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAACATTGGGACTATA GTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGC ATCAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGT GGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTG GAAGGTGAAGATTGTATCTGGAAGATCCAGTGGGAGAAGAGAAACGGATCTTCTTAGAT ATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTC ATGCCCCACATCTGGGGCAGTACCTTGGAACAGTGGCCCCCAGAACTGTACTCCTCC ACGCCAGACTTAACCATCCAGTTCATTGCGACCCCTGCTGGCCCTCATCTTTGAAAGGGC CAGGGATTTATCATGAACCTACGTCGAC	
	ORF Start: at 1	ORF Stop: end of sequence
	SEQ ID NO: 238	289 aa MW at 32172.6kD
NOV38f, 210120376 Protein Sequence	RSCGGAVHNATIGRVLSPSYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKDRMTVH SGQTNKSALLYDSLQTESVPFEGLLSEGNIRIEFTSDQARAASFNIRFEAFKKGHCYE PYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDEPLCRAMCG GELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEV MPHILGQYLGNSGPQKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNYVD	
	SEQ ID NO: 239	867 bp
NOV38g, 210120463 DNA Sequence	AGATCTTGTGGAGGGGCGAGTGACACAATGCCACCATCGGCCGCGTCTCTCCCCAAGTTAC CCTGAAAACACCAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCGG AAGCTGCACCTGCACCTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCAC AGCGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCT TTTGAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCGACAGGCC CGGGCGGCCTCCACCTTCAACATCCGATTGAAGCGTTTGAGAAAGGCCACTGCTATGAG CCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAACATTGGGACTATA GTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGC ATCAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGT GGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTG GAAGGTGAAGATTGTATCTGGAAGATCCAGTGGGAGAAGAGAAACGGATCTTCTTAGAT ATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTC ATGCCCCACATCTGGGGCAGTACCTTGGAACAGTGGCCCCCAGAACTGTACTCCTCC ACGCCAGACTTAACCATCCAGTTCATTGCGACCCCTGCTGGCCCTCATCTTTGAAAGGGC CAGGGATTTATCATGAACCTACGTCGAC	
	ORF Start: at 1	ORF Stop: end of sequence
	SEQ ID NO: 240	289 aa MW at 32200.7kD
NOV38g, 210120463 Protein Sequence	RSCGGAVHNATIGRVLSPSYPENTNGSQFCIWTIEAPEGRKLHLHFERLLLHDKDRMTVH SGQTNKSALLYDSLQTESVPFEGLLSEGNIRIEFTSDQARAASFNIRFEAFKKGHCYE PYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDEPLCRAMCG GELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEV MPHILGQYLGNSGPQKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNYVD	
	SEQ ID NO: 241	1434 bp
NOV38h, 210120269 DNA Sequence	AGATCTTGCAACTTCCCCCGCGGCCTGACTCTGGGGATGTACGGTGATGGACCTGCAC TCAGGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATG CTGACATGCATCAATGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCT CCTTGTGGAGGGGCGAGTGACACAATGCCACCATCGGCCGCGTCTCTCCCCAAGTTACCT GAAAACACCAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCAGAAG CTGCACCTGCACCTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCACAGC GGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTT GAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCGACAGGCCCGG GCGGCCTCCACCTTCAACATCCGATTGAAGCGTTTGAGAAAGGCCACTGCTATGAGCCC	

	TACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAACATTGGGACTATAGTG GAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGCATC AATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGG GAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTGGAA GGTGAAGATTGTATCTGGAAGATCCACGTGGGAGAAGAGAAACGGATCTTCTTAGATATC CAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTCATG CCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCACG CCAGACTTAACCATCCAGTTCATTCCGACCCCTGCTGGCCTCATCTTTGGAAGGGCCAG GGATTATCATGAACATACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAG ATCCAGAATGGCTGGAAAACCACTTCTCACACGGAGTTGGTGCGGGGAGCCAGAATCAC TACCAGTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCCCTCACCTGCCAGTGGGAC CTCAGCTGGAGCAGCGACCCCATTTTGTGAGAAAACGGAGGAGTCCCTGGCATGTGAC AAGCCAGGGCTGCTGAAAATGGATACCAAATCCTGTACAAGCGACTCTACCTGCCAGGA GAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGAAGTGACCATCCGC TGCATCCTGGGACAGCCATCCCACTGGAACGGGGCCCTGCCCGTGTGTGTCGAC		
	ORF Start: at 1		ORF Stop: end of sequence
	SEQ ID NO: 242	478 aa	MW at 53202.0kD
NOV38h, 210120269 Protein Sequence	RSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGA KMLTCINASKPHWSSQEPICSA PCGGAVHNATIGRVLS PSPYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKDRMTVHS GQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEGKHCEYP YIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDEPLCRAMCGG ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEV PHILGOYLGN SGPKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNYIEVSRNDS CSDLPE IQNGWKTTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCEKTEESLACD NPGLPENGYQILYKRLYLPGESLTFMCYEGFELMGEVTIRCI LGQPSHWNGPLPVCVD		
	SEQ ID NO: 243	867 bp	
NOV38i, CG97012-04 DNA Sequence	AGATCTTGTGGAGGGG CAGTGCAATGCCACCATCGGCCGCGTCTCTCCCCAAGTTAC CCTGAAAACACCAATGGGAGCCAATTCTGCATCTGGACGATTGAAGCTCCAGAGGGCCAG AAGCTGCACCTGCACCTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCAC AGCGGGCAGACCAACAAGTCAGCTCTTCTTACGACTCCCTTCAAACCGAGAGTGTCCCT TTTGAGGGCCTGCTGAGCGAAGGCAACACCATCCGCATCGAGTTCACGTCCGACCGGCC CGGGCGGCCTCCACCTTCAACATCCGATTTGAAGCGTTTGAGAAAGGCCACTGCTATGAG CCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAACATTGGGACTATA GTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGC ATCAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGT GGGGAGCTCTCTGCTGTGGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTG GAAGGTGAAGATTGTATCTGGAAGATCCACGTGGGAGAAGAGAAACGGATCTTCTTAGAT ATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGATGGCGACGAGGTC ATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCTCC ACGCCAGACTTAACCATCCAGTTCATTCCGACCCCTGCTGGCCTCATCTTTGGAAGGGC CAGGGATTATCATGAAC TACGTCGAC		
	ORF Start: at 7		ORF Stop: at 862
	SEQ ID NO: 244	285 aa	MW at 31715.2kD
NOV38i, CG97012-04 Protein Sequence	CGGAVHNATIGRVLS PSPYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKDRMTVHSG QTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEGKHCEYP YIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDEPLCRAMCGGE LSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEVMP HILGOYLGN SGPKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNY		
	SEQ ID NO: 245	2861 bp	
NOV38j, CG97012-05 DNA Sequence	AGCCACGATGCCCCGCGGCCCGGCCGCGCCCGCGGGACTCCGCGGGATCTCGCTGTTCTCT CGCTCTGCTCCTGGGGAGCCCGCGCGCAGCGCTGGAGCGAGATGCTCTTCCCGAGGGAGA TGCTAGCCCTTTGGTCTTACCTCTGCCCTCAGGAGCCCGGAGAGAGCGAGTCTCTGG CAAAGAGCACCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCCTCACAGTCGGCGGA AGTGTGGGCGAGCTGGTGTGGATGGGACCGCACCTCTGCACATCACGACATCCCAGC CCTGTACCGCTGCTTCCAGAGGAGGCCCGCCCCAAGCACGCTTGGCCCCCAAGAAGAA ACTGCCTTCGCTCAAGCAGGTGAACCTCTGCCAGGAAGCAGCTGAGGCCCAAGGCCACCTC		

	<p>CGCAGCCACTGTCCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCCTAGATCTCCTCTC CTCCTCCACGGAGAAGCCTGGCCACCGGGGGACCCGACCCCATCGTGGCCTCCGAGGA GGCATCAGAAGTGCCCTTTGGCTGGATCGAAAGGAGAGTGCAGTCCCTACAACACCCGC ACCCCTGCAAATCTCCCCCTTCACTTCGACGCCCTATGTGGCCACACACTCCCCAGAG GCCAGAACCCGGGGAGCCTGGGCTGACATGGCCAGGAGGCCCCCAGGAGACACAG CCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAG CCAGGAGACCACTACCTCCACCATTATCACCACCACGGTCATCACCACCAGCAAGCACC AGCTCTCTGCAGTGTGAGCTTCTCCAATCCTGAGGGGTACATGACTCCAGCGACTACCC ACTGCTGCCCTCAACAACCTTTCTGGAGTGCACATACAACGTGACAGTCTACACTGGCTA TGGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTCTCTCCATCCG CGGGTGGACGGCCCTACCCTGACCGTCTGGCCAACAGACACTCCTGGTGGAGGGCA GGTAATCCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGG CCTGGGACCTTCCAGCTTCACTACCAGGCTTCTATGCTGAGCTGCAACTTTCCCCGCG GCTGACTCTGGGATGTACGGTGTGACCTGCACTCAGTGGGGTGGCCACTTTCA CTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAATGCCTCCAA GCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGCAGTGCAAA TGCCACCATCGGCCGCTCTCTCCCAAGTTACCCTGAAAACACCAATGGGAGCCAATT CTGCATCTGGACGATTGAAGCTCCAGAGGGCCAGAAGCTGCACCTGCACCTTGAGAGGCT GTTGCTGCATGACAAGGACAGGATGACGGTTCACAGCGGGCAGACCAACAGTCAAGTCT TCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGGGCTGCTGAGCGAAGGCAA CACCATCCGCATCGAGTTACGTCCGACAGGCGGGCGCTCCACCTTCAACATCCG ATTTGAAGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTCAC TACATCCGACCCGACCTATAACATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCA CTCCTGGAGCAGGGCCCGCCATCATCGAATGCATCAATGTGCGGGACCCATACTGGAA TGACACAGAGCCCTGTGACAGGCCATGTGTGGTGGGGAGCTCTCTGCTGTGGCTGGGGT GGTATTGTCCCCAACTGGCCGAGCCCTACGTGAAGGTGAAGATTGTCTGGAAGAT CCAGTGGGAGAGAGAAACGGATCTTCTTAGATATCCAGTTCTGAATCTGAGCAACAG TGACATCTTGACCATCTACGATGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCT TGGGAACAGTGGCCCCAGAACTGTACTCCTCCAGCCAGACTTAACCATCCAGTTCCA TTCGGACCTGTGGCCTCATCTTTGAAAGGGCCAGGGATTATCATGAACCTACATAGA GGTATCAAGGAATGACTCCTGCTCGGATTTACCGAGATCCAGAATGGCTGGAAACAC TTCTCACACGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGCTATGA CATCGTGGGGAGTGACACCCTCACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCC ATTTGTGAGAAAACGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAAATGG ATACCAAATCCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTA CGAAGGCTTTGAGCTCATGGGTGAAGTGACCATCCGCTGCATCCTGGGACAGCCATCCCA CTGGAACGGGCCCTGCCGCTGTGTAAAGTAGCAGAAGCGGCAGCAGAGACTCGCTGGA AGGGGGGAACATGGCCCTGGCTATCTTCATCCCGGTCCTCATCATCTCCTTACTGCTGGG AGGAGCCTACATTTACATACAAGATGTCGCTACTATTCCAACCTCCGCTGCCTCTGAT GTACTCCACCCCTACAGCCAGATCACCCTGGAACCGAGTTTGACAACCCCATTTACGA GACAGGGGAACAGAGATATGAGGTTTCTATCTAAAGAG</p>
	<p>ORF Start: ATG at 8</p>
	<p>ORF Stop: TAA at 2855</p>
	<p>SEQ ID NO: 246</p>
	<p>949 aa</p>
	<p>MW at 103496.0kD</p>
<p>NOV38j, CG97012-05 Protein Sequence</p>	<p>MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKE HPEERVVTAPSSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPBEPARKHALPPKKLP SLKQVNSARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPIVASEEAS EVPLWLDRKESAVPTTPAPLQISPTSQPYVAHTLPQRPEPGEPPGDMAQEAPQEDTSPM ALMDKGENELTGSASEESQETTTSTIIITTVITTEQAPALCSVSFSNPEGYIDSSDYPLL PLNNFLECTYNVTYTYGYVELQVSVNLSDGELLSIRGVDGPTLTVLANTLLVEGQVI RSPNTISVYFRFTQDDGLGTFLHYQAFMLSCNFPRRPDSGDVTVMDLHSGGVAHFHCH LGYELQGAKMLTICINASKPHWSSQEPICSA PCGAVHNATIGRVLSPSYPENTNGSQFCI WTIEAPEGQKLHLHFERLLHDKDRMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEAFKGCYEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSL EQGPAAIECINVRDPYWNDEPLCRAMCGGELSAGVAVVLSPNWPEPYVEGEDCIWKIHV GEEKRIFLDIQFLNLSNSDILTIYDGEVMPHILGQYLGNSGPKLYSSTPDLTIQFHSD PAGLIFGKGQGFIMNYIEVSRNDSDDLPEIQNGWKTTSHTELVRGARITYQCDPGYDIV GSDTLTCQWDLSSWSDPPFCKTEESLACDNPLGPENGYQILYKRLYLPGESLTFMCEYEG FELMGVETIRCILGQPSHWNGPLPVCKVAEAAAETSLEGGMALAI FIPVLIISLLLGA</p>

YIYITRCRYYSNLRPLMYSHPYSQITVETEFDNPIYETGETREYEVSI
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 38B.

Table 38B. Comparison of NOV38a against NOV38b through NOV38j.		
Protein Sequence	NOV38a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV38b	228..1013 1..797	751/797 (94%) 752/797 (94%)
NOV38c	393..865 1..474	427/477 (89%) 439/477 (91%)
NOV38d	30..1013 30..1013	944/984 (95%) 944/984 (95%)
NOV38e	452..738 3..289	285/287 (99%) 287/287 (99%)
NOV38f	452..738 3..289	285/287 (99%) 287/287 (99%)
NOV38g	452..738 3..289	284/287 (98%) 287/287 (99%)
NOV38h	392..866 2..477	429/479 (89%) 441/479 (91%)
NOV38i	452..736 1..285	285/285 (100%) 285/285 (100%)
NOV38j	30..872 30..873	752/847 (88%) 765/847 (89%)

- Two polymorphic variants of NOV38a have been identified and are shown in Table 41P. Further analysis of the NOV38a protein yielded the following properties shown in Table 38C.

Table 38C. Protein Sequence Properties NOV38a	
PSort analysis:	0.6760 probability located in plasma membrane; 0.1800 probability located in nucleus; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 29 and 30

A search of the NOV38a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 38D.

Table 38D. Geneseq Results for NOV38a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV38a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU12271	Human PRO6094 polypeptide sequence - <i>Homo sapiens</i> , 1023 aa. [WO200140466-A2, 07- JUN-2001]	1..1013 1..1023	1013/1023 (99%) 1013/1023 (99%)	0.0
ABG22405	Novel human diagnostic protein #22396 - <i>Homo sapiens</i> , 990 aa. [WO200175067-A2, 11- OCT-2001]	29..1013 6..990	983/985 (99%) 984/985 (99%)	0.0
ABG05922	Novel human diagnostic protein #5913 - <i>Homo sapiens</i> , 990 aa. [WO200175067-A2, 11- OCT-2001]	29..1013 6..990	983/985 (99%) 984/985 (99%)	0.0
ABG01221	Novel human diagnostic protein #1212 - <i>Homo sapiens</i> , 982 aa. [WO200175067-A2, 11- OCT-2001]	33..1013 2..982	981/981 (100%) 981/981 (100%)	0.0
ABG22407	Novel human diagnostic protein #22398 - <i>Homo sapiens</i> , 997 aa. [WO200175067-A2, 11- OCT-2001]	29..1008 6..996	967/991 (97%) 971/991 (97%)	0.0

In a BLAST search of public sequence databases, the NOV38a protein was found to have homology to the proteins shown in the BLASTP data in Table 38E.

Table 38E. Public BLASTP Results for NOV38a				
Protein Accession Number	Protein/Organism/Length	NOV38a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BYH1	Seizure 6-like protein precursor - <i>Homo sapiens</i> (Human), 1024 aa.	1..1013 1..1024	1013/1024 (98%) 1013/1024 (98%)	0.0

Q9Y2E1	KIAA0927 protein - <i>Homo sapiens</i> (Human), 1001 aa (fragment).	1..872 53..925	821/876 (93%) 834/876 (94%)	0.0
Q9Y3J6	Hypothetical 87.6 kDa protein (DJ268D13.1.2) (seizure related gene 6 (mouse)-like (KIAA0927) (isoform 2)) - <i>Homo sapiens</i> (Human), 792 aa.	228..1008 1..791	778/791 (98%) 780/791 (98%)	0.0
Q9NUI3	DJ268D13.1.3 (Seizure related gene 6 (Mouse)-like (KIAA0927) (Isoform 3)) - <i>Homo sapiens</i> (Human), 777 aa (fragment).	228..1004 1..777	775/779 (99%) 775/779 (99%)	0.0
O95917	Hypothetical 79.0 kDa protein (DJ268D13.1.1) (seizure related gene 6 (mouse)-like (KIAA0927) (isoform 1)) - <i>Homo sapiens</i> (Human), 716 aa.	228..868 1..641	641/641 (100%) 641/641 (100%)	0.0

PFam analysis predicts that the NOV38a protein contains the domains shown in Table 38F.

Table 38F. Domain Analysis of NOV38a			
Pfam Domain	NOV38a Match Region	Identities/ Similarities for the Matched Region	Expect Value
sushi	393..448	16/65 (25%) 41/65 (63%)	6e-06
CUB	452..559	29/120 (24%) 72/120 (60%)	5.5e-09
sushi	567..624	19/67 (28%) 44/67 (66%)	4.5e-06
CUB	628..736	34/121 (28%) 69/121 (57%)	1.6e-15
sushi	745..800	22/64 (34%) 44/64 (69%)	1.3e-14
sushi	806..865	21/66 (32%) 47/66 (71%)	3.2e-11
sushi	873..930	20/65 (31%) 47/65 (72%)	4e-12

Example 39.

The NOV39 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 39A.

Table 39A. NOV39 Sequence Analysis			
	SEQ ID NO: 247	1957 bp	
NOV39a, CG99754-01 DNA Sequence	CAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCATGCCAGCCCCCTCTGGCC TGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTGAGGCTCGGCCACGGGC TGCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGCGC TTTGTGGCAGTCCCCGAGGGCATCCCCACCGAGACGCGCTGCTGGACCTAGGCAAGAAC CGCATCAAAACGCTCAACCAGGACGAGTTCGCCAGCTTCCCGCACCTGGAGGAGCTGGAG CTCAACGAGAACATCGTGAGCGCGTGAGGCCCGCGCCTTCAACAACCTCTTCAACCTC CGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCACTGGC CTCAGCAACCTGACCAAGCTGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTAC ATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTAC ATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGC AACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCTCATCGTCTGAGG CTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACCGACTC AAGGTCTTGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCAACTGCCTCTAC GGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTG GCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCTACAACCCCATCAGCACC ATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGCGGG CAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGTCAAT GTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTG GAGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGTCTCTGTGGGTGTTT CGGCGCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTT GTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGC CGCCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACG GTGCAGTTTGTGTGCCGGGCCGATGGCGACCCGCGCCCGCCCATCTCTGGCTCTACCC CGAAAGCACCTGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAG CTGGAGGTGCGCTACGCCAGGTACAGGACAACGGCAGTACCTGTGCATCGCGGCCAAC GCGGGCGGCAACGACTCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGG CCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCC AACAGCACCCGCGCACTGTGCCTTTCCTTTCGACATCAAGACCCCTCATCATGCCACC ACCATGGGCTTCATCTCTTCTGGGCGTCTGCTCTTCTGCGCTGGTGTGCTGTTTCTC TGGAGCCGGGGCAAGGGCAACAAAGCAACATCGAGATCGAGTATGTGCCCGGAAAG TCGGACGCAGGCATCAGTCCGCGACGCGCCCGCAAGTTCAACATGAAGATGATATGA GGCCGGGGCGGGGGCAGGGACCCCGGGCGGCCGGGCAGGGGAAGGGGCTGGCCGCCA CCTGCTCACTCTCAGTCCTTCCACCTCTCCCTAC		
	ORF Start: ATG at 16		ORF Stop: TGA at 1858
	SEQ ID NO: 248	614 aa	MW at 69145.1kD
NOV39a, CG99754-01 Protein Sequence	MLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRRFVAVP EGIPTETRLDLGKNRIKTLNDEFASFPHLELELNENIVSAVEPGAFNNLNLRLTLGL RSNRLKLIPLGVFTGLSNLTKLDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA FSGLSLEQLTLEKCNLTSTPTEALSHLHGLIVLRLRLNINAIIRDYSFKRLYLKVLEI SHWPYLDMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSM LHELLRLQEIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLEESVFHVSNGLETLIL DSNPLACDCRLLWVFRRLWLNFNRRQPTCATPEFVQGEKFKDFPDVLLPNYFTCRRARI RDRKAQQVFVDEGHTVQFVCRADGDPPIILWLSPRKHLVSAKSNRGLTVFPDGTLEVRY AQVQDNGTYLCIAANAGGNDSPAHLHVSYS PDWPHQPNKTFAFISNQPGGEANSTRA TVPPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNIEIEYVPRKSDAGI SSADAPRKFNMKMI		
	SEQ ID NO: 249	2015 bp	
NOV39b,	GAGCTGAGGCTGGTGGGGGGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAG		

CG99754-02 DNA Sequence	CCCATCCTCCTGCTGGTGGTGGGCTCAGTGCTGTGTCAGGCTCGGCCACGGGCTGCCCGCCC CGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGCGCTTTGTGGCA GTCCCCGAGGGCATCCCCACCGAGACGCGCTGTGCTGGACCTAGGCAAGAACC GCATCAAA ACGCTCAACCAGGACGAGTTCCGCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAG AACATCGTGAGCGCCGTGGAGCCCGGCGCTTCAACAACCTCTTCAACCTCCGGACGCTG GGTCTCCGCAGCAACCGCCTGAAGCTCATCCGCTAGGCGTCTTCACTGGCCTCAGCAAC CTGACCAAGCTGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAG GACCTGTACAACCTCAAGTCACTGGAGGTGGCGACAATGACCTCGTCTACATCTCTCAC CGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACC TCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCTCATCGTCTGAGGCTCCGGCAC CTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACCGACTCAAGGTCTTG GAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACCTGCCTCTACGGCCTCAAC CTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGC CACCTAGTCTATCTCGCTTCTCTCAACCTCTCCTACAACCCCATCAGCACCATTGAGGGC TCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGCGGGCAGCTGGCC GTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGTCTCAATGTCTCTGGC AACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTC ATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGGCGCCGC TGGCGGCTCAACTTCAACCGGCAGCAGCCACGTCGCCACGCCCGAGTTTGTCCAGGGC AAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCGCGCGGCC CGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACAGGTGCAGTTT GTGTGCCGGGCGGATGGCGACCCGCCGCCGCTCCTCTGGCTCTACCCCGAAAGCAC CTGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCTCTGATGGCACGCTGGAGGTG CGCTACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGC AACGACTCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAG CCCAACAGACCTTCGCTTTCATCTCCAACGAGCGGGCGAGGGCAACAGCACCC CGCGCACTGTGCCTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGC TTCATCTCTTCTGGGCGTCTCTCTCTGCTGGTGTGCTGTTTCTCTGGAGCCGG GGCAAGGGCAACACAAAGCACACATCGAGATCGAGTATGTGCCCAAAAGTCGGACGCA GGCATCAGCTCCGCGACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGC GGGGGCAGGGACCCCGGGCGGCGGGCAGGGGAAGGGCCTGGCCGCACTGCTCAC TCTCCAGTCCTTCCACCTCTCCTACCCTTCTACACACGTTCTTTCTCCCTCCCGC CTCCGTCCCCTGCTGCCCCCACCAGCCTCAGCTC		
	ORF Start: ATG at 31	ORF Stop: TGA at 1849	
	SEQ ID NO: 250	606 aa	MW at 68345.1kD
NOV39b, CG99754-02 Protein Sequence	MPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKRFFAVPEGIPTETR LLDLGNRIKTLNQDEFASFPHEELELNENIVSAVEPGAFNNLFLNRLTLGLRSNRLKLI PLGVFTGLSNLTKLDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLSLE QLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAI RDYSFKRLYRLKVLEISHWPYLDT MTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHLHELLRLQ EIQLVGGQLAVVEPYAFRLNLYLRVLNVSGNQLTTLEESVFHSGVGNLETILDSNPLACD CRLWVFRRRWRNLNFRQQPTCATPEFVQGEKDFDPVLLPNYFTCRRARIRDRKAQQV FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVDNGT YLCIAANAGGNDSPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDI KTLIIATTMGFISFLGVVLFCLVLLFLWSRGKNTKHNIEIEYVPQKSDAGISSADAPRK FNMKMI		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 39B.

Table 39B. Comparison of NOV39a against NOV39b.		
Protein Sequence	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV39b	9..614 1..606	563/606 (92%) 564/606 (92%)

Six polymorphic variants of NOV39a have been identified and are shown in Table 41Q. Further analysis of the NOV39a protein yielded the following properties shown in Table 39C.

Table 39C. Protein Sequence Properties NOV39a	
PSort analysis:	0.4600 probability located in plasma membrane; 0.1071 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 36 and 37

- A search of the NOV39a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 39D.

Table 39D. Geneseq Results for NOV39a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV39a Residues/- Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB74705	Human membrane associated protein MEMAP-11 - <i>Homo sapiens</i> , 620 aa. [WO200112662-A2, 22-FEB-2001]	1..614 7..620	614/614 (100%) 614/614 (100%)	0.0
AAW84596	Amino acid sequence of the human Tango-79 protein - <i>Homo sapiens</i> , 614 aa. [WO9906427-A1, 11-FEB-1999]	1..614 1..614	612/614 (99%) 612/614 (99%)	0.0
AAB80225	Human PRO227 protein - <i>Homo sapiens</i> , 620 aa. [WO200104311-A1, 18-JAN-2001]	1..614 7..620	612/614 (99%) 612/614 (99%)	0.0
AAU12333	Human PRO227 polypeptide sequence - <i>Homo sapiens</i> , 620 aa. [WO200140466-A2, 07-JUN-2001]	1..614 7..620	612/614 (99%) 612/614 (99%)	0.0
AAY13357	Amino acid sequence of protein PRO227 - <i>Homo sapiens</i> , 620 aa. [WO9914328-A2, 25-MAR-1999]	1..614 7..620	612/614 (99%) 612/614 (99%)	0.0

In a BLAST search of public sequence databases, the NOV39a protein was found to have homology to the proteins shown in the BLASTP data in Table 39E.

Table 39E. Public BLASTP Results for NOV39a				
Protein Accession Number	Protein/Organism/Length	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96FE5	Unknown (protein for MGC:17422) - <i>Homo sapiens</i> (Human), 614 aa.	1..614 1..614	614/614 (100%) 614/614 (100%)	0.0
Q9N008	Hypothetical 69.2 kDa protein - <i>Macaca fascicularis</i> (Crab eating macaque) (<i>Cynomolgus</i> monkey), 614 aa.	1..614 1..614	612/614 (99%) 613/614 (99%)	0.0
Q9D1T0	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930471K13, full insert sequence - <i>Mus musculus</i> (Mouse), 614 aa.	1..614 1..614	610/614 (99%) 611/614 (99%)	0.0
CAD38935	Hypothetical protein - <i>Homo sapiens</i> (Human), 577 aa (fragment).	38..614 1..577	577/577 (100%) 577/577 (100%)	0.0
Q9BZ20	BA438B23.1 (Neuronal leucine-rich repeat protein) (CDNA FLJ31810 fis, clone NT2RI2009289, weakly similar to carboxypeptidase N 83 kDa chain) - <i>Homo sapiens</i> (Human), 606 aa.	14..614 6..606	365/603 (60%) 468/603 (77%)	0.0

PFam analysis predicts that the NOV39a protein contains the domains shown in

5 Table 39F.

Table 39F. Domain Analysis of NOV39a			
Pfam Domain	NOV39a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRRNT	35..64	10/31 (32%) 22/31 (71%)	0.00079

LRR	114..137	9/25 (36%) 20/25 (80%)	0.061
LRR	186..209	10/25 (40%) 19/25 (76%)	0.012
LRR	282..305	7/25 (28%) 17/25 (68%)	0.72
LRR	330..353	7/25 (28%) 20/25 (80%)	0.19
LRRCT	363..416	17/59 (29%) 39/59 (66%)	0.0021
ig	433..493	15/64 (23%) 44/64 (69%)	2.1e-09

Example 40.

The NOV40 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 40A.

Table 40A. NOV40 Sequence Analysis			
	SEQ ID NO: 251	889 bp	
NOV40a, CG99777-01 DNA Sequence	GGGAGAATCCTTCTTGAACAGAGATGGGCCCAGAACTGAATCAGATGAAGAGAGATAAG GTGTGATGTGGGAAGACTATATAAAGAATGGACCCAGGGCTGCAGCAAGCACTCAACGG AATGGCCCCCTCTGGAGACACAGCCATGCATGTGCCGGCGGGCTCCGTGGCCAGCCACCT GGGGACCACGAGCCGAGCTATTCTATTGACCACAGCCACTCTGGCTCTGTGCCTTGT CTTCACGGTGGCCACTATTATGGTGTGGTTCGTTTCAGAGGACGGACTCCATTCCCAACTC ACCTGACAACGTCCCCCTCAAAGGAGGAAATTGCTCAGAAGACCTCTTATGTATCCTGAA AAGGGCTCCATTCAAGAAGTCATGGGCCTACCTCCAAGTGGCAAAGCATCTAAACAAAAC CAAGTTGTCTTGAACAAAGATGGCATTCTCCATGGAGTCAGATATCAGGATGGGAATCT GGTGATCCAATTCCCTGGTTTGTACTTCATCATTGCCAACTGCAGTTCTTGTACAATG CCCAAATAATTCTGTGATCTGAAGTTGGAGCTTCTCATCAACAAGCATATCAAAAAACA GGCCCTGGTGACAGTGTGTGAGTCTGGAATGCAACGAAACACGTATACCAGAATCTCTC TCAATTCTGTCTGGATTACCTGCAGGTCAACACCACCATATCAGTCAATGTGGATACATT CCAGTACATAGATACAAGCACCTTTCTCTTGAGAATGTGTTGTCCATCTTCTTATACAG TAATTCACTGAACAGTTTCTCTTGGCCTTCAGGAAGAAAGCGCCTCTCCACCATACAG TATTTTCATCCCTCCAACACTTGGGCAAAAAGAAAACCTTAGACCAAGA		
	ORF Start: ATG at 89		ORF Stop: TGA at 791
	SEQ ID NO: 252	234 aa	MW at 26016.9kD
NOV40a, CG99777-01 Protein Sequence	MDPGLQQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL VVQRTDSIPNSPDNVPLKGGNCSEDLCLIKRAPFKKSWAYLQVAKHLNKTKLSWNKDG LHGVRYQDGNLVIQFPGLYFIICQLQFLVQCPNNSVDLKLELLINKHIKKQALVTVCESG MQTKHVVQNLSQFLLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD		
	SEQ ID NO: 253	829 bp	
NOV40b, CG99777-02 DNA Sequence	GGGAGAATCCTTCTTGAACAGAGATGGGCCCAGAACTGAATCAGATGAAGAGAGATAAG GTGTGATGTGGGAAGACTATATAAAGAATGGACCCAGGGCTGCAGCAAGCACTCAACGG AATGGCCCCCTCTGGAGACACAGCCATGCATGTGCCGGCGGGCTCCGTGGCCAGCCACCT GGGGACCACGAGCCGAGCTATTCTATTGACCACAGCCACTCTGGCTCTGTGCCTTGT CTTCACGGTGGCCACTATTATGGTGTGGTTCGTTTCAGAGGACGGACTCCATTCCCAACTC ACCTGACAACGTCCCCCTCAAAGGAGTGGCAAAGCATCTAAACAAAACCAAGTTGTCTTG GAACAAAGATGGCATTCTCCATGGAGTCAGATATCAGGATGGGAATCTGGTGATCCAATT CCCTGGTTTGTACTTCATCATTGCCAACTGCAGTTTCTGTACAATGCCCAATAATTC		

	TGTCGATCTGAAGTTGGAGCTTCTCATCAACAAGCATATCAAAAAACAGGCCCTGGTGAC AGTGTGTGAGTCTGGAATGCAAACGAAACACGTATACCAGAATCTCTCTCAATTCTTGCT GGATTACCTGCAGGTCAACACCACCATATCAGTCAATGTGGATACATTCCAGTACATAGA TACAAGCACCTTTCTCTCTTGAGAATGTGTTGTCCATCTTCTCTATACAGTAATTCAGACTG AACAGTTTCTCTTGGCCTTCAGGAAGAAAGCGCCTCTCTACCATAACGATTTTCATCCCT CCAAACACTTGGGCAAAAAGAAACTTTAGACCAAGAAGGATTCTCCTC		
	ORF Start: ATG at 89		ORF Stop: TGA at 719
	SEQ ID NO: 254	210 aa	MW at 23250.6kD
NOV40b, CG99777-02 Protein Sequence	MDPGLQQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL VVQRTDSIPNSPDNVPLKGVAKHLNKTCLSWNKDGLHGVRYQDGNLVIQFPGLYFIICQ LQFLVQCPNNSVDLKLELLINKHIKKQALVTVCESGMQTKHVYQNLSQLLDYLVNTTI SVNVDTFQYIDTSTFPLENVLSIFLYSNSD		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 40B.

Table 40B. Comparison of NOV40a against NOV40b.		
Protein Sequence	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV40b	1..234	210/234 (89%)
	1..210	210/234 (89%)

Three polymorphic variants of NOV40b have been identified and are shown in Table 41R.

- 5 Further analysis of the NOV40a protein yielded the following properties shown in Table 40C.

Table 40C. Protein Sequence Properties NOV40a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.3000 probability located in microbody (peroxisome); 0.3000 probability located in Golgi body; 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Cleavage site between residues 68 and 69

A search of the NOV40a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 40D.

10

Table 40D. Geneseq Results for NOV40a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAU78086	Human CD30-ligand (CD30L) protein sequence - <i>Homo sapiens</i> , 234 aa. [WO200211767-A2, 14-FEB-2002]	1..234 1..234	234/234 (100%) 234/234 (100%)	e-135
AAR45009	Sequence encoded by a human CD30-L cDNA clone encoding additional N-terminal amino acids - <i>Homo sapiens</i> , 234 aa. [WO9324135-A, 09-DEC-1993]	1..234 1..234	234/234 (100%) 234/234 (100%)	e-135
AAR45007	Sequence encoded by a human CD30-L cDNA clone - <i>Homo sapiens</i> , 215 aa. [WO9324135-A, 09-DEC-1993]	20..234 1..215	215/215 (100%) 215/215 (100%)	e-123
AAU78087	Mouse CD30-ligand (CD30L) protein sequence - <i>Mus sp.</i> , 239 aa. [WO200211767-A2, 14-FEB-2002]	1..234 1..239	167/240 (69%) 195/240 (80%)	4e-92
AAR45008	Sequence encoded by a murine CD30-L cDNA clone encoding additional N-terminal amino acids - <i>Acomys cahirinus</i> , 239 aa. [WO9324135-A, 09-DEC-1993]	1..234 1..239	167/240 (69%) 195/240 (80%)	4e-92

In a BLAST search of public sequence databases, the NOV40a protein was found to have homology to the proteins shown in the BLASTP data in Table 40E.

Table 40E. Public BLASTP Results for NOV40a				
Protein Accession Number	Protein/Organism/Length	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P32971	Tumor necrosis factor ligand superfamily member 8 (CD30 ligand) (CD30- L) (CD153 antigen) - <i>Homo sapiens</i> (Human), 234 aa.	1..234 1..234	234/234 (100%) 234/234 (100%)	e-134

P32972	Tumor necrosis factor ligand superfamily member 8 (CD30 ligand) (CD30- L) - <i>Mus musculus</i> (Mouse), 239 aa.	1..234 1..239	167/240 (69%) 195/240 (80%)	1e-91
AAD46392	CD30 LIGAND-EXOTOXIN A FUSION PROTEIN - synthetic construct, 220 aa (fragment).	86..234 48..196	149/149 (100%) 149/149 (100%)	9e-83
P41047	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand) - <i>Mus musculus</i> (Mouse), 279 aa.	97..195 142..264	31/123 (25%) 53/123 (42%)	0.056
Q9WV90	Fas ligand - <i>Marmota monax</i> (Woodchuck), 169 aa (fragment).	100..154 44..101	20/58 (34%) 29/58 (49%)	0.49

PFam analysis predicts that the NOV40a protein contains the domains shown in Table 40F.

Table 40F. Domain Analysis of NOV40a			
Pfam Domain	NOV40a Match Region	Identities/ Similarities for the Matched Region	Expect Value
TNF	93..230	55/159 (35%) 136/159 (86%)	1.6e-53

Example B: Sequencing Methodology and Identification of NOVX Clones

- 5 1. **GeneCalling™ Technology:** This is a proprietary method of performing differential gene expression profiling between two or more samples developed at CuraGen and described by Shimkets, *et al.*, "Gene expression analysis by transcript profiling coupled to a gene database query" Nature Biotechnology 17:198-803 (1999). cDNA was derived from various human samples representing multiple tissue types, normal and diseased states,
- 10 physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then digested with up to as many as 120 pairs of restriction enzymes and pairs of
- 15 linker-adaptors specific for each pair of restriction enzymes were ligated to the appropriate

end. The restriction digestion generates a mixture of unique cDNA gene fragments. Limited PCR amplification is performed with primers homologous to the linker adapter sequence where one primer is biotinylated and the other is fluorescently labeled. The doubly labeled material is isolated and the fluorescently labeled single strand is resolved by capillary gel electrophoresis. A computer algorithm compares the electropherograms from an experimental and control group for each of the restriction digestions. This and additional sequence-derived information is used to predict the identity of each differentially expressed gene fragment using a variety of genetic databases. The identity of the gene fragment is confirmed by additional, gene-specific competitive PCR or by isolation and sequencing of the gene fragment.

2. **SeqCalling™ Technology:** cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

3. **PathCalling™ Technology:** The NOVX nucleic acid sequences are derived by laboratory screening of cDNA library by the two-hybrid approach. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, are sequenced. In silico prediction was based on sequences available in CuraGen Corporation's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory screening was performed using the methods summarized below:

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents 6,057,101 and 6,083,693, incorporated herein by reference in their entireties).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries. Such PCR product was sequenced; sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Physical clone: the cDNA fragment derived by the screening procedure, covering the entire open reading frame is, as a recombinant DNA, cloned into pACT2 plasmid (Clontech) used to make the cDNA library. The recombinant plasmid is inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693).

4. **RACE:** Techniques based on the polymerase chain reaction such as rapid amplification of cDNA ends (RACE), were used to isolate or complete the predicted sequence of the cDNA of the invention. Usually multiple clones were sequenced from one

or more human samples to derive the sequences for fragments. Various human tissue samples from different donors were used for the RACE reaction. The sequences derived from these procedures were included in the SeqCalling Assembly process described in preceding paragraphs.

5 **5. Exon Linking:** The NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding
10 sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were
15 then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen,
20 stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The PCR product derived from exon linking was cloned into the pCR2.1 vector from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in
25 CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

30 **6. Physical Clone:** Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN,

BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the
5 full-length protein.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clones used for expression and screening purposes.

**Example C: Quantitative expression analysis of clones in various cells and
10 tissues**

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an Applied Biosystems ABI PRISM[®] 7700 or an ABI PRISM[®] 7900 HT Sequence Detection
15 System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on
20 metabolic diseases), AI_comprehensive_panel (containing normal tissue and samples from autoimmune/autoinflammatory diseases), Panel CNSD.01 (containing samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of
25 agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

30 First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l)

was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 µg of total RNA were performed in a volume of 20 µl and incubated for 60 minutes at 42 °C. This reaction can be scaled up to 50 µg of total RNA in a final volume of 100 µl. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58 °-60 °C, primer optimal T_m = 59 °C, maximum primer difference = 2 °C, probe does not have 5'G, probe T_m must be 10 °C greater than primer T_m, amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200 nM.

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95 °C for 15 seconds, 60 °C for 1 minute. Results were recorded as CT values

(cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying
5 by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR
10 amplification was performed as follows: 95 °C 10 min, then 40 cycles of 95 °C for 15 seconds, 60 °C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The
15 samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through
20 the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on these panels are comprised of samples derived from all major organ systems from single adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney,
25 adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:
30 ca. = carcinoma,
* = established from metastasis,

met = metastasis,

s cell var = small cell variant,

non-s = non-sm = non-small,

squam = squamous,

5 pl. eff = pl effusion = pleural effusion,

glio = glioma,

astro = astrocytoma, and

neuro = neuroblastoma.

General_screening_panel_v1.4, v1.5 and v1.6

10 The plates for Panels 1.4, v1.5 and v1.6 include two control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panels 1.4, v1.5 and v1.6 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon
15 cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in Panels 1.4, v1.5 and v1.6 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on Panels 1.4, v1.5 and v1.6 are comprised of pools of
20 samples derived from all major organ systems from 2 to 5 different adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small
25 intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose. Abbreviations are as described for Panels 1, 1.1, 1.2, and 1.3D.

Panels 2D, 2.2, 2.3 and 2.4

The plates for Panels 2D, 2.2, 2.3 and 2.4 generally include two control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons
30 working in close cooperation with the National Cancer Institute's Cooperative Human

Tissue Network (CHTN) or the National Disease Research Initiative (NDRI) or from Ardaïs or Clinomics. The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted

5 "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologist at NDRI/CHTN/Ardaïs/Clinomics). Unmatched RNA samples from tissues without malignancy (normal tissues) were also obtained from Ardaïs or Clinomics. This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples

10 include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (*i.e.* immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims

15 (accidents, *etc.*). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen. General oncology screening panel_v_2.4 is an updated version of Panel 2D.

HASS Panel v 1.0

The HASS panel v 1.0 plates are comprised of 93 cDNA samples and two controls.

20 Specifically, 81 of these samples are derived from cultured human cancer cell lines that had been subjected to serum starvation, acidosis and anoxia for different time periods as well as controls for these treatments, 3 samples of human primary cells, 9 samples of malignant brain cancer (4 medulloblastomas and 5 glioblastomas) and 2 controls. The human cancer cell lines are obtained from ATCC (American Type Culture Collection) and fall into the

25 following tissue groups: breast cancer, prostate cancer, bladder carcinomas, pancreatic cancers and CNS cancer cell lines. These cancer cells are all cultured under standard recommended conditions. The treatments used (serum starvation, acidosis and anoxia) have been previously published in the scientific literature. The primary human cells were obtained from Clonetics (Walkersville, MD) and were grown in the media and conditions

30 recommended by Clonetics. The malignant brain cancer samples are obtained as part of a collaboration (Henry Ford Cancer Center) and are evaluated by a pathologist prior to

CuraGen receiving the samples. RNA was prepared from these samples using the standard procedures. The genomic and chemistry control wells have been described previously.

ARDAIS Panel v 1.0

The plates for ARDAIS panel v 1.0 generally include 2 control wells and 22 test
 5 samples composed of RNA isolated from human tissue procured by surgeons working in
 close cooperation with Ardais Corporation. The tissues are derived from human lung
 malignancies (lung adenocarcinoma or lung squamous cell carcinoma) and in cases where
 indicated many malignant samples have "matched margins" obtained from noncancerous
 lung tissue just adjacent to the tumor. These matched margins are taken from the tissue
 10 surrounding (*i.e.* immediately proximal) to the zone of surgery (designated "NAT", for
 normal adjacent tissue) in the results below. The tumor tissue and the "matched margins"
 are evaluated by independent pathologists (the surgical pathologists and again by a
 pathologist at Ardais). Unmatched malignant and non-malignant RNA samples from lungs
 were also obtained from Ardais. Additional information from Ardais provides a gross
 15 histopathological assessment of tumor differentiation grade and stage. Moreover, most
 samples include the original surgical pathology report that provides information regarding
 the clinical state of the patient.

Panels 3D and 3.1

The plates of Panels 3D and 3.1 are comprised of 94 cDNA samples and two control
 20 samples. Specifically, 92 of these samples are derived from cultured human cancer cell
 lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are
 generally obtained from ATCC (American Type Culture Collection), NCI or the German
 tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the
 tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder
 25 carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas,
 ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there
 are two independent samples of cerebellum. These cells are all cultured under standard
 recommended conditions and RNA extracted using the standard procedures. The cell lines
 in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.
 30 Oncology_cell_line_screening_panel_v3.2 is an updated version of Panel 3. The cell lines
 in panel 3D, 3.1, 1.3D and oncology_cell_line_screening_panel_v3.2 are of the most
 common cell lines used in the scientific literature.

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) was employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5ng/ml, TNF alpha at approximately 5-10ng/ml, IFN gamma at approximately 20-50ng/ml, IL-4 at approximately 5-10ng/ml, IL-9 at approximately 5-10ng/ml, IL-13 at approximately 5-10ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20ng/ml PMA and 1-2µg/ml ionomycin, IL-12 at 5-10ng/ml, IFN gamma at 20-50ng/ml and IL-18 at 5-10ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 µg/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte

reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol
5 (5.5 $\times 10^{-5}$ M) (Gibco), and 10 mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum
10 (FCS) (Hyclone, Logan, UT), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 $\times 10^{-5}$ M (Gibco), and 10 mM Hepes (Gibco), 50ng/ml GMCSF and 5ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 $\times 10^{-5}$ M (Gibco), 10 mM
15 Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 μ g/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from
20 mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. CD45RO beads were then used to isolate the CD45RO CD4 lymphocytes with the
25 remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 $\times 10^{-5}$ M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μ g/ml anti-CD28 (Pharmingen) and 3 μ g/ml anti-CD3
30 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested

the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and
5 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with
10 sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10 ng/ml. Cells were harvested for
15 RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100
20 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for
25 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and
30 Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours

following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at
5 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco). RNA was either prepared from resting cells or cells
10 activated with PMA at 10ng/ml and ionomycin at 1 μ g/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). CCD106 cells were activated for 6 and 14 hours with approximately 5
15 ng/ml TNF alpha and 1ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5ng/ml IL-4, 5ng/ml IL-9, 5ng/ml IL-13 and 25ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane
20 (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15ml Falcon Tube. An equal volume of isopropanol was added and left at -20°C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was
25 redissolved in 300 μ l of RNase-free water and 35 μ l buffer (Promega) 5 μ l DTT, 7 μ l RNAsin and 8 μ l DNase were added. The tube was incubated at 37°C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80°C .

30 AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained

from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other tissues was obtained from Clinomics.

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohns disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and four female patients. Four of the patients were taking lebvid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims with no disease or with emphysema, asthma or COPD was purchased from Clinomics. Emphysema patients ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

AI = Autoimmunity

Syn = Synovial

Normal = No apparent disease

Rep22 /Rep20 = individual patients

RA = Rheumatoid arthritis

Backus = From Backus Hospital

5 OA = Osteoarthritis

(SS) (BA) (MF) = Individual patients

Adj = Adjacent tissue

Match control = adjacent tissues

-M = Male

10 -F = Female

COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases.

15 Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study. Cells were obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective)
20 Caesarean section. After delivery of the infant, when the surgical incisions were being repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and
25 kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

Patient 2 Diabetic Hispanic, overweight, not on insulin

Patient 7-9 Nondiabetic Caucasian and obese (BMI>30)

Patient 10 Diabetic Hispanic, overweight, on insulin
Patient 11 Nondiabetic African American and overweight
Patient 12 Diabetic Hispanic on insulin

Adipocyte differentiation was induced in donor progenitor cells obtained from
5 Osirus (a division of Clonetics/BioWhittaker) in triplicate, except for Donor 3U which had
only two replicates. Scientists at Clonetics isolated, grew and differentiated human
mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in
Mark F. Pittenger, *et al.*, Multilineage Potential of Adult Human Mesenchymal Stem Cells
Science Apr 2 1999: 143-147. Clonetics provided Trizol lysates or frozen pellets suitable
10 for mRNA isolation and ds cDNA production. A general description of each donor is as
follows:

Donor 2 and 3 U: Mesenchymal Stem cells, Undifferentiated Adipose

Donor 2 and 3 AM: Adipose, AdiposeMidway Differentiated

Donor 2 and 3 AD: Adipose, Adipose Differentiated

15 Human cell lines were generally obtained from ATCC (American Type Culture
Collection), NCI or the German tumor cell bank and fall into the following tissue groups:
kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver
HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These
cells are all cultured under standard recommended conditions and RNA extracted using the
20 standard procedures. All samples were processed at CuraGen to produce single stranded
cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic
islets from a 58 year old female patient obtained from the Diabetes Research Institute at the
University of Miami School of Medicine. Islet tissue was processed to total RNA at an
25 outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following
abbreviations are used:

GO Adipose = Greater Omentum Adipose

SK = Skeletal Muscle

UT = Uterus

PL = Placenta

AD = Adipose Differentiated

AM = Adipose Midway Differentiated

5 U = Undifferentiated Stem Cells

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors
10 between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains two brains from each of the following diagnoses: Alzheimer's disease, Parkinson's disease,
15 Huntington's disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus palladus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area 17 (occipital cortex). Not all brain regions are represented in all cases; *e.g.*, Huntington's
20 disease is characterized in part by neurodegeneration in the globus palladus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

25 In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy

Sub Nigra = Substantia nigra

Glob Palladus= Globus palladus

Temp Pole = Temporal pole

Cing Gyr = Cingulate gyrus

BA 4 = Brodman Area 4

Panel CNS_Neurodegeneration_V1.0

5 The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and
47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained
from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain
and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are
removed from calvaria of donors between 4 and 24 hours after death, sectioned by
10 neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and
examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from
Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no
evidence of dementia prior to death. The eight normal control brains are divided into two
15 categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and
controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically
senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe
AD senile plaque load). Within each of these brains, the following regions are represented:
hippocampus, temporal cortex (Brodman Area 21), parietal cortex (Brodman area 7), and
20 occipital cortex (Brodman area 17). These regions were chosen to encompass all levels of
neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in
AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus;
the parietal cortex shows moderate neuronal death in the late stages of the disease; the
occipital cortex is spared in AD and therefore acts as a "control" region within AD patients.
25 Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0
panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like
pathology upon autopsy

30 Control = Control brains; patient not demented, showing no neuropathology

Control (Path) = Control brains; pateint not demented but showing sever
AD-like pathology

SupTemporal Ctx = Superior Temporal Cortex

Inf Temporal Ctx = Inferior Temporal Cortex

5

A. CG133274-02: Induced Myeloid Leukemia Cell

Differentiation Protein MCL-1-like Protein.

Expression of gene CG133274-02 was assessed using the primer-probe set Ag7050,
described in Table AA. Results of the RTQ-PCR runs are shown in Table AB.

10 Table AA. Probe Name Ag7050

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtctcgtgggtgcgctg-3'	17	450	255
Probe	TET-5'- tcgtaagggtctccagcgcccttcctg- 3'-TAMRA	25	485	256
Reverse	5'-gattggcgccaaggaca-3'	17	541	257

Table AB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7050, Run 282273858	Tissue Name	Rel. Exp.(%) Ag7050, Run 282273858
Adipose	100.0	Renal ca. TK-10	59.5
Melanoma* Hs688(A).T	33.7	Bladder	60.7
Melanoma* Hs688(B).T	34.9	Gastric ca. (liver met.) NCI-N87	87.1
Melanoma* M14	33.0	Gastric ca. KATO III	59.0
Melanoma* LOXIMVI	49.0	Colon ca. SW-948	19.8
Melanoma* SK-MEL-5	22.8	Colon ca. SW480	36.1
Squamous cell carcinoma SCC-4	19.2	Colon ca.* (SW480 met) SW620	25.0
Testis Pool	12.7	Colon ca. HT29	28.7
Prostate ca.* (bone met) PC-3	44.4	Colon ca. HCT-116	56.6
Prostate Pool	18.3	Colon ca. CaCo-2	24.0
Placenta	27.2	Colon cancer tissue	69.3
Uterus Pool	14.0	Colon ca. SW1116	12.1

Ovarian ca. OVCAR-3	46.3	Colon ca. Colo-205	10.2
Ovarian ca. SK-OV-3	53.6	Colon ca. SW-48	11.0
Ovarian ca. OVCAR-4	32.1	Colon Pool	14.4
Ovarian ca. OVCAR-5	55.5	Small Intestine Pool	24.5
Ovarian ca. IGROV-1	31.4	Stomach Pool	19.3
Ovarian ca. OVCAR-8	34.4	Bone Marrow Pool	11.5
Ovary	21.5	Fetal Heart	13.5
Breast ca. MCF-7	72.2	Heart Pool	13.9
Breast ca. MDA-MB-231	60.3	Lymph Node Pool	16.0
Breast ca. BT 549	81.2	Fetal Skeletal Muscle	8.5
Breast ca. T47D	18.2	Skeletal Muscle Pool	17.0
Breast ca. MDA-N	12.3	Spleen Pool	59.9
Breast Pool	14.6	Thymus Pool	24.0
Trachea	44.1	CNS cancer (glio/astro) U87-MG	82.4
Lung	11.5	CNS cancer (glio/astro) U-118-MG	42.3
Fetal Lung	81.2	CNS cancer (neuro;met) SK-N-AS	46.7
Lung ca. NCI-N417	15.3	CNS cancer (astro) SF-539	22.1
Lung ca. LX-1	61.6	CNS cancer (astro) SNB-75	45.4
Lung ca. NCI-H146	17.8	CNS cancer (glio) SNB-19	31.9
Lung ca. SHP-77	55.9	CNS cancer (glio) SF-295	60.7
Lung ca. A549	28.1	Brain (Amygdala) Pool	6.9
Lung ca. NCI-H526	25.2	Brain (cerebellum)	12.7
Lung ca. NCI-H23	90.1	Brain (fetal)	10.0
Lung ca. NCI-H460	37.1	Brain (Hippocampus) Pool	10.2
Lung ca. HOP-62	27.2	Cerebral Cortex Pool	8.4
Lung ca. NCI-H522	33.9	Brain (Substantia nigra) Pool	7.0
Liver	2.7	Brain (Thalamus) Pool	7.6
Fetal Liver	14.1	Brain (whole)	4.5
Liver ca. HepG2	20.4	Spinal Cord Pool	22.8
Kidney Pool	40.9	Adrenal Gland	19.9
Fetal Kidney	11.3	Pituitary gland Pool	5.9
Renal ca. 786-0	31.6	Salivary Gland	7.3
Renal ca. A498	12.3	Thyroid (female)	30.6
Renal ca. ACHN	31.9	Pancreatic ca. CAPAN2	25.7
Renal ca. UO-31	33.9	Pancreas Pool	29.7

General_screening_panel_v1.6 Summary: Ag7050 Highest expression of this gene is seen in adipose (CT=25). This gene is ubiquitously expressed in this panel, with high to moderate expression seen in brain, colon, gastric, lung, breast, ovarian, and melanoma cancer cell lines. This expression profile suggests a role for this gene product in cell survival and proliferation. Modulation of this gene product may be useful in the treatment of cancer.

Among tissues with metabolic function, this gene is expressed at high to moderate levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed at moderate levels in the CNS, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

B. CG134430-01: RIKEN cDNA 2310034L04 Like Gene.

Expression of gene CG134430-01 was assessed using the primer-probe set Ag7372, described in Table BA. Results of the RTQ-PCR runs are shown in Table BB.

Table BA. Probe Name Ag7372

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - catttgaagtgggtgtctacacttataaa -3'	28	789	258
Probe	TET-5' - agtcctgtccctctggtgcttctcac- 3' -TAMRA	26	818	259
Reverse	5' - ggcatagatatttcttgattacttcata t-3'	29	860	260

Table BB. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7372, Run 305065597	Tissue Name	Rel. Exp.(%) Ag7372, Run 305065597
Secondary Th1 act	46.7	HUVEC IL-1beta	19.1
Secondary Th2 act	51.1	HUVEC IFN gamma	17.9
Secondary Tr1 act	27.0	HUVEC TNF alpha + IFN gamma	3.2
Secondary Th1 rest	6.1	HUVEC TNF alpha + IL4	3.9
Secondary Th2 rest	16.8	HUVEC IL-11	8.5
Secondary Tr1 rest	13.9	Lung Microvascular EC none	36.9
Primary Th1 act	25.2	Lung Microvascular EC TNFalpha + IL-1beta	8.1
Primary Th2 act	80.7	Microvascular Dermal EC none	3.6
Primary Tr1 act	58.2	Microvascular Dermal EC TNFalpha + IL-1beta	4.0
Primary Th1 rest	4.4	Bronchial epithelium TNFalpha + IL1beta	1.4
Primary Th2 rest	5.4	Small airway epithelium none	4.6
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	31.6
CD45RA CD4 lymphocyte act	100.0	Coronary artery SMC rest	6.0
CD45RO CD4 lymphocyte act	37.9	Coronary artery SMC TNFalpha + IL-1beta	10.4
CD8 lymphocyte act	18.2	Astrocytes rest	2.2
Secondary CD8 lymphocyte rest	3.5	Astrocytes TNFalpha + IL- 1beta	1.7
Secondary CD8 lymphocyte act	6.9	KU-812 (Basophil) rest	8.1
CD4 lymphocyte none	13.1	KU-812 (Basophil) PMA/ionomycin	11.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	21.2	CCD1106 (Keratinocytes) none	18.3
LAK cells rest	5.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	4.6
LAK cells IL-2	41.8	Liver cirrhosis	3.9
LAK cells IL-2+IL-12	1.3	NCI-H292 none	8.4
LAK cells IL-2+IFN gamma	4.0	NCI-H292 IL-4	6.4
LAK cells IL-2+ IL-18	3.4	NCI-H292 IL-9	9.0
LAK cells PMA/ionomycin	36.3	NCI-H292 IL-13	7.5
NK Cells IL-2 rest	82.4	NCI-H292 IFN gamma	2.1
Two Way MLR 3 day	14.0	HPAEC none	7.4
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	32.1

Two Way MLR 7 day	9.1	Lung fibroblast none	11.9
PBMC rest	8.3	Lung fibroblast TNF alpha + IL-1 beta	10.0
PBMC PWM	8.2	Lung fibroblast IL-4	9.5
PBMC PHA-L	6.6	Lung fibroblast IL-9	6.4
Ramos (B cell) none	9.1	Lung fibroblast IL-13	10.6
Ramos (B cell) ionomycin	30.1	Lung fibroblast IFN gamma	9.1
B lymphocytes PWM	9.5	Dermal fibroblast CCD1070 rest	25.7
B lymphocytes CD40L and IL-4	41.2	Dermal fibroblast CCD1070 TNF alpha	47.3
EOL-1 dbcAMP	29.7	Dermal fibroblast CCD1070 IL-1 beta	22.2
EOL-1 dbcAMP PMA/ionomycin	22.8	Dermal fibroblast IFN gamma	8.9
Dendritic cells none	13.8	Dermal fibroblast IL-4	11.8
Dendritic cells LPS	9.2	Dermal Fibroblasts rest	15.0
Dendritic cells anti-CD40	9.8	Neutrophils TNFa+LPS	31.2
Monocytes rest	13.1	Neutrophils rest	98.6
Monocytes LPS	16.2	Colon	5.4
Macrophages rest	4.9	Lung	4.5
Macrophages LPS	9.1	Thymus	16.2
HUVEC none	37.1	Kidney	30.8
HUVEC starved	10.8		

Panel 4.1D Summary: Ag7372 This gene is widely expressed at low levels in many samples on this panel. Highest expression of this gene is seen in CD45RA CD4 cells, naive T cells that have been activated with CD3 and CD28 (CT=32.6). Significant expression is also seen in both acutely and chronically activated T cells, resting neutrophils and NK cells. Based on the widespread expression of this gene in cells of significance to the autoimmune response, modulation of the expression or function of this gene may be useful in the treatment of autoimmune disease, including T cell mediated diseases such as asthma, arthritis, psoriasis, inflammatory bowel disease, and lupus.

C. CG137677-01 and CG137697-01: RIKEN 5730409G15-like protein.

Expression of gene CG137677-01 and CG137697-01 was assessed using the primer-probe sets Ag4928 and Ag4927, described in Tables CA and CB. Results of the RTQ-PCR runs are shown in Tables CC, CD and CE.

Table CA. Probe Name Ag4928

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tcagatgggaagtggaagct-3'	20	935	261
Probe	TET-5'- ccagaaactgtttccctacagagagca -3'-TAMRA	27	963	262
Reverse	5'-aggttcagcattgccatct-3'	19	995	263

Table CB. Probe Name Ag4927

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccccaggcatacatcttca-3'	19	571	264
Probe	TET-5'- actgtcacagccgggtcctcgag- 3'-TAMRA	23	593	265
Reverse	5'-gaggccattgagaaggacat- 3'	20	629	266

Table CC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4927, Run 224735008	Rel. Exp.(%) Ag4928, Run 224735009	Tissue Name	Rel. Exp.(%) Ag4927, Run 224735008	Rel. Exp.(%) Ag4928, Run 224735009
AD 1 Hippo	4.7	14.2	Control (Path) 3 Temporal Ctx	8.7	11.7
AD 2 Hippo	42.3	66.9	Control (Path) 4 Temporal Ctx	32.8	51.8
AD 3 Hippo	4.9	7.9	AD 1 Occipital Ctx	14.4	9.1
AD 4 Hippo	9.8	12.6	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	65.5	83.5	AD 3 Occipital Ctx	3.9	4.9
AD 6 Hippo	40.6	82.9	AD 4 Occipital Ctx	23.7	18.2
Control 2 Hippo	23.5	25.7	AD 5 Occipital Ctx	0.0	66.4
Control 4 Hippo	16.0	17.7	AD 6 Occipital Ctx	33.0	13.4
Control (Path) 3 Hippo	0.0	15.7	Control 1 Occipital Ctx	6.1	10.2
AD 1 Temporal Ctx	12.7	22.5	Control 2 Occipital Ctx	61.6	47.0
AD 2 Temporal Ctx	44.4	70.2	Control 3 Occipital Ctx	25.3	54.3
AD 3 Temporal Ctx	5.3	2.9	Control 4 Occipital Ctx	8.7	8.4

AD 4 Temporal Ctx	4.1	27.0	Control (Path) 1 Occipital Ctx	100.0	100.0
AD 5 Inf Temporal Ctx	55.9	86.5	Control (Path) 2 Occipital Ctx	4.2	18.3
AD 5 Sup Temporal Ctx	33.9	70.2	Control (Path) 3 Occipital Ctx	3.8	4.6
AD 6 Inf Temporal Ctx	38.4	40.3	Control (Path) 4 Occipital Ctx	27.5	31.9
AD 6 Sup Temporal Ctx	54.3	49.3	Control 1 Parietal Ctx	8.9	19.5
Control 1 Temporal Ctx	8.7	12.0	Control 2 Parietal Ctx	33.2	46.7
Control 2 Temporal Ctx	37.4	51.8	Control 3 Parietal Ctx	4.1	30.6
Control 3 Temporal Ctx	18.7	23.0	Control (Path) 1 Parietal Ctx	76.3	73.2
Control 4 Temporal Ctx	17.1	20.7	Control (Path) 2 Parietal Ctx	31.6	29.3
Control (Path) 1 Temporal Ctx	62.4	77.9	Control (Path) 3 Parietal Ctx	5.0	15.9
Control (Path) 2 Temporal Ctx	59.5	48.6	Control (Path) 4 Parietal Ctx	57.0	52.9

Table CD. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4927, Run 228839257	Rel. Exp.(%) Ag4928, Run 228839262	Tissue Name	Rel. Exp.(%) Ag4927, Run 228839257	Rel. Exp.(%) Ag4928, Run 228839262
Adipose	1.4	3.1	Renal ca. TK-10	35.1	41.8
Melanoma* Hs688(A).T	12.9	18.4	Bladder	13.2	10.4
Melanoma* Hs688(B).T	12.7	18.4	Gastric ca. (liver met.) NCI-N87	82.4	98.6
Melanoma* M14	33.4	34.4	Gastric ca. KATO III	100.0	68.3
Melanoma* LOXIMVI	34.9	25.2	Colon ca. SW-948	15.8	10.2
Melanoma* SK-MEL-5	37.1	68.8	Colon ca. SW480	43.8	55.5
Squamous cell carcinoma SCC-4	21.8	21.5	Colon ca.* (SW480 met) SW620	41.8	44.4
Testis Pool	9.5	6.5	Colon ca. HT29	22.8	15.8
Prostate ca.* (bone met) PC-3	11.7	26.8	Colon ca. HCT-116	54.0	47.0

Prostate Pool	4.4	4.8	Colon ca. CaCo-2	31.0	47.3
Placenta	3.2	3.8	Colon cancer tissue	9.4	7.0
Uterus Pool	2.0	4.2	Colon ca. SW1116	8.4	6.1
Ovarian ca. OVCAR-3	25.7	34.9	Colon ca. Colo-205	5.9	7.3
Ovarian ca. SK-OV-3	20.6	19.5	Colon ca. SW-48	9.2	7.5
Ovarian ca. OVCAR-4	8.1	9.9	Colon Pool	17.3	8.5
Ovarian ca. OVCAR-5	44.8	44.8	Small Intestine Pool	17.7	10.8
Ovarian ca. IGROV-1	8.8	27.0	Stomach Pool	11.8	3.7
Ovarian ca. OVCAR-8	16.0	10.2	Bone Marrow Pool	5.2	3.2
Ovary	7.5	8.0	Fetal Heart	3.1	4.1
Breast ca. MCF-7	24.7	28.9	Heart Pool	4.6	3.7
Breast ca. MDA-MB-231	14.7	20.9	Lymph Node Pool	21.2	15.5
Breast ca. BT 549	24.3	12.8	Fetal Skeletal Muscle	5.8	5.0
Breast ca. T47D	8.7	11.1	Skeletal Muscle Pool	5.3	4.4
Breast ca. MDA-N	18.0	18.6	Spleen Pool	3.8	2.7
Breast Pool	18.6	8.7	Thymus Pool	15.9	9.5
Trachea	9.4	8.0	CNS cancer (glio/astro) U87-MG	35.1	49.3
Lung	5.3	4.5	CNS cancer (glio/astro) U-118-MG	40.9	40.6
Fetal Lung	17.3	13.7	CNS cancer (neuro;met) SK-N-AS	16.7	22.4
Lung ca. NCI-N417	8.2	5.7	CNS cancer (astro) SF-539	10.7	7.1
Lung ca. LX-1	70.2	77.4	CNS cancer (astro) SNB-75	27.4	17.9
Lung ca. NCI-H146	9.7	4.3	CNS cancer (glio) SNB-19	12.0	15.7
Lung ca. SHP-77	34.2	26.6	CNS cancer (glio) SF-295	38.2	43.2
Lung ca. A549	25.5	29.7	Brain (Amygdala) Pool	8.2	3.4
Lung ca. NCI-H526	3.1	5.4	Brain (cerebellum)	22.5	16.2
Lung ca. NCI-H23	43.5	100.0	Brain (fetal)	25.5	7.9

Lung ca. NCI-H460	25.2	24.1	Brain (Hippocampus) Pool	7.7	4.4
Lung ca. HOP-62	12.7	11.8	Cerebral Cortex Pool	10.5	5.0
Lung ca. NCI-H522	51.1	48.6	Brain (Substantia nigra) Pool	9.3	4.4
Liver	1.2	1.6	Brain (Thalamus) Pool	15.0	6.7
Fetal Liver	9.5	9.9	Brain (whole)	11.2	5.1
Liver ca. HepG2	22.1	23.2	Spinal Cord Pool	11.0	5.1
Kidney Pool	25.9	13.4	Adrenal Gland	10.7	8.9
Fetal Kidney	15.7	17.6	Pituitary gland Pool	6.7	9.6
Renal ca. 786-0	12.6	14.9	Salivary Gland	3.7	4.7
Renal ca. A498	7.9	7.0	Thyroid (female)	3.4	4.8
Renal ca. ACHN	27.2	23.8	Pancreatic ca. CAPAN2	37.4	31.9
Renal ca. UO-31	21.5	20.2	Pancreas Pool	23.0	13.3

Table CE, Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4927, Run 223598856	Rel. Exp.(%) Ag4928, Run 223597247	Tissue Name	Rel. Exp.(%) Ag4927, Run 223598856	Rel. Exp.(%) Ag4928, Run 223597247
Secondary Th1 act	25.2	13.8	HUVEC IL-1beta	15.8	9.7
Secondary Th2 act	23.5	8.7	HUVEC IFN gamma	11.2	6.5
Secondary Tr1 act	12.5	8.9	HUVEC TNF alpha + IFN gamma	16.4	6.7
Secondary Th1 rest	6.6	4.2	HUVEC TNF alpha + IL4	20.9	10.8
Secondary Th2 rest	6.4	4.2	HUVEC IL-11	10.4	4.3
Secondary Tr1 rest	6.3	2.1	Lung Microvascular EC none	29.1	12.9
Primary Th1 act	31.0	18.2	Lung Microvascular EC TNFalpha + IL-1beta	27.0	13.0
Primary Th2 act	22.8	13.0	Microvascular Dermal EC none	11.2	2.5
Primary Tr1 act	29.9	15.9	Microvascular Dermal EC TNFalpha + IL-1beta	13.8	6.9
Primary Th1 rest	5.7	1.6	Bronchial epithelium TNFalpha + IL1beta	10.1	6.7

Primary Th2 rest	3.8	2.5	Small airway epithelium none	7.3	2.5
Primary Tr1 rest	7.9	6.3	Small airway epithelium TNFalpha + IL-1beta	9.9	4.8
CD45RA CD4 lymphocyte act	10.5	10.2	Coronary artery SMC rest	6.7	4.6
CD45RO CD4 lymphocyte act	0.0	17.8	Coronary artery SMC TNFalpha + IL-1beta	4.9	3.5
CD8 lymphocyte act	28.5	15.1	Astrocytes rest	11.6	5.2
Secondary CD8 lymphocyte rest	10.6	16.2	Astrocytes TNFalpha + IL-1beta	6.1	5.3
Secondary CD8 lymphocyte act	10.2	2.6	KU-812 (Basophil) rest	15.7	11.2
CD4 lymphocyte none	4.2	2.8	KU-812 (Basophil) PMA/ionomycin	18.9	16.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	5.7	4.7	CCD1106 (Keratinocytes) none	32.8	13.4
LAK cells rest	11.1	8.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	17.2	2.1
LAK cells IL-2	15.9	11.8	Liver cirrhosis	3.7	2.7
LAK cells IL-2+IL-12	14.1	11.2	NCI-H292 none	10.4	14.6
LAK cells IL-2+IFN gamma	18.4	11.9	NCI-H292 IL-4	14.9	19.6
LAK cells IL-2+ IL-18	23.0	8.4	NCI-H292 IL-9	18.2	27.2
LAK cells PMA/ionomycin	5.5	0.8	NCI-H292 IL-13	15.6	16.4
NK Cells IL-2 rest	11.7	6.1	NCI-H292 IFN gamma	26.2	17.0
Two Way MLR 3 day	13.5	7.4	HPAEC none	12.1	8.0
Two Way MLR 5 day	11.3	6.0	HPAEC TNF alpha + IL-1 beta	19.6	14.1
Two Way MLR 7 day	13.3	7.9	Lung fibroblast none	36.9	24.3
PBMC rest	2.8	1.0	Lung fibroblast TNF alpha + IL-1 beta	20.9	11.8
PBMC PWM	22.5	10.3	Lung fibroblast IL-4	37.4	17.6
PBMC PHA-L	21.2	9.0	Lung fibroblast IL-9	86.5	39.8
Ramos (B cell) none	54.7	23.8	Lung fibroblast IL-13	43.5	20.4
Ramos (B cell) ionomycin	53.2	25.9	Lung fibroblast IFN gamma	49.0	20.7
B lymphocytes PWM	24.1	17.4	Dermal fibroblast CCD1070 rest	46.3	15.2

B lymphocytes CD40L and IL-4	20.4	4.0	Dermal fibroblast CCD1070 TNF alpha	23.7	5.9
EOL-1 dbcAMP	21.8	2.9	Dermal fibroblast CCD1070 IL-1 beta	15.1	6.0
EOL-1 dbcAMP PMA/ionomycin	10.2	0.0	Dermal fibroblast IFN gamma	10.2	6.4
Dendritic cells none	7.5	4.0	Dermal fibroblast IL-4	31.4	10.7
Dendritic cells LPS	6.3	0.8	Dermal Fibroblasts rest	14.6	8.1
Dendritic cells anti- CD40	7.1	5.2	Neutrophils TNFa+LPS	10.4	1.5
Monocytes rest	3.8	4.2	Neutrophils rest	11.5	1.7
Monocytes LPS	4.7	0.1	Colon	3.5	2.5
Macrophages rest	11.7	9.9	Lung	9.9	3.7
Macrophages LPS	2.3	1.3	Thymus	11.2	18.8
HUVEC none	13.5	5.5	Kidney	100.0	100.0
HUVEC starved	11.5	8.2			

CNS_neurodegeneration_v1.0 Summary: Ag4927/Ag4928 These results confirm the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.5 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.5 Summary: Ag4927/Ag4928 Two experiments with two different probe and primer sets produce results that are in excellent agreement. Highest expression of this gene is detected in a lung cancer and a gastric cancer cell line (CTs=25-26). Moderate levels of expression of this gene is also seen in cluster of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of gastric, colon, lung, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

5 Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4.1D Summary: Ag4927/Ag4928 Highest expression of this gene is detected in kidney (CTs=28-29.5). This gene is expressed at moderate to low levels in a wide range of cell types of significance in the immune response in health and disease. These cells

10 include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement

15 with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus

20 erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

D. CG137717-01: FLJ37712 is protein-like protein.

Expression of gene CG137717-01 was assessed using the primer-probe set Ag4929, described in Table DA. Results of the RTQ-PCR runs are shown in Tables DB, DC, DD and DE.

25 Table DA. Probe Name Ag4929

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctcttcacacctgcattccta-3'	22	1003	267
Probe	TET-5'- tcctctactttaccaaagtgaatactgg a-3'-TAMRA	30	1028	268
Reverse	5'-ccatggaatgtcatcaaagag-3'	22	1059	269

Table DB. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4929, Run 305464508	Tissue Name	Rel. Exp.(%) Ag4929, Run 305464508
110967 COPD-F	57.0	112427 Match Control Psoriasis-F	35.6
110980 COPD-F	2.7	112418 Psoriasis-M	71.2
110968 COPD-M	73.7	112723 Match Control Psoriasis-M	14.8
110977 COPD-M	14.4	112419 Psoriasis-M	82.4
110989 Emphysema-F	46.3	112424 Match Control Psoriasis-M	4.5
110992 Emphysema-F	3.7	112420 Psoriasis-M	34.4
110993 Emphysema-F	28.9	112425 Match Control Psoriasis-M	34.2
110994 Emphysema-F	7.9	104689 (MF) OA Bone- Backus	23.3
110995 Emphysema-F	8.1	104690 (MF) Adj "Normal" Bone-Backus	9.0
110996 Emphysema-F	1.5	104691 (MF) OA Synovium-Backus	6.0
110997 Asthma-M	1.4	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	4.2	104694 (BA) OA Bone- Backus	5.9
111002 Asthma-F	3.9	104695 (BA) Adj "Normal" Bone-Backus	3.9
111003 Atopic Asthma- F	11.0	104696 (BA) OA Synovium-Backus	4.1
111004 Atopic Asthma- F	13.0	104700 (SS) OA Bone- Backus	16.3
111005 Atopic Asthma- F	7.5	104701 (SS) Adj "Normal" Bone-Backus	8.7
111006 Atopic Asthma- F	0.5	104702 (SS) OA Synovium-Backus	7.7
111417 Allergy-M	4.6	117093 OA Cartilage Rep7	15.4
112347 Allergy-M	0.4	112672 OA Bone5	30.6
112349 Normal Lung-F	0.3	112673 OA Synovium5	11.6
112357 Normal Lung-F	4.2	112674 OA Synovial Fluid cells5	23.3
112354 Normal Lung- M	5.4	117100 OA Cartilage Rep14	6.6
112374 Crohns-F	34.9	112756 OA Bone9	6.9
112389 Match Control Crohns-F	53.6	112757 OA Synovium9	14.4

112375 Crohns-F	33.4	112758 OA Synovial Fluid Cells9	7.8
112732 Match Control Crohns-F	40.1	117125 RA Cartilage Rep2	100.0
112725 Crohns-M	8.9	113492 Bone2 RA	10.7
112387 Match Control Crohns-M	26.6	113493 Synovium2 RA	9.1
112378 Crohns-M	1.2	113494 Syn Fluid Cells RA	7.8
112390 Match Control Crohns-M	36.1	113499 Cartilage4 RA	15.8
112726 Crohns-M	17.7	113500 Bone4 RA	24.7
112731 Match Control Crohns-M	43.8	113501 Synovium4 RA	7.0
112380 Ulcer Col-F	16.6	113502 Syn Fluid Cells4 RA	13.3
112734 Match Control Ulcer Col-F	88.3	113495 Cartilage3 RA	16.5
112384 Ulcer Col-F	54.7	113496 Bone3 RA	16.7
112737 Match Control Ulcer Col-F	7.1	113497 Synovium3 RA	8.9
112386 Ulcer Col-F	6.6	113498 Syn Fluid Cells3 RA	24.0
112738 Match Control Ulcer Col-F	3.3	117106 Normal Cartilage Rep20	5.6
112381 Ulcer Col-M	0.0	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	5.7	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	94.0	113665 Syn Fluid Cells3 Normal	0.5
112394 Match Control Ulcer Col-M	4.1	117107 Normal Cartilage Rep22	10.9
112383 Ulcer Col-M	36.6	113667 Bone4 Normal	14.8
112736 Match Control Ulcer Col-M	37.4	113668 Synovium4 Normal	12.0
112423 Psoriasis-F	26.6	113669 Syn Fluid Cells4 Normal	17.1

Table DC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4929, Run 224735010	Tissue Name	Rel. Exp.(%) Ag4929, Run 224735010
AD 1 Hippo	5.9	Control (Path) 3 Temporal Ctx	1.1

AD 2 Hippo	8.0	Control (Path) 4 Temporal Ctx	25.7
AD 3 Hippo	2.2	AD 1 Occipital Ctx	10.8
AD 4 Hippo	1.0	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	2.6
AD 6 Hippo	26.6	AD 4 Occipital Ctx	10.7
Control 2 Hippo	8.8	AD 5 Occipital Ctx	17.6
Control 4 Hippo	1.2	AD 6 Occipital Ctx	18.7
Control (Path) 3 Hippo	1.0	Control 1 Occipital Ctx	0.3
AD 1 Temporal Ctx	6.3	Control 2 Occipital Ctx	48.0
AD 2 Temporal Ctx	21.2	Control 3 Occipital Ctx	14.2
AD 3 Temporal Ctx	1.6	Control 4 Occipital Ctx	1.0
AD 4 Temporal Ctx	9.5	Control (Path) 1 Occipital Ctx	59.5
AD 5 Inf Temporal Ctx	90.1	Control (Path) 2 Occipital Ctx	9.9
AD 5 SupTemporal Ctx	27.7	Control (Path) 3 Occipital Ctx	0.4
AD 6 Inf Temporal Ctx	43.5	Control (Path) 4 Occipital Ctx	17.1
AD 6 Sup Temporal Ctx	41.8	Control 1 Parietal Ctx	1.9
Control 1 Temporal Ctx	1.5	Control 2 Parietal Ctx	33.2
Control 2 Temporal Ctx	24.0	Control 3 Parietal Ctx	17.3
Control 3 Temporal Ctx	10.4	Control (Path) 1 Parietal Ctx	42.6
Control 4 Temporal Ctx	2.3	Control (Path) 2 Parietal Ctx	16.3
Control (Path) 1 Temporal Ctx	39.8	Control (Path) 3 Parietal Ctx	0.9
Control (Path) 2 Temporal Ctx	27.7	Control (Path) 4 Parietal Ctx	31.6

Table DD. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4929, Run 228839297	Tissue Name	Rel. Exp.(%) Ag4929, Run 228839297
Adipose	0.0	Renal ca. TK-10	65.5
Melanoma* Hs688(A).T	0.0	Bladder	0.1
Melanoma* Hs688(B).T	0.1	Gastric ca. (liver met.) NCI-N87	3.3
Melanoma* M14	40.9	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	7.2

Melanoma* SK-MEL-5	0.0	Colon ca. SW480	1.8
Squamous cell carcinoma SCC-4	17.1	Colon ca.* (SW480 met) SW620	0.2
Testis Pool	1.4	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	40.9	Colon ca. HCT-116	46.7
Prostate Pool	1.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.2
Uterus Pool	0.7	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	1.7	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	88.3	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.5	Colon Pool	0.9
Ovarian ca. OVCAR-5	44.1	Small Intestine Pool	1.4
Ovarian ca. IGROV-1	3.4	Stomach Pool	1.5
Ovarian ca. OVCAR-8	9.1	Bone Marrow Pool	0.0
Ovary	3.3	Fetal Heart	0.0
Breast ca. MCF-7	0.3	Heart Pool	1.6
Breast ca. MDA-MB-231	67.8	Lymph Node Pool	3.0
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	0.2
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.6
Breast ca. MDA-N	0.2	Spleen Pool	1.1
Breast Pool	1.6	Thymus Pool	3.5
Trachea	3.5	CNS cancer (glio/astro) U87-MG	0.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	1.2
Fetal Lung	2.5	CNS cancer (neuro;met) SK-N-AS	48.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	2.1
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	5.6
Lung ca. SHP-77	6.1	CNS cancer (glio) SF-295	0.4
Lung ca. A549	32.8	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	5.3	Brain (cerebellum)	14.5
Lung ca. NCI-H23	1.3	Brain (fetal)	4.7
Lung ca. NCI-H460	21.2	Brain (Hippocampus) Pool	10.1
Lung ca. HOP-62	15.0	Cerebral Cortex Pool	0.5
Lung ca. NCI-H522	0.6	Brain (Substantia nigra) Pool	1.7
Liver	0.0	Brain (Thalamus) Pool	27.9
Fetal Liver	2.9	Brain (whole)	39.0

Liver ca. HepG2	0.0	Spinal Cord Pool	14.7
Kidney Pool	8.3	Adrenal Gland	1.7
Fetal Kidney	2.2	Pituitary gland Pool	4.0
Renal ca. 786-0	3.3	Salivary Gland	5.9
Renal ca. A498	12.0	Thyroid (female)	0.9
Renal ca. ACHN	51.1	Pancreatic ca. CAPAN2	100.0
Renal ca. UO-31	19.8	Pancreas Pool	1.6

Table DE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4929, Run 223597249	Tissue Name	Rel. Exp.(%) Ag4929, Run 223597249
Secondary Th1 act	55.1	HUVEC IL-1beta	0.0
Secondary Th2 act	22.2	HUVEC IFN gamma	0.1
Secondary Tr1 act	34.4	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	3.6	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	3.8	HUVEC IL-11	0.7
Secondary Tr1 rest	13.8	Lung Microvascular EC none	0.4
Primary Th1 act	60.3	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	40.1	Microvascular Dermal EC none	0.0
Primary Tr1 act	100.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	10.4	Bronchial epithelium TNFalpha + IL1beta	4.5
Primary Th2 rest	9.6	Small airway epithelium none	5.4
Primary Tr1 rest	42.6	Small airway epithelium TNFalpha + IL-1beta	7.2
CD45RA CD4 lymphocyte act	7.2	Coronary artery SMC rest	0.4
CD45RO CD4 lymphocyte act	5.9	Coronary artery SMC TNFalpha + IL-1beta	2.2
CD8 lymphocyte act	11.3	Astrocytes rest	3.4
Secondary CD8 lymphocyte rest	5.7	Astrocytes TNFalpha + IL- 1beta	2.6
Secondary CD8 lymphocyte act	14.7	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	2.0	KU-812 (Basophil) PMA/ionomycin	0.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	9.7	CCD1106 (Keratinocytes) none	14.1

LAK cells rest	4.1	CCD1106 (Keratinocytes) TNFalpha + IL-1 beta	6.7
LAK cells IL-2	1.0	Liver cirrhosis	0.4
LAK cells IL-2+IL-12	6.9	NCI-H292 none	3.2
LAK cells IL-2+IFN gamma	12.7	NCI-H292 IL-4	2.5
LAK cells IL-2+ IL-18	16.2	NCI-H292 IL-9	4.4
LAK cells PMA/ionomycin	0.3	NCI-H292 IL-13	2.9
NK Cells IL-2 rest	4.1	NCI-H292 IFN gamma	1.7
Two Way MLR 3 day	3.6	HPAEC none	0.0
Two Way MLR 5 day	8.1	HPAEC TNF alpha + IL-1 beta	0.2
Two Way MLR 7 day	3.4	Lung fibroblast none	0.3
PBMC rest	0.7	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.7	Lung fibroblast IL-4	0.0
PBMC PHA-L	5.8	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	16.4	Dermal fibroblast CCD1070 rest	0.2
B lymphocytes CD40L and IL-4	0.9	Dermal fibroblast CCD1070 TNF alpha	3.5
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	1.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.5
Dendritic cells none	1.4	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.4	Dermal Fibroblasts rest	0.2
Dendritic cells anti-CD40	1.0	Neutrophils TNFa+LPS	0.5
Monocytes rest	1.0	Neutrophils rest	0.9
Monocytes LPS	0.2	Colon	0.3
Macrophages rest	0.8	Lung	2.0
Macrophages LPS	0.2	Thymus	8.1
HUVEC none	0.0	Kidney	42.3
HUVEC starved	0.0		

AI_comprehensive panel_v1.0 Summary: Ag4929 Highest expression of this gene is detected in RA cartilage (CT=30.6). In addition, moderate levels of expression are seen in samples from Crohn's, ulcerative colitis, psoriasis, and COPD derived tissue. Thus, modulation of the expression or function of this gene may be useful in the treatment of these

5 conditions.

CNS_neurodegeneration_v1.0 Summary: Ag4929 This panel does not show differential expression of this gene in Alzheimer's disease. However, this profile confirms the expression of this gene at moderate levels in the brain. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurological disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

General_screening_panel_v1.5 Summary: Ag4929 Highest expression of this gene is seen in a pancreatic cancer cell line (CT=28). Expression in this panel appears to be predominantly associated with samples derived from cancer cell lines, including brain, renal, lung, breast, ovarian, prostate and melanoma cancer cell lines. Thus, expression of this gene could be used as a marker of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of cancer.

Panel 4.1D Summary: Ag4929 Expression of this gene is most prominent in T cells including both acutely and chronically activated T cells (CTs=29-30). Therefore, therapeutics designed with the protein encoded by this transcript may help to regulate T cell function and be effective in treating T cell mediated diseases such as asthma, arthritis, psoriasis, , and lupus.

E. CG137793-02: High Affinity Immunoglobulin Epsilon

Receptor Alpha-Subunit Precursor Protein-like Protein.

Expression of gene CG137793-02 was assessed using the primer-probe set Ag6866, described in Table EA.

Table EA. Probe Name Ag6866

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agaatacaaatgccatgggtt-3'	20	292	270
Probe	TET-5'- tccttataatagatcaccttgacacatcc ca-3'-TAMRA	32	320	271
Reverse	5'-ggttctcataccagtacttgaga-3'	23	361	272

F. CG137873-02: Human fibrinogen alpha chain precursor protein-likew protein

Expression of gene CG137873-02 was assessed using the primer-probe set Ag7411, described in Table FA. Results of the RTQ-PCR runs are shown in Table FB.

Table FA. Probe Name Ag7411

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-acccagactggggctca-3'	17	1196	273
Probe	TET-5'- atctggcatcttcacaaatacaaagg -3'-TAMRA	26	1215	274
Reverse	5'-atttaccacgggaaggga-3'	19	1273	275

5

Table FB. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7411, Run 305065220	Tissue Name	Rel. Exp.(%) Ag7411, Run 305065220
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0

CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

Panel 4.1D Summary: Ag7411 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 33.8). Furthermore, expression of this gene is not detected in normal liver on Panel 1.6, suggesting that its expression is unique to liver cirrhosis.

Therefore, therapeutic modulation of the expression or function of this gene may be used to diagnose this condition or to reduce or inhibit fibrosis that occurs in liver cirrhosis.

G. CG137873-03 (205101513edited2): Fibrinogen Alpha Chain

Precursor Protein-like Protein.

- 5 Expression of gene CG137873-03 (205101513edited2) was assessed using the primer-probe set Ag7412, described in Table GA. Results of the RTQ-PCR runs are shown in Tables GB and GC.

Table GA. Probe Name Ag7412

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggaagctggaagctggaagta-3'	21	970	276
Probe	TET-5'-ccaaaaccctgggagccctagacctg-3'-TAMRA	26	998	277
Reverse	5'-ctgccaggattccaggtt-3'	18	1034	278

Table GB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7412, Run 306067375	Tissue Name	Rel. Exp.(%) Ag7412, Run 306067375
Adipose	0.0	Renal ca. TK-10	3.3
Melanoma* Hs688(A).T	0.0	Bladder	1.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	6.4
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.1

Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.5	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	4.6	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	100.0	Brain (whole)	4.6
Liver ca. HepG2	6.7	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table GC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7412, Run 305065272	Tissue Name	Rel. Exp.(%) Ag7412, Run 305065272
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0

Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0

PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

General_screening_panel_v1.6 Summary: Ag7412 Highest expression of this gene is seen in fetal liver (CT=27). Thus, expression of this gene could be used to differentiate between fetal and adult liver (CT=40). Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of liver disorders.

- 5 **Panel 4.1D Summary:** Ag7412 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 28.3). Therefore, therapeutic modulation of the expression or function of this gene may be used to diagnose this condition and to reduce or inhibit fibrosis that occurs in liver cirrhosis.

H. CG137882-02: Membrane Protein FLJ212269-like Protein.

- 10 Expression of gene CG137882-02 was assessed using the primer-probe set Ag7046, described in Table HA.

Table HA. Probe Name Ag7046

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tgtgaacgtcgaagcaacc-3'	19	391	279
Probe	TET-5'- agtctcaccttccagcgacaagcttcc -3'-TAMRA	27	421	280

Reverse	5' - tgggagagatatattggaaggaat - 3'	23	461	281
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General_screening_panel_v1.6 Summary: Ag7046 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

I. CG137910-01: FLJ21432-like protein.

Expression of gene CG137910-01 was assessed using the primer-probe set Ag7448,
5 described in Table IA. Results of the RTQ-PCR runs are shown in Tables IB and IC.

Table IA. Probe Name Ag7448

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - aggagccattctctgccttt -3'	20	315	282
Probe	TET-5' - catggctcttccacacagtctactgcc -3' - TAMRA	28	341	283
Reverse	5' - cagtttagagaagagccgagaga - 3'	23	380	284

Table IB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag7448, Run 306067416	Tissue Name	Rel. Exp.(%) Ag7448, Run 306067416
AD 1 Hippo	12.5	Control (Path) 3 Temporal Ctx	5.2
AD 2 Hippo	29.1	Control (Path) 4 Temporal Ctx	12.2
AD 3 Hippo	9.9	AD 1 Occipital Ctx	14.3
AD 4 Hippo	6.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	48.3	AD 3 Occipital Ctx	16.3
AD 6 Hippo	41.2	AD 4 Occipital Ctx	17.3
Control 2 Hippo	16.4	AD 5 Occipital Ctx	11.2
Control 4 Hippo	10.4	AD 6 Occipital Ctx	25.5
Control (Path) 3 Hippo	2.9	Control 1 Occipital Ctx	5.8
AD 1 Temporal Ctx	7.3	Control 2 Occipital Ctx	30.8
AD 2 Temporal Ctx	27.5	Control 3 Occipital Ctx	11.6
AD 3 Temporal Ctx	9.5	Control 4 Occipital Ctx	11.6
AD 4 Temporal Ctx	16.2	Control (Path) 1 Occipital Ctx	47.0
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	5.1
AD 5 SupTemporal Ctx	52.9	Control (Path) 3 Occipital Ctx	9.5

AD 6 Inf Temporal Ctx	58.2	Control (Path) 4 Occipital Ctx	9.6
AD 6 Sup Temporal Ctx	36.1	Control 1 Parietal Ctx	4.1
Control 1 Temporal Ctx	5.6	Control 2 Parietal Ctx	37.9
Control 2 Temporal Ctx	32.1	Control 3 Parietal Ctx	10.2
Control 3 Temporal Ctx	8.5	Control (Path) 1 Parietal Ctx	27.9
Control 4 Temporal Ctx	7.4	Control (Path) 2 Parietal Ctx	12.8
Control (Path) 1 Temporal Ctx	20.6	Control (Path) 3 Parietal Ctx	9.8
Control (Path) 2 Temporal Ctx	16.6	Control (Path) 4 Parietal Ctx	17.2

Table IC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7448, Run 306067435	Tissue Name	Rel. Exp.(%) Ag7448, Run 306067435
Secondary Th1 act	53.2	HUVEC IL-1beta	55.1
Secondary Th2 act	81.2	HUVEC IFN gamma	50.7
Secondary Tr1 act	8.6	HUVEC TNF alpha + IFN gamma	8.2
Secondary Th1 rest	5.6	HUVEC TNF alpha + IL4	21.6
Secondary Th2 rest	6.7	HUVEC IL-11	20.3
Secondary Tr1 rest	3.8	Lung Microvascular EC none	84.1
Primary Th1 act	10.7	Lung Microvascular EC TNFalpha + IL-1beta	24.3
Primary Th2 act	51.8	Microvascular Dermal EC none	18.0
Primary Tr1 act	62.9	Microvascular Dermal EC TNFalpha + IL-1beta	11.0
Primary Th1 rest	3.7	Bronchial epithelium TNFalpha + IL1beta	26.1
Primary Th2 rest	5.0	Small airway epithelium none	29.9
Primary Tr1 rest	0.6	Small airway epithelium TNFalpha + IL-1beta	58.6
CD45RA CD4 lymphocyte act	45.7	Coronary artery SMC rest	16.0
CD45RO CD4 lymphocyte act	68.3	Coronary artery SMC TNFalpha + IL-1beta	23.8
CD8 lymphocyte act	10.4	Astrocytes rest	5.5
Secondary CD8 lymphocyte rest	12.3	Astrocytes TNFalpha + IL-1beta	4.8
Secondary CD8 lymphocyte act	12.0	KU-812 (Basophil) rest	34.2

CD4 lymphocyte none	1.0	KU-812 (Basophil) PMA/ionomycin	79.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	9.8	CCD1106 (Keratinocytes) none	16.8
LAK cells rest	18.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.9
LAK cells IL-2	18.9	Liver cirrhosis	9.4
LAK cells IL-2+IL-12	1.3	NCI-H292 none	40.3
LAK cells IL-2+IFN gamma	9.2	NCI-H292 IL-4	68.8
LAK cells IL-2+ IL-18	10.4	NCI-H292 IL-9	75.3
LAK cells PMA/ionomycin	77.9	NCI-H292 IL-13	39.5
NK Cells IL-2 rest	82.4	NCI-H292 IFN gamma	19.6
Two Way MLR 3 day	9.5	HPAEC none	7.2
Two Way MLR 5 day	5.4	HPAEC TNF alpha + IL-1 beta	58.6
Two Way MLR 7 day	10.4	Lung fibroblast none	36.3
PBMC rest	3.8	Lung fibroblast TNF alpha + IL-1 beta	23.7
PBMC PWM	20.9	Lung fibroblast IL-4	30.8
PBMC PHA-L	15.6	Lung fibroblast IL-9	55.5
Ramos (B cell) none	33.4	Lung fibroblast IL-13	7.6
Ramos (B cell) ionomycin	97.3	Lung fibroblast IFN gamma	51.4
B lymphocytes PWM	32.5	Dermal fibroblast CCD1070 rest	63.7
B lymphocytes CD40L and IL-4	45.4	Dermal fibroblast CCD1070 TNF alpha	100.0
EOL-1 dbcAMP	64.2	Dermal fibroblast CCD1070 IL-1 beta	40.9
EOL-1 dbcAMP PMA/ionomycin	13.1	Dermal fibroblast IFN gamma	24.7
Dendritic cells none	10.7	Dermal fibroblast IL-4	30.8
Dendritic cells LPS	4.9	Dermal Fibroblasts rest	23.2
Dendritic cells anti-CD40	18.2	Neutrophils TNFa+LPS	7.6
Monocytes rest	7.4	Neutrophils rest	15.4
Monocytes LPS	79.0	Colon	8.1
Macrophages rest	17.8	Lung	4.8
Macrophages LPS	13.2	Thymus	4.7
HUVEC none	27.9	Kidney	18.6
HUVEC starved	51.1		

CNS_neurodegeneration_v1.0 Summary: Ag7448 This gene appears to be upregulated in the temporal cortex of Alzheimer's disease patients when compared with

non-demented controls. Therefore, modulation of the expression or function of this gene may slow or stop the progression of Alzheimer's disease.

Panel 4.1D Summary: Ag7448 This gene is ubiquitously expressed in this panel with highest expression in TNF- α treated dermal fibroblasts (CT=29). This gene is also expressed at moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues as well as in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

J. CG138013-01: Sialic acid-binding immunoglobulin like lectin-9-like protein.

Expression of gene CG138013-01 was assessed using the primer-probe set Ag4957, described in Table JA. Results of the RTQ-PCR runs are shown in Tables JB, JC and JD.

Table JA. Probe Name Ag4957

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggggagatacttctttcgtat-3'	22	422	285
Probe	TET-5'- tggaattataaacatcacccggtctctg -3'-TAMRA	28	463	286
Reverse	5'-ggccaaggctgtcacattca-3'	20	491	287

Table JB. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4957, Run 222176655	Tissue Name	Rel. Exp.(%) Ag4957, Run 222176655
110967 COPD-F	6.1	112427 Match Control Psoriasis-F	5.7
110980 COPD-F	3.2	112418 Psoriasis-M	4.4

110968 COPD-M	6.4	112723 Match Control Psoriasis-M	2.6
110977 COPD-M	4.0	112419 Psoriasis-M	9.0
110989 Emphysema-F	4.2	112424 Match Control Psoriasis-M	4.2
110992 Emphysema-F	2.3	112420 Psoriasis-M	8.1
110993 Emphysema-F	3.8	112425 Match Control Psoriasis-M	3.5
110994 Emphysema-F	1.4	104689 (MF) OA Bone-Backus	29.3
110995 Emphysema-F	7.1	104690 (MF) Adj "Normal" Bone-Backus	11.1
110996 Emphysema-F	2.7	104691 (MF) OA Synovium-Backus	37.9
110997 Asthma-M	5.1	104692 (BA) OA Cartilage-Backus	0.9
111001 Asthma-F	6.7	104694 (BA) OA Bone-Backus	29.5
111002 Asthma-F	5.6	104695 (BA) Adj "Normal" Bone-Backus	10.4
111003 Atopic Asthma-F	1.4	104696 (BA) OA Synovium-Backus	100.0
111004 Atopic Asthma-F	4.0	104700 (SS) OA Bone-Backus	31.0
111005 Atopic Asthma-F	2.0	104701 (SS) Adj "Normal" Bone-Backus	19.2
111006 Atopic Asthma-F	0.5	104702 (SS) OA Synovium-Backus	28.3
111417 Allergy-M	4.0	117093 OA Cartilage Rep7	4.0
112347 Allergy-M	0.0	112672 OA Bone5	8.8
112349 Normal Lung-F	0.5	112673 OA Synovium5	4.5
112357 Normal Lung-F	16.7	112674 OA Synovial Fluid cells5	2.7
112354 Normal Lung-M	7.7	117100 OA Cartilage Rep14	3.1
112374 Crohns-F	7.2	112756 OA Bone9	6.0
112389 Match Control Crohns-F	5.5	112757 OA Synovium9	0.7
112375 Crohns-F	1.6	112758 OA Synovial Fluid Cells9	5.5
112732 Match Control Crohns-F	5.2	117125 RA Cartilage Rep2	5.0
112725 Crohns-M	1.1	113492 Bone2 RA	17.9
112387 Match Control Crohns-M	3.4	113493 Synovium2 RA	8.1

112378 Crohns-M	0.8	113494 Syn Fluid Cells RA	14.0
112390 Match Control Crohns-M	3.9	113499 Cartilage4 RA	17.4
112726 Crohns-M	2.2	113500 Bone4 RA	16.3
112731 Match Control Crohns-M	1.7	113501 Synovium4 RA	12.5
112380 Ulcer Col-F	1.9	113502 Syn Fluid Cells4 RA	10.7
112734 Match Control Ulcer Col-F	15.5	113495 Cartilage3 RA	24.7
112384 Ulcer Col-F	6.7	113496 Bone3 RA	23.8
112737 Match Control Ulcer Col-F	1.2	113497 Synovium3 RA	12.6
112386 Ulcer Col-F	1.1	113498 Syn Fluid Cells3 RA	26.2
112738 Match Control Ulcer Col-F	4.1	117106 Normal Cartilage Rep20	2.5
112381 Ulcer Col-M	0.0	113663 Bone3 Normal	0.7
112735 Match Control Ulcer Col-M	5.6	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	5.1	113665 Syn Fluid Cells3 Normal	0.0
112394 Match Control Ulcer Col-M	0.4	117107 Normal Cartilage Rep22	1.7
112383 Ulcer Col-M	15.1	113667 Bone4 Normal	1.8
112736 Match Control Ulcer Col-M	1.4	113668 Synovium4 Normal	1.5
112423 Psoriasis-F	4.0	113669 Syn Fluid Cells4 Normal	4.1

Table JC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4957, Run 219311035	Tissue Name	Rel. Exp.(%) Ag4957, Run 219311035
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.2
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0

Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.1
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.4	Coronary artery SMC TNFalpha + IL-1beta	0.2
CD8 lymphocyte act	0.3	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.4	Astrocytes TNFalpha + IL- 1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.5	KU-812 (Basophil) PMA/ionomycin	0.4
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	17.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.2	Liver cirrhosis	1.0
LAK cells IL-2+IL-12	0.4	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.5	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.3	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	8.5	NCI-H292 IL-13	0.1
NK Cells IL-2 rest	1.7	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	10.4	HPAEC none	0.0
Two Way MLR 5 day	3.9	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.8	Lung fibroblast none	0.0
PBMC rest	7.5	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	2.4	Lung fibroblast IL-4	0.0
PBMC PHA-L	4.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.2	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.1	Dermal fibroblast CCD1070 TNF alpha	0.1
EOL-1 dbcAMP	1.4	Dermal fibroblast CCD1070 IL-1 beta	0.0

EOL-1 dbcAMP PMA/ionomycin	5.7	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	35.6	Dermal fibroblast IL-4	0.3
Dendritic cells LPS	25.5	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	57.4	Neutrophils TNFa+LPS	3.9
Monocytes rest	51.8	Neutrophils rest	40.3
Monocytes LPS	100.0	Colon	0.1
Macrophages rest	29.1	Lung	19.9
Macrophages LPS	12.2	Thymus	0.5
HUVEC none	0.0	Kidney	0.1
HUVEC starved	0.0		

Table JD. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4957, Run 260281958	Tissue Name	Rel. Exp.(%) Ag4957, Run 260281958
Colon cancer 1	20.9	Bladder cancer NAT 2	0.0
Colon cancer NAT 1	14.6	Bladder cancer NAT 3	0.0
Colon cancer 2	34.9	Bladder cancer NAT 4	0.0
Colon cancer NAT 2	5.5	Prostate adenocarcinoma 1	13.5
Colon cancer 3	22.5	Prostate adenocarcinoma 2	1.5
Colon cancer NAT 3	4.2	Prostate adenocarcinoma 3	3.3
Colon malignant cancer 4	44.1	Prostate adenocarcinoma 4	17.1
Colon normal adjacent tissue 4	5.6	Prostate cancer NAT 5	3.0
Lung cancer 1	33.4	Prostate adenocarcinoma 6	1.4
Lung NAT 1	12.2	Prostate adenocarcinoma 7	3.0
Lung cancer 2	22.4	Prostate adenocarcinoma 8	0.0
Lung NAT 2	4.8	Prostate adenocarcinoma 9	10.4
Squamous cell carcinoma 3	43.2	Prostate cancer NAT 10	0.0
Lung NAT 3	2.9	Kidney cancer 1	73.2
metastatic melanoma 1	16.6	Kidney NAT 1	11.1
Melanoma 2	3.2	Kidney cancer 2	80.7
Melanoma 3	0.0	Kidney NAT 2	4.0
metastatic melanoma 4	70.7	Kidney cancer 3	20.0
metastatic melanoma 5	100.0	Kidney NAT 3	3.1
Bladder cancer 1	3.5	Kidney cancer 4	23.5

Bladder cancer NAT 1	0.0	Kidney NAT 4	5.0
Bladder cancer 2	4.2		

AI_comprehensive panel_v1.0 Summary: Ag4957 Highest expression of this gene is detected in orthoarthritis synovium (CT=31.5). In addition, moderate to low levels of expression of this gene is also seen in samples derived from osteoarthritic (OA) bone and adjacent bone as well as OA and normal bone, and OA synovium. Low level expression is also detected in cartilage, bone, synovium and synovial fluid samples from rheumatoid arthritis patients. This gene codes for a variant of sialic acid-binding immunoglobulin-like lectin-9 (SIGLEC-9) protein. Siglec-9 was found to be expressed at high or intermediate levels by monocytes, neutrophils, and a minor population of CD16(+), CD56(-) cells and at lower levels in B cells, NK cells and minor subsets of CD8(+) T cells and CD4(+) T cells (Zhang *et al.*, 2000, J Biol Chem 275(29):22121-6, PMID: 10801862). Similar pattern of expression of SIGLEC-9 encoded by this gene in monocytes, neutrophils and T cells, is also seen in panel 4.1D. Monocytes and T cells are known to play a role in the pathogenesis of arthritis (VanderBorghet *et al.*, 2001, Semin Arthritis Rheum 31(3):160-75, PMID: 11740797; Jenkins JK *et al.*, 2002, Am J Med Sci 323(4):171-80, PMID: 12003371). Therefore, therapeutic modulation of the SIGLEC-9 protein encoded by this gene may be useful in the treatment of osteoarthritis and rheumatoid arthritis.

Panel 4.1D Summary: Ag4957 Highest expression of this gene is detected in LPS treated monocytes (CT=28.5). In addition, moderate levels of expression of this gene is also seen in resting monocytes, dendritic cell, and macrophages. Thus, therapeutic modalities that block the function of the this gene product may be useful in the reduction or elimination of the symptoms in patients with autoimmune and inflammatory diseases in which monocytes, dendritic cells and macrophages play an important role in antigen presentation and other functions. Furthermore, moderate to low levels of expression of this gene is also seen in eosinophils, PBMC cells, two way MLR, LAK cells, stimulated neutrophils and lung. Therefore, therapeutic modulation of this gene product may be beneficial in the treatment of autoimmune and inflammatory diseases, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, or rheumatoid arthritis.

general oncology screening panel_v_2.4 Summary: Ag4957 Highest expression of this gene is detected in metastatic melanoma (CT=33.2). Moderate to low levels of

expression of this gene is also seen in malignant colon cancer, lung cancer, and kidney cancer. Expression of this gene is higher in cancer as compared to the corresponding adjacent normal tissue. Therefore, expression of this gene may be used as diagnostic marker for detection of these cancers and therapeutic modulation of this gene or its product through the use of small molecule drug or antibodies may be useful in the treatment of these cancers and also their metastasis.

K. CG138074-01: RIKEN 2310012P03-like protein.

Expression of gene CG138074-01 was assessed using the primer-probe set Ag4952, described in Table KA.

10 Table KA. Probe Name Ag4952

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tacaccaccatgctgtccat-3'	20	574	288
Probe	TET-5'- ccatatccattctgccttgacacct -3'-TAMRA	26	609	289
Reverse	5'-actcgtgtcactcatcatgtca- 3'	22	648	290

L. CG138573-01: FOLATE RECEPTOR 3-LIKE PROTEIN.

Expression of gene CG138573-01 was assessed using the primer-probe set Ag4964, described in Table LA.

15 Table LA. Probe Name Ag4964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctggatgtatccccactctaca- 3'	22	256	291
Probe	TET-5'- ttcagcctgtttcactgtggactgct -3'-TAMRA	26	280	292
Reverse	5'-tagaagcagatagcctggatga- 3'	22	329	293

General_screening_panel_v1.5 Summary: Ag4964 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Panel 4.1D Summary: Ag4964 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

**M. CG138606-01: BRUSH BORDER 61.9 KDA PROTEIN
PRECURSOR-LIKE PROTEIN.**

Expression of gene CG138606-01 was assessed using the primer-probe set Ag4970, described in Table MA. Results of the RTQ-PCR runs are shown in Tables MB and MC.

5 Table MA. Probe Name Ag4970

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttatatccctcgggaaattgac-3'	22	1248	294
Probe	TET-5'- aaacacagccatcgatcacctttg -3'-TAMRA	26	1287	295
Reverse	5'-tgtcaatgggaaatgggtctaaa-3'	22	1321	296

Table MB. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4970, Run 228926385	Tissue Name	Rel. Exp.(%) Ag4970, Run 228926385
Adipose	5.1	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	1.4	Bladder	2.9
Melanoma* Hs688(B).T	3.1	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	4.1
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	1.3
Squamous cell carcinoma SCC-4	0.7	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	21.6	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.7	Colon ca. HCT-116	1.2
Prostate Pool	2.7	Colon ca. CaCo-2	2.6
Placenta	0.0	Colon cancer tissue	3.5
Uterus Pool	3.4	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	10.7	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.6	Colon Pool	16.7
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	100.0
Ovarian ca. IGROV-1	0.5	Stomach Pool	4.9
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	6.0
Ovary	5.0	Fetal Heart	4.2
Breast ca. MCF-7	0.5	Heart Pool	3.2
Breast ca. MDA-MB-231	0.5	Lymph Node Pool	13.5

Breast ca. BT 549	5.4	Fetal Skeletal Muscle	1.8
Breast ca. T47D	0.0	Skeletal Muscle Pool	5.7
Breast ca. MDA-N	0.0	Spleen Pool	3.3
Breast Pool	9.4	Thymus Pool	8.0
Trachea	0.9	CNS cancer (glio/astro) U87-MG	0.0
Lung	4.3	CNS cancer (glio/astro) U-118-MG	2.2
Fetal Lung	5.1	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	4.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	0.5
Lung ca. SHP-77	1.1	CNS cancer (glio) SF-295	1.7
Lung ca. A549	0.0	Brain (Amygdala) Pool	1.5
Lung ca. NCI-H526	0.0	Brain (cerebellum)	1.2
Lung ca. NCI-H23	1.2	Brain (fetal)	1.3
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	2.0
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	1.9
Lung ca. NCI-H522	0.3	Brain (Substantia nigra) Pool	1.1
Liver	0.0	Brain (Thalamus) Pool	0.9
Fetal Liver	3.7	Brain (whole)	0.5
Liver ca. HepG2	0.6	Spinal Cord Pool	2.1
Kidney Pool	21.0	Adrenal Gland	0.4
Fetal Kidney	13.6	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	4.6
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	1.1	Pancreas Pool	9.5

Table MC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4970, Run 223692673	Tissue Name	Rel. Exp.(%) Ag4970, Run 223692673
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.8
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	3.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0

Secondary Tr1 rest	1.1	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.9
Primary Th2 act	0.0	Microvascular Dermal EC none	0.4
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL-1beta	2.6
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	1.1	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	0.7
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	3.2
CD4 lymphocyte none	0.8	KU-812 (Basophil) PMA/ionomycin	8.4
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	1.2
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.9
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	1.3
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	1.8
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.8
Two Way MLR 7 day	0.0	Lung fibroblast none	3.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	1.5
PBMC PWM	0.0	Lung fibroblast IL-4	0.9
PBMC PHA-L	0.0	Lung fibroblast IL-9	2.8
Ramos (B cell) none	0.0	Lung fibroblast IL-13	1.8
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.9

B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.8
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	3.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	1.7
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	2.4
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	15.6
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.9
HUVEC none	0.0	Kidney	7.0
HUVEC starved	0.7		

General_screening_panel_v1.5 Summary: Ag4970 Expression of this gene is almost exclusive to small intestine (CT=31.2). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel.

Panel 4.1D Summary: Ag4970 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 30.2). Furthermore, expression of this gene is not detected in normal liver in Panel 1.3D, suggesting that its expression is unique to liver cirrhosis. Therefore, therapeutic modulation of the expression or function of this gene may be used to diagnose this condition and to reduce or inhibit fibrosis that occurs in liver cirrhosis.

10 N. CG138751-01: CAMP INDUCIBLE 2 PROTEIN-LIKE-PROTEIN.

Expression of gene CG138751-01 was assessed using the primer-probe set Ag4971, described in Table NA. Results of the RTQ-PCR runs are shown in Tables NB, NC and ND.

Table NA. Probe Name Ag4971

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggaagcctatcagtatcgtaa-3'	22	179	297
Probe	TET-5'-cggagcagatcaaaccatcaatgat-3'-TAMRA	26	224	298
Reverse	5'-cacatgggtgtcattgagactgt-3'	22	254	299

Table NB. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4971, Run 296465693	Tissue Name	Rel. Exp.(%) Ag4971, Run 296465693
110967 COPD-F	0.8	112427 Match Control Psoriasis-F	0.1
110980 COPD-F	0.7	112418 Psoriasis-M	0.7
110968 COPD-M	1.0	112723 Match Control Psoriasis-M	0.5
110977 COPD-M	1.4	112419 Psoriasis-M	0.9
110989 Emphysema-F	0.6	112424 Match Control Psoriasis-M	0.2
110992 Emphysema-F	0.4	112420 Psoriasis-M	1.6
110993 Emphysema-F	0.9	112425 Match Control Psoriasis-M	0.0
110994 Emphysema-F	0.5	104689 (MF) OA Bone- Backus	63.3
110995 Emphysema-F	1.6	104690 (MF) Adj "Normal" Bone-Backus	10.4
110996 Emphysema-F	0.3	104691 (MF) OA Synovium-Backus	39.0
110997 Asthma-M	0.2	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	0.7	104694 (BA) OA Bone- Backus	100.0
111002 Asthma-F	1.0	104695 (BA) Adj "Normal" Bone-Backus	32.5
111003 Atopic Asthma- F	1.2	104696 (BA) OA Synovium-Backus	38.4
111004 Atopic Asthma- F	1.3	104700 (SS) OA Bone- Backus	8.9
111005 Atopic Asthma- F	0.7	104701 (SS) Adj "Normal" Bone-Backus	20.4
111006 Atopic Asthma- F	0.2	104702 (SS) OA Synovium-Backus	17.9
111417 Allergy-M	0.4	117093 OA Cartilage Rep7	1.0
112347 Allergy-M	0.0	112672 OA Bone5	0.1
112349 Normal Lung-F	0.0	112673 OA Synovium5	0.0
112357 Normal Lung-F	0.4	112674 OA Synovial Fluid cells5	0.0
112354 Normal Lung- M	0.0	117100 OA Cartilage Rep14	0.6
112374 Crohns-F	1.0	112756 OA Bone9	0.4

112389 Match Control Crohns-F	2.6	112757 OA Synovium9	0.2
112375 Crohns-F	1.0	112758 OA Synovial Fluid Cells9	0.4
112732 Match Control Crohns-F	3.2	117125 RA Cartilage Rep2	2.2
112725 Crohns-M	0.1	113492 Bone2 RA	2.2
112387 Match Control Crohns-M	0.6	113493 Synovium2 RA	0.3
112378 Crohns-M	0.0	113494 Syn Fluid Cells RA	1.5
112390 Match Control Crohns-M	0.0	113499 Cartilage4 RA	1.0
112726 Crohns-M	0.9	113500 Bone4 RA	1.2
112731 Match Control Crohns-M	0.0	113501 Synovium4 RA	0.6
112380 Ulcer Col-F	0.3	113502 Syn Fluid Cells4 RA	0.6
112734 Match Control Ulcer Col-F	6.1	113495 Cartilage3 RA	1.3
112384 Ulcer Col-F	1.1	113496 Bone3 RA	1.5
112737 Match Control Ulcer Col-F	0.2	113497 Synovium3 RA	0.9
112386 Ulcer Col-F	0.7	113498 Syn Fluid Cells3 RA	2.0
112738 Match Control Ulcer Col-F	1.1	117106 Normal Cartilage Rep20	0.5
112381 Ulcer Col-M	0.0	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	0.1	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	2.3	113665 Syn Fluid Cells3 Normal	0.0
112394 Match Control Ulcer Col-M	0.3	117107 Normal Cartilage Rep22	0.2
112383 Ulcer Col-M	1.8	113667 Bone4 Normal	0.1
112736 Match Control Ulcer Col-M	2.7	113668 Synovium4 Normal	0.2
112423 Psoriasis-F	0.4	113669 Syn Fluid Cells4 Normal	0.2

Table NC. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4971, Run 228926585	Tissue Name	Rel. Exp.(%) Ag4971, Run 228926585
Adipose	4.0	Renal ca. TK-10	1.0
Melanoma ^a Hs688(A).T	0.0	Bladder	4.9

Melanoma* Hs688(B).T	0.4	Gastric ca. (liver met.) NCI-N87	1.4
Melanoma* M14	19.2	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.1	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	67.4	Colon ca. SW480	1.8
Squamous cell carcinoma SCC-4	24.8	Colon ca.* (SW480 met) SW620	0.1
Testis Pool	0.7	Colon ca. HT29	0.1
Prostate ca.* (bone met) PC-3	6.2	Colon ca. HCT-116	2.5
Prostate Pool	0.9	Colon ca. CaCo-2	0.5
Placenta	4.2	Colon cancer tissue	9.7
Uterus Pool	0.6	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.5
Ovarian ca. SK-OV-3	1.2	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.7
Ovarian ca. OVCAR-5	3.3	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.5
Ovarian ca. OVCAR-8	0.1	Bone Marrow Pool	0.5
Ovary	0.8	Fetal Heart	0.2
Breast ca. MCF-7	0.3	Heart Pool	0.4
Breast ca. MDA-MB-231	43.5	Lymph Node Pool	0.7
Breast ca. BT 549	0.1	Fetal Skeletal Muscle	0.7
Breast ca. T47D	0.1	Skeletal Muscle Pool	0.2
Breast ca. MDA-N	0.7	Spleen Pool	13.8
Breast Pool	0.4	Thymus Pool	0.6
Trachea	9.7	CNS cancer (glio/astro) U87-MG	2.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	25.5
Fetal Lung	0.6	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.5
Lung ca. LX-1	0.1	CNS cancer (astro) SNB- 75	12.7
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB- 19	0.0
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	11.3
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.8
Lung ca. NCI-H526	0.0	Brain (cerebellum) -	1.1
Lung ca. NCI-H23	0.0	Brain (fetal)	0.7
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	0.7
Lung ca. HOP-62	2.0	Cerebral Cortex Pool	0.2

Lung ca. NCI-H522	0.3	Brain (Substantia nigra) Pool	0.8
Liver	2.2	Brain (Thalamus) Pool	0.4
Fetal Liver	3.4	Brain (whole)	1.5
Liver ca. HepG2	2.3	Spinal Cord Pool	0.4
Kidney Pool	1.7	Adrenal Gland	100.0
Fetal Kidney	0.1	Pituitary gland Pool	0.1
Renal ca. 786-0	0.3	Salivary Gland	59.0
Renal ca. A498	0.1	Thyroid (female)	0.8
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	57.8
Renal ca. UO-31	0.6	Pancreas Pool	1.0

Table ND. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4971, Run 223692675	Tissue Name	Rel. Exp.(%) Ag4971, Run 223692675
Secondary Th1 act	0.2	HUVEC IL-1beta	0.1
Secondary Th2 act	0.4	HUVEC IFN gamma	0.2
Secondary Tr1 act	0.9	HUVEC TNF alpha + IFN gamma	0.1
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.3
Secondary Th2 rest	0.7	HUVEC IL-11	0.1
Secondary Tr1 rest	0.2	Lung Microvascular EC none	0.0
Primary Th1 act	0.1	Lung Microvascular EC TNFalpha + IL-1beta	2.2
Primary Th2 act	0.4	Microvascular Dermal EC none	0.4
Primary Tr1 act	0.1	Microvascular Dermal EC TNFalpha + IL-1beta	0.9
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	4.8
Primary Th2 rest	0.0	Small airway epithelium none	5.4
Primary Tr1 rest	0.1	Small airway epithelium TNFalpha + IL-1beta	3.9
CD45RA CD4 lymphocyte act	0.1	Coronary artery SMC rest	0.2
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.2
CD8 lymphocyte act	0.2	Astrocytes rest	0.1
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.1
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.1
CD4 lymphocyte none	0.1	KU-812 (Basophil) PMA/ionomycin	3.0

2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	CCD1106 (Keratinocytes) none	39.5
LAK cells rest	45.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	28.5
LAK cells IL-2	0.1	Liver cirrhosis	0.4
LAK cells IL-2+IL-12	0.4	NCI-H292 none	15.4
LAK cells IL-2+IFN gamma	0.4	NCI-H292 IL-4	10.3
LAK cells IL-2+ IL-18	0.2	NCI-H292 IL-9	21.8
LAK cells PMA/ionomycin	17.8	NCI-H292 IL-13	8.1
NK Cells IL-2 rest	0.1	NCI-H292 IFN gamma	17.7
Two Way MLR 3 day	4.6	HPAEC none	0.1
Two Way MLR 5 day	1.7	HPAEC TNF alpha + IL-1 beta	0.4
Two Way MLR 7 day	0.4	Lung fibroblast none	0.2
PBMC rest	3.1	Lung fibroblast TNF alpha + IL-1 beta	0.2
PBMC PWM	0.1	Lung fibroblast IL-4	0.1
PBMC PHA-L	0.3	Lung fibroblast IL-9	0.3
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.5
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.1
B lymphocytes PWM	0.2	Dermal fibroblast CCD1070 rest	0.2
B lymphocytes CD40L and IL-4	0.6	Dermal fibroblast CCD1070 TNF alpha	0.9
EOL-1 dbcAMP	2.6	Dermal fibroblast CCD1070 IL-1 beta	0.3
EOL-1 dbcAMP PMA/ionomycin	1.9	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	59.9	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	21.9	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	100.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	32.3	Neutrophils rest	0.7
Monocytes LPS	5.9	Colon	1.5
Macrophages rest	30.6	Lung	7.3
Macrophages LPS	8.7	Thymus	1.0
HUVEC none	0.3	Kidney	0.1
HUVEC starved	0.7		

AI_comprehensive panel_v1.0 Summary: Ag4971 Highest expression of this gene is detected in orthoarthritis (OA) bone (CT=26.7). High to moderate levels of expression of this gene is also seen in OA and adjacent normal bone and OA synovium. In addition, moderate to low levels of expression of this gene is also seen in bone, cartilage,

synovium and synovial fluid samples derived from rheumatoid arthritis patient, OA cartilage, as well as, in samples derived from COPD lung, emphysema, atopic asthma, asthma, allergy, Crohn's disease (normal matched control and diseased), ulcerative colitis (normal matched control and diseased), and psoriasis (normal matched control and diseased).

- 5 Therefore, therapeutic modulation of this gene product may ameliorate symptoms/conditions associated with autoimmune and inflammatory disorders including psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

General_screening_panel_v1.5 Summary: Ag4971 Highest expression of this
10 gene is detected in adrenal gland (CT=27.8). Moderate to low levels of expression of this gene is also seen in tissues with metabolic/endocrine function such as pancreas, adipose, thyroid, and liver. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

15 Moderate levels of expression of this gene is also seen in number of cancer cell lines derived from melanoma, pancreatic, brain, colon, breast and prostate cancers. Therefore, expression of this gene may be used as diagnostic marker to detect the presence of these cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of these cancers.

20 In addition, low levels of expression of this gene is also seen in whole and fetal brain, amygdala, cerebellum and substantia nigra. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

25 **Panel 4.1D Summary:** Ag4971 Highest expression of this gene is detected in anti-CD40 treated dendritic cells (CT=29). Moderate levels of expression of this gene is detected in dendritic cells, monocytes, macrophages, LAK cells, keratinocytes and mucoepidermoid NCI-H292 cells. Moderate to low levels of expression of this gene is also seen in
30 PMA/ionomycin activated LAK cells, two way MLR, PBMC, eosinophils, small airway epithelium, TNFalpha + IL-1beta activated bronchial epithelium and microvascular dermal epithelium and lung. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead

to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

A. CG139363-01 and CG139363-02: Transmembrane protein

5 HTMPI0-like protein.

Expression of gene CG139363-01 and CG139363-02 was assessed using the primer-probe set Ag4978, described in Table OA. Results of the RTQ-PCR runs are shown in Tables OB, OC and OD. Note that CG139363-02 represents a full-length physical clone.

Table OA. Probe Name Ag4978

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccctctcttggattagc-3'	19	134	300
Probe	TET-5'- cacagccctgctggtggctttactat -3'-TAMRA	26	177	301
Reverse	5'-cttcttcttcggtgaatcaaag-3'	22	206	302

10 Table OB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4978, Run 224757409	Tissue Name	Rel. Exp.(%) Ag4978, Run 224757409
AD 1 Hippo	4.1	Control (Path) 3 Temporal Ctx	4.4
AD 2 Hippo	8.7	Control (Path) 4 Temporal Ctx	20.4
AD 3 Hippo	2.6	AD 1 Occipital Ctx	6.2
AD 4 Hippo	9.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	11.3	AD 3 Occipital Ctx	1.8
AD 6 Hippo	29.9	AD 4 Occipital Ctx	24.7
Control 2 Hippo	43.8	AD 5 Occipital Ctx	40.3
Control 4 Hippo	11.3	AD 6 Occipital Ctx	23.7
Control (Path) 3 Hippo	4.9	Control 1 Occipital Ctx	4.4
AD 1 Temporal Ctx	7.2	Control 2 Occipital Ctx	43.8
AD 2 Temporal Ctx	23.2	Control 3 Occipital Ctx	20.0
AD 3 Temporal Ctx	2.5	Control 4 Occipital Ctx	9.0
AD 4 Temporal Ctx	33.0	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	40.3	Control (Path) 2 Occipital Ctx	15.8

AD 5 Sup Temporal Ctx	17.3	Control (Path) 3 Occipital Ctx	4.4
AD 6 Inf Temporal Ctx	44.4	Control (Path) 4 Occipital Ctx	13.3
AD 6 Sup Temporal Ctx	34.9	Control 1 Parietal Ctx	7.7
Control 1 Temporal Ctx	5.1	Control 2 Parietal Ctx	23.7
Control 2 Temporal Ctx	41.8	Control 3 Parietal Ctx	19.3
Control 3 Temporal Ctx	23.3	Control (Path) 1 Parietal Ctx	57.8
Control 3 Temporal Ctx	12.8	Control (Path) 2 Parietal Ctx	20.4
Control (Path) 1 Temporal Ctx	49.7	Control (Path) 3 Parietal Ctx	4.1
Control (Path) 2 Temporal Ctx	31.4	Control (Path) 4 Parietal Ctx	25.9

Table OC. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4978, Run 228940920	Tissue Name	Rel. Exp.(%) Ag4978, Run 228940920
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0

Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	2.8
Trachea	0.1	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	62.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	25.9
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	51.8
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	66.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	48.6
Liver	0.0	Brain (Thalamus) Pool	100.0
Fetal Liver	0.0	Brain (whole)	64.6
Liver ca. HepG2	0.0	Spinal Cord Pool	24.3
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table OD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4978, Run 223693384	Tissue Name	Rel. Exp.(%) Ag4978, Run 223693384
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0

Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.6
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	1.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.7
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.5
Two Way MLR 3 day	0.0	HPAEC none	0.6
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0

B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.5
Macrophages LPS	0.0	Thymus	100.0
HUVEC none	0.0	Kidney	0.6
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag4978 This panel does not show differential expression of this gene in Alzheimer's disease. However, this profile confirms the expression of this gene at moderate levels in the brain. See Panel 1.5 for discussion of this gene in the central nervous system.

- 5 **General_screening_panel_v1.5 Summary:** Ag4978 Highest expression of this gene is seen in the thalamus (CT=26.7). Overall, expression of this gene appears to be highly associated with the brain. High levels of expression are seen in all regions of the CNS examined, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or
- 10 function of this gene may be useful in the treatment of neurological disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

- 15 **Panel 4.1D Summary:** Ag4978 This transcript is expressed at significant levels only in the thymus (CT = 30.2). The putative protein encoded by this gene could therefore play an important role in T cell development. Therapeutic modulation of the expression or function of this gene may modulate immune function (T cell development) and be important for organ transplant, AIDS treatment or post chemotherapy immune reconstitution.

P. CG140188-01: DC2-Like Protein.

Expression of gene CG140188-01 was assessed using the primer-probe set Ag7417, described in Table PA. Results of the RTQ-PCR runs are shown in Table PB.

Table PA. Probe Name Ag7417

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - cattggctctatgactgatgaac- 3'	23	194	303
Probe	TET-5' - ccaagaaagctactggcctctgat- 3' -TAMRA	24	223	304
Reverse	5' - ggatgcaagtccctccataata-3'	22	269	305

Table PB. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7417, Run 305065593	Tissue Name	Rel. Exp.(%) Ag7417, Run 305065593
Secondary Th1 act	21.0	HUVEC IL-1 beta	48.0
Secondary Th2 act	29.5	HUVEC IFN gamma	37.9
Secondary Tr1 act	14.6	HUVEC TNF alpha + IFN gamma	18.8
Secondary Th1 rest	1.2	HUVEC TNF alpha + IL4	24.8
Secondary Th2 rest	3.6	HUVEC IL-11	22.2
Secondary Tr1 rest	4.2	Lung Microvascular EC none	100.0
Primary Th1 act	3.4	Lung Microvascular EC TNFalpha + IL-1 beta	41.8
Primary Th2 act	24.0	Microvascular Dermal EC none	9.5
Primary Tr1 act	20.6	Microvascular Dermal EC TNFalpha + IL-1 beta	18.7
Primary Th1 rest	1.4	Bronchial epithelium TNFalpha + IL1 beta	22.4
Primary Th2 rest	2.5	Small airway epithelium none	9.2
Primary Tr1 rest	1.2	Small airway epithelium TNFalpha + IL-1 beta	14.9
CD45RA CD4 lymphocyte act	22.8	Coronary artery SMC rest	49.0
CD45RO CD4 lymphocyte act	21.3	Coronary artery SMC TNFalpha + IL-1 beta	45.1
CD8 lymphocyte act	13.8	Astrocytes rest	10.7
Secondary CD8 lymphocyte rest	2.2	Astrocytes TNFalpha + IL- 1 beta	24.3
Secondary CD8 lymphocyte act	6.3	KU-812 (Basophil) rest	22.8

CD4 lymphocyte none	1.6	KU-812 (Basophil) PMA/ionomycin	31.4
2ry Th1/Th2/Tr1_anti- CD95 CH11	3.2	CCD1106 (Keratinocytes) none	23.8
LAK cells rest	6.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	10.7
LAK cells IL-2	4.2	Liver cirrhosis	11.3
LAK cells IL-2+IL-12	1.4	NCI-H292 none	25.2
LAK cells IL-2+IFN gamma	5.8	NCI-H292 IL-4	17.3
LAK cells IL-2+ IL-18	2.6	NCI-H292 IL-9	33.2
LAK cells PMA/ionomycin	9.5	NCI-H292 IL-13	20.6
NK Cells IL-2 rest	20.9	NCI-H292 IFN gamma	6.8
Two Way MLR 3 day	4.8	HPAEC none	15.2
Two Way MLR 5 day	2.5	HPAEC TNF alpha + IL-1 beta	54.3
Two Way MLR 7 day	4.3	Lung fibroblast none	22.2
PBMC rest	1.5	Lung fibroblast TNF alpha + IL-1 beta	21.0
PBMC PWM	5.1	Lung fibroblast IL-4	27.5
PBMC PHA-L	3.6	Lung fibroblast IL-9	30.1
Ramos (B cell) none	36.3	Lung fibroblast IL-13	15.2
Ramos (B cell) ionomycin	59.0	Lung fibroblast IFN gamma	38.4
B lymphocytes PWM	3.9	Dermal fibroblast CCD1070 rest	40.1
B lymphocytes CD40L and IL-4	10.4	Dermal fibroblast CCD1070 TNF alpha	49.7
EOL-1 dbcAMP	26.6	Dermal fibroblast CCD1070 IL-1 beta	31.9
EOL-1 dbcAMP PMA/ionomycin	14.1	Dermal fibroblast IFN gamma	17.0
Dendritic cells none	10.2	Dermal fibroblast IL-4	28.7
Dendritic cells LPS	5.1	Dermal Fibroblasts rest	8.4
Dendritic cells anti-CD40	3.5	Neutrophils TNFa+LPS	0.0
Monocytes rest	5.4	Neutrophils rest	1.2
Monocytes LPS	22.7	Colon	0.7
Macrophages rest	5.6	Lung	1.4
Macrophages LPS	3.7	Thymus	4.1
HUVEC none	43.8	Kidney	6.0
HUVEC starved	38.2		

CNS_neurodegeneration_v1.0 Summary: Ag7417 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Panel 4.1D Summary: Ag7417 Highest expression of this gene is seen in untreated lung microvascular endothelial cells (CT=30.8). This gene is also expressed at moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, endothelial cell, basophil, astrocyte, monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues as well as in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

**Q. CG140305-01: COMPLEMENT-c1q TUMOR NECROSIS
FACTOR-RELATED PROTEIN-LIKE PROTEIN.**

Expression of gene CG140305-01 was assessed using the primer-probe set Ag6486, described in Table QA. Results of the RTQ-PCR runs are shown in Tables QB, QC and QD.

Table QA. Probe Name Ag6486

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tgctggatgtatctgatttgc-3'	21	581	306
Probe	TET-5'-caacacagtcttccagcatgtacagct-3'-TAMRA	26	543	307
Reverse	5'-gtatgtgtaccttatgcacaatgg-3'	24	519	308

Table QB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6486, Run 277240051	Tissue Name	Rel. Exp.(%) Ag6486, Run 277240051
Adipose	13.9	Renal ca. TK-10	12.4
Melanoma* Hs688(A).T	35.4	Bladder	14.7
Melanoma* Hs688(B).T	55.9	Gastric ca. (liver met.) NCI-N87	10.8
Melanoma* M14	1.4	Gastric ca. KATO III	0.3
Melanoma* LOXIMVI	1.3	Colon ca. SW-948	0.4
Melanoma* SK-MEL-5	2.0	Colon ca. SW480	0.6

Squamous cell carcinoma SCC-4	1.7	Colon ca.* (SW480 met) SW620	4.4
Testis Pool	30.8	Colon ca. HT29	2.6
Prostate ca.* (bone met) PC-3	2.8	Colon ca. HCT-116	4.9
Prostate Pool	15.2	Colon ca. CaCo-2	9.0
Placenta	2.6	Colon cancer tissue	33.7
Uterus Pool	3.8	Colon ca. SW1116	1.7
Ovarian ca. OVCAR-3	4.4	Colon ca. Colo-205	2.0
Ovarian ca. SK-OV-3	14.0	Colon ca. SW-48	1.0
Ovarian ca. OVCAR-4	1.0	Colon Pool	9.1
Ovarian ca. OVCAR-5	9.1	Small Intestine Pool	22.8
Ovarian ca. IGROV-1	4.6	Stomach Pool	15.5
Ovarian ca. OVCAR-8	1.2	Bone Marrow Pool	4.6
Ovary	3.1	Fetal Heart	10.5
Breast ca. MCF-7	7.2	Heart Pool	3.9
Breast ca. MDA-MB-231	5.0	Lymph Node Pool	5.8
Breast ca. BT 549	4.2	Fetal Skeletal Muscle	39.5
Breast ca. T47D	0.5	Skeletal Muscle Pool	1.8
Breast ca. MDA-N	1.1	Spleen Pool	4.4
Breast Pool	11.0	Thymus Pool	14.3
Trachea	26.8	CNS cancer (glio/astro) U87-MG	2.2
Lung	4.7	CNS cancer (glio/astro) U-118-MG	4.5
Fetal Lung	34.9	CNS cancer (neuro;met) SK-N-AS	3.8
Lung ca. NCI-N417	0.3	CNS cancer (astro) SF-539	2.2
Lung ca. LX-1	6.8	CNS cancer (astro) SNB-75	8.8
Lung ca. NCI-H146	12.9	CNS cancer (glio) SNB-19	3.7
Lung ca. SHP-77	19.8	CNS cancer (glio) SF-295	7.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	9.1
Lung ca. NCI-H526	2.5	Brain (cerebellum)	100.0
Lung ca. NCI-H23	9.4	Brain (fetal)	20.2
Lung ca. NCI-H460	1.0	Brain (Hippocampus) Pool	13.5
Lung ca. HOP-62	4.9	Cerebral Cortex Pool	10.8
Lung ca. NCI-H522	1.2	Brain (Substantia nigra) Pool	7.4
Liver	0.4	Brain (Thalamus) Pool	14.7
Fetal Liver	5.7	Brain (whole)	8.0
Liver ca. HepG2	5.2	Spinal Cord Pool	24.8

Kidney Pool	20.2	Adrenal Gland	3.2
Fetal Kidney	65.1	Pituitary gland Pool	2.2
Renal ca. 786-0	10.4	Salivary Gland	18.7
Renal ca. A498	2.1	Thyroid (female)	2.1
Renal ca. ACHN	2.2	Pancreatic ca. CAPAN2	5.6
Renal ca. UO-31	1.2	Pancreas Pool	3.3

Table QC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6486, Run 269282929	Tissue Name	Rel. Exp.(%) Ag6486, Run 269282929
Secondary Th1 act	15.8	HUVEC IL-1beta	9.7
Secondary Th2 act	27.9	HUVEC IFN gamma	8.8
Secondary Tr1 act	17.0	HUVEC TNF alpha + IFN gamma	7.5
Secondary Th1 rest	9.5	HUVEC TNF alpha + IL4	5.3
Secondary Th2 rest	9.4	HUVEC IL-11	8.5
Secondary Tr1 rest	8.8	Lung Microvascular EC none	92.0
Primary Th1 act	3.8	Lung Microvascular EC TNFalpha + IL-1beta	5.8
Primary Th2 act	38.2	Microvascular Dermal EC none	9.4
Primary Tr1 act	31.0	Microvascular Dermal EC TNFalpha + IL-1beta	8.5
Primary Th1 rest	9.5	Bronchial epithelium TNFalpha + IL1beta	5.4
Primary Th2 rest	13.2	Small airway epithelium none	0.0
Primary Tr1 rest	1.4	Small airway epithelium TNFalpha + IL-1beta	6.4
CD45RA CD4 lymphocyte act	34.6	Coronary artery SMC rest	3.9
CD45RO CD4 lymphocyte act	40.3	Coronary artery SMC TNFalpha + IL-1beta	5.4
CD8 lymphocyte act	21.9	Astrocytes rest	8.0
Secondary CD8 lymphocyte rest	6.9	Astrocytes TNFalpha + IL- 1beta	0.0
Secondary CD8 lymphocyte act	5.2	KU-812 (Basophil) rest	52.1
CD4 lymphocyte none	13.5	KU-812 (Basophil) PMA/ionomycin	33.2
2ry Th1/Th2/Tr1 _anti- CD95 CH11	24.1	CCD1106 (Keratinocytes) none	8.0
LAK cells rest	8.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	5.7
LAK cells IL-2	10.4	Liver cirrhosis	20.7
LAK cells IL-2+IL-12	1.9	NCI-H292 none	34.6

LAK cells IL-2+IFN gamma	14.3	NCI-H292 IL-4	24.3
LAK cells IL-2+ IL-18	21.0	NCI-H292 IL-9	34.4
LAK cells PMA/ionomycin	7.0	NCI-H292 IL-13	29.9
NK Cells IL-2 rest	70.2	NCI-H292 IFN gamma	17.2
Two Way MLR 3 day	23.2	HPAEC none	7.0
Two Way MLR 5 day	2.0	HPAEC TNF alpha + IL-1 beta	8.0
Two Way MLR 7 day	6.9	Lung fibroblast none	5.0
PBMC rest	1.6	Lung fibroblast TNF alpha + IL-1 beta	9.6
PBMC PWM	7.2	Lung fibroblast IL-4	0.0
PBMC PHA-L	15.2	Lung fibroblast IL-9	5.3
Ramos (B cell) none	9.7	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	17.2	Lung fibroblast IFN gamma	14.1
B lymphocytes PWM	6.8	Dermal fibroblast CCD1070 rest	12.9
B lymphocytes CD40L and IL-4	56.6	Dermal fibroblast CCD1070 TNF alpha	100.0
EOL-1 dbcAMP	50.0	Dermal fibroblast CCD1070 IL-1 beta	8.0
EOL-1 dbcAMP PMA/ionomycin	8.1	Dermal fibroblast IFN gamma	9.2
Dendritic cells none	13.2	Dermal fibroblast IL-4	28.1
Dendritic cells LPS	3.1	Dermal Fibroblasts rest	7.9
Dendritic cells anti-CD40	3.6	Neutrophils TNFa+LPS	2.9
Monocytes rest	0.0	Neutrophils rest	6.2
Monocytes LPS	7.7	Colon	46.0
Macrophages rest	2.4	Lung	9.0
Macrophages LPS	0.0	Thymus	51.4
HUVEC none	1.7	Kidney	78.5
HUVEC starved	22.7		

Table QD. Panel CNS_1.1

Tissue Name	Rel. Exp.(%) Ag6486, Run 271481506	Tissue Name	Rel. Exp.(%) Ag6486, Run 271481506
Cing Gyr Depression2	26.8	BA17 PSP2	5.6
Cing Gyr Depression	13.8	BA17 PSP	11.3
Cing Gyr PSP2	4.8	BA17 Huntington's2	17.2
Cing Gyr PSP	52.9	BA17 Huntington's	20.0
Cing Gyr Huntington's2	33.2	BA17 Parkinson's2	26.4
Cing Gyr Huntington's	53.2	BA17 Parkinson's	31.4

Cing Gyr Parkinson's2	0.0	BA17 Alzheimer's2	7.5
Cing Gyr Parkinson's	53.6	BA17 Control2	12.6
Cing Gyr Alzheimer's2	14.6	BA17 Control	19.8
Cing Gyr Alzheimer's	23.5	BA9 Depression2	4.9
Cing Gyr Control2	16.6	BA9 Depression	0.4
Cing Gyr Control	52.9	BA9 PSP2	6.0
Temp Pole Depression2	15.6	BA9 PSP	15.6
Temp Pole PSP2	0.0	BA9 Huntington's2	28.3
Temp Pole PSP	2.1	BA9 Huntington's	36.3
Temp Pole Huntington's	28.3	BA9 Parkinson's2	26.4
Temp Pole Parkinson's2	31.4	BA9 Parkinson's	32.8
Temp Pole Parkinson's	16.2	BA9 Alzheimer's2	4.6
Temp Pole Alzheimer's2	5.9	BA9 Alzheimer's	1.8
Temp Pole Alzheimer's	4.7	BA9 Control2	59.9
Temp Pole Control2	33.9	BA9 Control	14.3
Temp Pole Control	4.0	BA7 Depression	17.4
Glob Palladus Depression	12.1	BA7 PSP2	12.1
Glob Palladus PSP2	7.0	BA7 PSP	14.5
Glob Palladus PSP	14.7	BA7 Huntington's2	76.8
Glob Palladus Parkinson's2	30.4	BA7 Huntington's	26.1
Glob Palladus Parkinson's	73.2	BA7 Parkinson's2	17.4
Glob Palladus Alzheimer's2	7.4	BA7 Parkinson's	19.3
Glob Palladus Alzheimer's	9.1	BA7 Alzheimer's2	2.8
Glob Palladus Control2	6.7	BA7 Control2	14.4
Glob Palladus Control	19.5	BA7 Control	9.9
Sub Nigra Depression2	9.3	BA4 Depression2	6.7
Sub Nigra Depression	4.5	BA4 Depression	13.5
Sub Nigra PSP2	17.4	BA4 PSP2	10.2
Sub Nigra Huntington's2	46.0	BA4 PSP	7.5
Sub Nigra Huntington's	63.7	BA4 Huntington's2	13.5
Sub Nigra Parkinson's2	76.3	BA4 Huntington's	14.5
Sub Nigra Alzheimer's2	27.4	BA4 Parkinson's2	34.2
Sub Nigra Control2	36.9	BA4 Parkinson's	39.2
Sub Nigra Control	100.0	BA4 Alzheimer's2	2.3

BA17 Depression2	25.3	BA4 Control2	22.5
BA17 Depression	19.2	BA4 Control	15.0

General_screening_panel_v1.6 Summary: Ag6486 Highest expression of this gene is detected in brain cerebellum (CT=27.8). In addition, moderate levels of expression of this gene is also seen in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Moderate levels of expression of this gene is also seen in cluster of cancer cell lines derived from pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, fetal liver and the gastrointestinal tract. This gene encodes a splice variant of the complement C1q tumor necrosis factor-related protein, a member of the C1q family. This family includes proteins such as complement subunit C1q, adiponectin, gliacolin, C1q-related protein, cerebellin, CORS26 etc., all of which are secreted. These proteins have been implicated in tissue differentiation, immune regulation, energy homeostasis, synaptic function and in diseases such as obesity, diabetes and neurodegeneration. Adiponectin, a member of C1q family and protein closely related to complement C1q tumor necrosis factor-related protein, is induced over 100-fold in adipocyte differentiation (Scherer *et al.*, 1995, J Biol Chem 270(45):26746-9 PMID: 7592907) and is involved in adipocyte signaling (Hu *et al.*, 1996, J Biol Chem 271(18):10697-703 PMID: 8631877). Recently, adiponectin has been shown to reverse insulin resistance in mouse models of lipotrophy and obesity (Yamauchi *et al.*, 2001, Nat Med 7(8):941-6 PMID: 11479627). Therefore this protein, and proteins related to it, are potential antigens for development protein therapeutics for use in the treatment of obesity and type II diabetes.

This gene is expressed at much higher levels in fetal (CTs=29-32) when compared to adult skeletal muscle, lung and liver (CTs=32-35.9). This observation suggests that expression of this gene can be used to distinguish fetal from adult skeletal muscle, lung and liver. In addition, the relative overexpression of this gene in fetal tissue suggests that the protein product may enhance growth or development of these tissues in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the protein encoded by this gene could be useful in treatment of muscle, lung and liver related diseases.

Panel 4.1D Summary: Ag6486 Highest expression of this gene is detected in TNF alpha treated dermal fibroblast (CT=32.4). In addition, moderate to low levels of expression of this gene is also seen in activated T cells, IL-2 treated NK Cells, CD40L and IL-4 treated B lymphocytes, eosinophils, lung microvascular endothelial cells, basophils, NCI-H292 mucoepidermoid cells, and normal tissues represented by colon, thymus and kidney. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of protein therapeutics or antibodies, might be beneficial in the treatment of autoimmune and inflammatory diseases that involve these cell and tissue types, such as lupus erythematosus, asthma, emphysema, Crohn's disease, ulcerative colitis, rheumatoid arthritis, osteoarthritis, and psoriasis.

Panel CNS_1.1 Summary: Ag6486 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. See Panel 1.6 for a discussion of this gene in treatment of central nervous system disorders.

R. CG140639-01 and CG140639-02: Flotillin-2 (Reggie-1) (REG-1)-like protein.

Expression of gene CG140639-01 and CG140639-02 was assessed using the primer-probe set Ag5036, described in Table RA. Results of the RTQ-PCR runs are shown in Tables RB and RC. Note that CG140639-02 represents a full-length physical clone.

Table RA. Probe Name Ag5036

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gggtaagaatgtgcaggacat-3'	21	349	309
Probe	TET-5'- aaaacgtcgtcctgcagaccctg-3'-TAMRA	23	372	310

Reverse	5' - tgataaatctgctccactgtca-3'	22	426	311
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Table RB. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5036, Run 228967203	Tissue Name	Rel. Exp.(%) Ag5036, Run 228967203
Adipose	10.4	Renal ca. TK-10	44.4
Melanoma* Hs688(A).T	23.0	Bladder	33.4
Melanoma* Hs688(B).T	18.4	Gastric ca. (liver met.) NCI-N87	25.9
Melanoma* M14	45.4	Gastric ca. KATO III	41.5
Melanoma* LOXIMV1	13.9	Colon ca. SW-948	14.5
Melanoma* SK-MEL-5	23.2	Colon ca. SW480	61.6
Squamous cell carcinoma SCC-4	6.1	Colon ca.* (SW480 met) SW620	47.3
Testis Pool	6.3	Colon ca. HT29	37.1
Prostate ca.* (bone met) PC-3	15.4	Colon ca. HCT-116	39.5
Prostate Pool	17.2	Colon ca. CaCo-2	68.3
Placenta	33.7	Colon cancer tissue	20.3
Uterus Pool	11.0	Colon ca. SW1116	8.9
Ovarian ca. OVCAR-3	57.0	Colon ca. Colo-205	12.1
Ovarian ca. SK-OV-3	100.0	Colon ca. SW-48	11.7
Ovarian ca. OVCAR-4	27.5	Colon Pool	15.3
Ovarian ca. OVCAR-5	39.8	Small Intestine Pool	11.3
Ovarian ca. IGROV-1	44.4	Stomach Pool	8.2
Ovarian ca. OVCAR-8	26.1	Bone Marrow Pool	4.8
Ovary	9.3	Fetal Heart	16.4
Breast ca. MCF-7	24.8	Heart Pool	9.9
Breast ca. MDA-MB-231	89.5	Lymph Node Pool	12.7
Breast ca. BT 549	47.6	Fetal Skeletal Muscle	11.0
Breast ca. T47D	16.2	Skeletal Muscle Pool	22.2
Breast ca. MDA-N	11.7	Spleen Pool	14.6
Breast Pool	10.7	Thymus Pool	10.9
Trachea	22.7	CNS cancer (glio/astro) U87-MG	39.8
Lung	2.2	CNS cancer (glio/astro) U-118-MG	23.0
Fetal Lung	29.9	CNS cancer (neuro;met) SK-N-AS	19.6
Lung ca. NCI-N417	6.6	CNS cancer (astro) SF- 539	13.9

Lung ca. LX-1	68.8	CNS cancer (astro) SNB-75	34.4
Lung ca. NCI-H146	13.4	CNS cancer (glio) SNB-19	43.8
Lung ca. SHP-77	41.2	CNS cancer (glio) SF-295	48.0
Lung ca. A549	52.1	Brain (Amygdala) Pool	18.2
Lung ca. NCI-H526	23.7	Brain (cerebellum)	47.0
Lung ca. NCI-H23	44.1	Brain (fetal)	27.5
Lung ca. NCI-H460	29.1	Brain (Hippocampus) Pool	15.8
Lung ca. HOP-62	43.8	Cerebral Cortex Pool	23.5
Lung ca. NCI-H522	36.9	Brain (Substantia nigra) Pool	18.6
Liver	5.8	Brain (Thalamus) Pool	22.8
Fetal Liver	47.6	Brain (whole)	23.2
Liver ca. HepG2	15.3	Spinal Cord Pool	11.7
Kidney Pool	20.9	Adrenal Gland	13.8
Fetal Kidney	8.7	Pituitary gland Pool	2.7
Renal ca. 786-0	21.9	Salivary Gland	14.1
Renal ca. A498	19.1	Thyroid (female)	11.3
Renal ca. ACHN	50.0	Pancreatic ca. CAPAN2	21.8
Renal ca. UO-31	39.2	Pancreas Pool	18.2

Table RC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag5036, Run 223740995	Tissue Name	Rel. Exp.(%) Ag5036, Run 223740995
Secondary Th1 act	42.9	HUVEC IL-1beta	27.2
Secondary Th2 act	54.3	HUVEC IFN gamma	42.0
Secondary Tr1 act	35.4	HUVEC TNF alpha + IFN gamma	21.8
Secondary Th1 rest	21.2	HUVEC TNF alpha + IL4	31.9
Secondary Th2 rest	35.6	HUVEC IL-11	32.1
Secondary Tr1 rest	20.7	Lung Microvascular EC none	72.2
Primary Th1 act	13.3	Lung Microvascular EC TNFalpha + IL-1beta	36.6
Primary Th2 act	34.6	Microvascular Dermal EC none	54.7
Primary Tr1 act	37.1	Microvascular Dermal EC TNFalpha + IL-1beta	26.6
Primary Th1 rest	19.5	Bronchial epithelium TNFalpha + IL1beta	25.5
Primary Th2 rest	23.0	Small airway epithelium none	14.2
Primary Tr1 rest	40.1	Small airway epithelium TNFalpha + IL-1beta	26.2

CD45RA CD4 lymphocyte act	34.6	Coronary artery SMC rest	16.2
CD45RO CD4 lymphocyte act	51.8	Coronary artery SMC TNFalpha + IL-1beta	19.3
CD8 lymphocyte act	28.3	Astrocytes rest	14.4
Secondary CD8 lymphocyte rest	31.0	Astrocytes TNFalpha + IL-1beta	12.9
Secondary CD8 lymphocyte act	17.3	KU-812 (Basophil) rest	50.0
CD4 lymphocyte none	16.4	KU-812 (Basophil) PMA/ionomycin	67.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	39.0	CCD1106 (Keratinocytes) none	31.4
LAK cells rest	32.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	53.2
LAK cells IL-2	38.7	Liver cirrhosis	10.4
LAK cells IL-2+IL-12	11.1	NCI-H292 none	44.4
LAK cells IL-2+IFN gamma	13.2	NCI-H292 IL-4	69.7
LAK cells IL-2+ IL-18	21.0	NCI-H292 IL-9	66.9
LAK cells PMA/ionomycin	11.3	NCI-H292 IL-13	57.0
NK Cells IL-2 rest	49.3	NCI-H292 IFN gamma	49.3
Two Way MLR 3 day	27.9	HPAEC none	29.7
Two Way MLR 5 day	22.1	HPAEC TNF alpha + IL-1 beta	25.2
Two Way MLR 7 day	28.7	Lung fibroblast none	42.3
PBMC rest	20.6	Lung fibroblast TNF alpha + IL-1 beta	28.3
PBMC PWM	26.1	Lung fibroblast IL-4	25.3
PBMC PHA-L	34.9	Lung fibroblast IL-9	31.0
Ramos (B cell) none	19.8	Lung fibroblast IL-13	22.1
Ramos (B cell) ionomycin	35.1	Lung fibroblast IFN gamma	40.1
B lymphocytes PWM	21.9	Dermal fibroblast CCD1070 rest	19.6
B lymphocytes CD40L and IL-4	51.8	Dermal fibroblast CCD1070 TNF alpha	65.1
EOL-1 dbcAMP	19.1	Dermal fibroblast CCD1070 IL-1 beta	12.1
EOL-1 dbcAMP PMA/ionomycin	11.2	Dermal fibroblast IFN gamma	17.1
Dendritic cells none	27.5	Dermal fibroblast IL-4	22.1
Dendritic cells LPS	25.5	Dermal Fibroblasts rest	26.8
Dendritic cells anti-CD40	26.4	Neutrophils TNFa+LPS	16.5
Monocytes rest	53.2	Neutrophils rest	100.0
Monocytes LPS	31.4	Colon	6.5

Macrophages rest	27.2	Lung	22.4
Macrophages LPS	16.5	Thymus	13.5
HUVEC none	17.1	Kidney	25.2
HUVEC starved	38.4		

General_screening_panel_v1.5 Summary: Ag5036 Highest expression of this gene is seen in an ovarian cancer cell line (CT=27). This gene is widely expressed in this panel, with moderate expression seen in brain, colon, gastric, lung, breast, ovarian, and melanoma cancer cell lines. This gene encodes a protein with homology to flotillin-2, an
5 integral membrane protein of the plasmalemmal microdomains involved in vesicular trafficking and signal transduction. Cho has suggested that this molecule is involved in cell adhesion (Genomics 27: 251-258, 1995.). Thus, based on this expression profile and the homology of this gene to flotillin, this protein product may be involved in cell survival and/or proliferation. Modulation of this gene product may be useful in the treatment of
10 cancer.

Among tissues with metabolic function, this gene is expressed at moderate levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. Flotillin-2 may play a role in the glucose uptake pathway (Baumann, Nature 2000 Sep 14;407(6801):202-7). This widespread expression among these metabolic tissues
15 and the homology to flotillin suggest that this gene product may play a role in normal neuroendocrine and metabolic function and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at much higher levels in fetal liver tissue (CT=28) when compared to expression in the adult counterpart (CT=31). Thus, expression of this
20 gene may be used to differentiate between the fetal and adult source of this tissue.

This gene is also expressed at moderate levels in the CNS, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease,
25 schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 4.1D Summary: Ag5036 Highest expression of this gene is seen in neutrophils (CT=28.2). This gene is also expressed at moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include

members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

S. CG140843-01: INTEGRIN BETA-5 PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG140843-01 was assessed using the primer-probe set Ag7404, described in Table SA. Results of the RTQ-PCR runs are shown in Table SB. Table SA.
Probe Name Ag7404

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - ctgcatggggaggtcaa - 3'	17	852	312
Probe	TET- 5' - aagtaccaacacccactgacgtctc - 3' - TAMRA	26	873	313
Reverse	5' - gctggggcactcaaagact - 3'	19	907	314

Table SB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7404, Run 306066735	Tissue Name	Rel. Exp.(%) Ag7404, Run 306066735
Adipose	6.4	Renal ca. TK-10	38.2
Melanoma* Hs688(A).T	21.6	Bladder	0.0
Melanoma* Hs688(B).T	14.2	Gastric ca. (liver met.) NCI-N87	34.2
Melanoma* M14	9.5	Gastric ca. KATO III	16.6
Melanoma* LOXIMV1	2.9	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	9.3	Colon ca. SW480	100.0
Squamous cell carcinoma SCC-4	2.9	Colon ca.* (SW480 met) SW620	11.0
Testis Pool	5.1	Colon ca. HT29	17.7

Prostate ca.* (bone met) PC-3	8.2	Colon ca. HCT-116	18.2
Prostate Pool	3.4	Colon ca. CaCo-2	16.4
Placenta	0.0	Colon cancer tissue	7.6
Uterus Pool	10.2	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	50.0	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV-3	27.4	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	26.1
Ovarian ca. OVCAR-5	40.1	Small Intestine Pool	11.3
Ovarian ca. IGROV-1	4.2	Stomach Pool	18.7
Ovarian ca. OVCAR-8	6.5	Bone Marrow Pool	4.5
Ovary	13.3	Fetal Heart	3.3
Breast ca. MCF-7	24.1	Heart Pool	10.3
Breast ca. MDA-MB-231	46.3	Lymph Node Pool	20.4
Breast ca. BT 549	10.6	Fetal Skeletal Muscle	0.0
Breast ca. T47D	7.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	5.6	Spleen Pool	15.5
Breast Pool	23.2	Thymus Pool	6.7
Trachea	9.0	CNS cancer (glio/astro) U87-MG	10.2
Lung	9.4	CNS cancer (glio/astro) U-118-MG	18.8
Fetal Lung	11.4	CNS cancer (neuro;met) SK-N-AS	30.8
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	17.8
Lung ca. LX-1	21.3	CNS cancer (astro) SNB- 75	43.8
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	6.8
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	20.7
Lung ca. A549	35.4	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	5.6
Lung ca. NCI-H23	2.8	Brain (fetal)	0.0
Lung ca. NCI-H460	10.7	Brain (Hippocampus) Pool	7.3
Lung ca. HOP-62	12.8	Cerebral Cortex Pool	3.2
Lung ca. NCI-H522	7.1	Brain (Substantia nigra) Pool	7.1
Liver	0.0	Brain (Thalamus) Pool	3.3
Fetal Liver	0.0	Brain (whole)	3.4
Liver ca. HepG2	19.9	Spinal Cord Pool	13.4
Kidney Pool	9.0	Adrenal Gland	6.6
Fetal Kidney	12.2	Pituitary gland Pool	0.0
Renal ca. 786-0	16.5	Salivary Gland	0.0

Renal ca. A498	3.6	Thyroid (female)	0.0
Renal ca. ACHN	13.4	Pancreatic ca. CAPAN2	35.6
Renal ca. UO-31	19.6	Pancreas Pool	4.2

CNS_neurodegeneration_v1.0 Summary: Ag7404 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

General_screening_panel_v1.6 Summary: Ag7404 Expression of this gene is restricted to a sample derived from a colon cancer cell line (CT=34.8). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of colon cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon cancer.

T. CG141540-01: IL1 receptor -type-2-like protein

Expression of gene CG141540-01 was assessed using the primer-probe sets Ag5237 and Ag5236, described in Tables TA and TB. Results of the RTQ-PCR runs are shown in Tables TC, TD and TE.

Table TA. Probe Name Ag5237

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agatggtctgactgtgctatg-3'	21	1143	315
Probe	TET-5'- tcacatcaagactttcaatcctatccc a-3'-TAMRA	29	1167	316
Reverse	5'-gaattatttcattccatttatttc- 3'	24	1199	317

Table TB. Probe Name Ag5236

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-acgcatcaagagggtcaagact- 3'	21	744	318
Probe	TET-5'- ccggcacacccttaaccaccat- 3'-TAMRA	22	794	319
Reverse	5'-gtgtcattggcgcgtcca-3'	17	823	320

Table TC. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag5236, Run 229545061	Tissue Name	Rel. Exp.(%) Ag5236, Run 229545061
110967 COPD-F	0.0	112427 Match Control Psoriasis-F	0.0
110980 COPD-F	0.0	112418 Psoriasis-M	0.0

110968 COPD-M	1.4	112723 Match Control Psoriasis-M	0.0
110977 COPD-M	0.0	112419 Psoriasis-M	0.0
110989 Emphysema-F	0.0	112424 Match Control Psoriasis-M	1.6
110992 Emphysema-F	2.7	112420 Psoriasis-M	3.8
110993 Emphysema-F	1.8	112425 Match Control Psoriasis-M	0.0
110994 Emphysema-F	0.0	104689 (MF) OA Bone-Backus	3.4
110995 Emphysema-F	11.4	104690 (MF) Adj "Normal" Bone-Backus	1.7
110996 Emphysema-F	6.1	104691 (MF) OA Synovium-Backus	1.7
110997 Asthma-M	4.6	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	0.0	104694 (BA) OA Bone-Backus	1.8
111002 Asthma-F	0.0	104695 (BA) Adj "Normal" Bone-Backus	0.9
111003 Atopic Asthma-F	0.7	104696 (BA) OA Synovium-Backus	0.0
111004 Atopic Asthma-F	0.0	104700 (SS) OA Bone-Backus	4.4
111005 Atopic Asthma-F	0.0	104701 (SS) Adj "Normal" Bone-Backus	3.0
111006 Atopic Asthma-F	0.0	104702 (SS) OA Synovium-Backus	1.5
111417 Allergy-M	0.0	117093 OA Cartilage Rep7	1.4
112347 Allergy-M	0.0	112672 OA Bone5	0.0
112349 Normal Lung-F	0.0	112673 OA Synovium5	0.0
112357 Normal Lung-F	0.0	112674 OA Synovial Fluid cells5	1.2
112354 Normal Lung-M	0.0	117100 OA Cartilage Rep14	0.0
112374 Crohns-F	0.0	112756 OA Bone9	0.0
112389 Match Control Crohns-F	6.1	112757 OA Synovium9	0.7
112375 Crohns-F	0.0	112758 OA Synovial Fluid Cells9	1.5
112732 Match Control Crohns-F	30.8	117125 RA Cartilage Rep2	0.0
112725 Crohns-M	0.0	113492 Bone2 RA	0.9
112387 Match Control Crohns-M	1.5	113493 Synovium2 RA	0.0

112378 Crohns-M	0.0	113494 Syn Fluid Cells RA	2.0
112390 Match Control Crohns-M	0.0	113499 Cartilage4 RA	2.5
112726 Crohns-M	1.1	113500 Bone4 RA	2.2
112731 Match Control Crohns-M	1.7	113501 Synovium4 RA	1.9
112380 Ulcer Col-F	0.0	113502 Syn Fluid Cells4 RA	0.0
112734 Match Control Ulcer Col-F	100.0	113495 Cartilage3 RA	4.5
112384 Ulcer Col-F	1.8	113496 Bone3 RA	5.3
112737 Match Control Ulcer Col-F	0.6	113497 Synovium3 RA	2.3
112386 Ulcer Col-F	1.2	113498 Syn Fluid Cells3 RA	2.0
112738 Match Control Ulcer Col-F	4.6	117106 Normal Cartilage Rep20	0.0
112381 Ulcer Col-M	0.0	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	0.0	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	7.9	113665 Syn Fluid Cells3 Normal	0.0
112394 Match Control Ulcer Col-M	0.0	117107 Normal Cartilage Rep22	0.0
112383 Ulcer Col-M	1.9	113667 Bone4 Normal	0.0
112736 Match Control Ulcer Col-M	0.0	113668 Synovium4 Normal	0.0
112423 Psoriasis-F	2.3	113669 Syn Fluid Cells4 Normal	0.0

Table TD. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5236, Run 237228536	Tissue Name	Rel. Exp.(%) Ag5236, Run 237228536
Adipose	22.2	Renal ca. TK-10	3.2
Melanoma* Hs688(A).T	0.0	Bladder	16.8
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	11.4
Melanoma* M14	0.0	Gastric ca. KATO III	40.1
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	29.3
Melanoma* SK-MEL-5	0.7	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	8.2	Colon ca.* (SW480 met) SW620	4.9
Testis Pool	1.4	Colon ca. HT29	13.3
Prostate ca.* (bone met) PC-3	1.0	Colon ca. HCT-116	0.0

Prostate Pool	0.0	Colon ca. CaCo-2	42.0
Placenta	13.4	Colon cancer tissue	35.1
Uterus Pool	3.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	26.2	Colon ca. Colo-205	67.4
Ovarian ca. SK-OV-3	100.0	Colon ca. SW-48	3.3
Ovarian ca. OVCAR-4	80.7	Colon Pool	2.7
Ovarian ca. OVCAR-5	1.3	Small Intestine Pool	2.9
Ovarian ca. IGROV-1	25.3	Stomach Pool	2.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	5.0
Ovary	18.6	Fetal Heart	0.8
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	3.2	Fetal Skeletal Muscle	0.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	59.5
Breast Pool	1.2	Thymus Pool	17.4
Trachea	12.6	CNS cancer (glio/astro) U87-MG	6.8
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	6.6	CNS cancer (neuro;met) SK-N-AS	6.3
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	1.1
Lung ca. LX-1	2.1	CNS cancer (astro) SNB-75	18.7
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	85.3
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	3.4
Lung ca. A549	8.0	Brain (Amygdala) Pool	2.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	3.4
Lung ca. NCI-H460	3.4	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	2.7	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.8	Brain (Thalamus) Pool	0.8
Fetal Liver	4.1	Brain (whole)	1.8
Liver ca. HepG2	7.0	Spinal Cord Pool	0.0
Kidney Pool	2.8	Adrenal Gland	3.2
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	11.3	Salivary Gland	1.0
Renal ca. A498	3.3	Thyroid (female)	0.8
Renal ca. ACHN	0.6	Pancreatic ca. CAPAN2	0.0

Renal ca. UO-31	0.0	Pancreas Pool	13.9
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Table TE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag5236, Run 229788311	Tissue Name	Rel. Exp.(%) Ag5236, Run 229788311
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	5.9
CD45RA CD4 lymphocyte act	2.1	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	1.1	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.7
Secondary CD8 lymphocyte rest	1.4	Astrocytes TNFalpha + IL- 1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.9
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	2.5
LAK cells rest	3.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.4
LAK cells IL-2	0.0	Liver cirrhosis	2.5
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0

LAK cells PMA/ionomycin	12.4	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	2.2	HPAEC none	0.0
Two Way MLR 5 day	1.1	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.9	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.9	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	4.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	1.6	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	10.3	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	4.7	Neutrophils TNFa+LPS	85.3
Monocytes rest	0.0	Neutrophils rest	100.0
Monocytes LPS	1.0	Colon	0.0
Macrophages rest	0.0	Lung	1.0
Macrophages LPS	0.0	Thymus	2.8
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

AI_comprehensive_panel_v1.0 Summary: Ag5236 Expression of this gene is limited to a normal tissue sample adjacent to Crohn's and normal tissue sample adjacent to ulcerative colitis (CTs=32-34). Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel.

- 5 **General_screening_panel_v1.5 Summary:** Ag5236 Highest expression of this gene is seen in an ovarian cancer cell line (CT=32). Low but significant levels of expression are also seen in clusters of cell lines derived from brain, ovarian, colon and gastric cancers. Thus, this gene product may be involved in these cancers. Low levels of expression are also seen in adipose and pancreas suggesting a role for this gene product in the pathogenesis of
- 10 metabolic disorders including obesity and diabetes.

Panel 4.1D Summary: Ag5236 This gene is expressed exclusively in neutrophils. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker of neutrophils.

U. CG141580-01: KIAA 1467 protein-like protein.

- 5 Expression of gene CG141580-01 was assessed using the primer-probe set Ag7248, described in Table UA. Results of the RTQ-PCR runs are shown in Tables UB and UC.

Table UA. Probe Name Ag7248

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - gtctatgactaggaacattttgttgtag -3'	29	2255	321
Probe	TET-5' - ccacaacactaaaatatacacacacacag c-3' -TAMRA	30	2289	322
Reverse	5' - cttaggacatacctggaaaataacttc- 3'	27	2320	323

Table UB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag7248, Run 296423801	Tissue Name	Rel. Exp.(%) Ag7248, Run 296423801
AD 1 Hippo	6.3	Control (Path) 3 Temporal Ctx	1.2
AD 2 Hippo	14.1	Control (Path) 4 Temporal Ctx	12.9
AD 3 Hippo	2.5	AD 1 Occipital Ctx	6.1
AD 4 Hippo	1.9	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	1.2
AD 6 Hippo	27.2	AD 4 Occipital Ctx	9.9
Control 2 Hippo	13.3	AD 5 Occipital Ctx	25.5
Control 4 Hippo	1.8	AD 6 Occipital Ctx	23.5
Control (Path) 3 Hippo	2.5	Control 1 Occipital Ctx	0.9
AD 1 Temporal Ctx	3.5	Control 2 Occipital Ctx	43.8
AD 2 Temporal Ctx	8.2	Control 3 Occipital Ctx	7.6
AD 3 Temporal Ctx	1.7	Control 4 Occipital Ctx	1.2
AD 4 Temporal Ctx	17.8	Control (Path) 1 Occipital Ctx	66.4
AD 5 Inf Temporal Ctx	60.7	Control (Path) 2 Occipital Ctx	7.6

AD 5 Sup Temporal Ctx	20.7	Control (Path) 3 Occipital Ctx	0.5
AD 6 Inf Temporal Ctx	25.5	Control (Path) 4 Occipital Ctx	6.7
AD 6 Sup Temporal Ctx	30.8	Control 1 Parietal Ctx	1.8
Control 1 Temporal Ctx	1.3	Control 2 Parietal Ctx	16.3
Control 2 Temporal Ctx	24.5	Control 3 Parietal Ctx	14.4
Control 3 Temporal Ctx	5.5	Control (Path) 1 Parietal Ctx	67.8
Control 3 Temporal Ctx	2.8	Control (Path) 2 Parietal Ctx	14.6
Control (Path) 1 Temporal Ctx	37.9	Control (Path) 3 Parietal Ctx	1.7
Control (Path) 2 Temporal Ctx	21.0	Control (Path) 4 Parietal Ctx	35.6

Table UC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7248, Run 296417628	Tissue Name	Rel. Exp.(%) Ag7248, Run 296417628
Secondary Th1 act	53.6	HUVEC IL-1beta	36.1
Secondary Th2 act	50.0	HUVEC IFN gamma	37.6
Secondary Tr1 act	16.8	HUVEC TNF alpha + IFN gamma	7.1
Secondary Th1 rest	1.7	HUVEC TNF alpha + IL4	14.3
Secondary Th2 rest	2.0	HUVEC IL-11	11.3
Secondary Tr1 rest	6.7	Lung Microvascular EC none	100.0
Primary Th1 act	5.6	Lung Microvascular EC TNFalpha + IL-1beta	12.3
Primary Th2 act	33.7	Microvascular Dermal EC none	18.2
Primary Tr1 act	27.7	Microvascular Dermal EC TNFalpha + IL-1beta	8.0
Primary Th1 rest	1.2	Bronchial epithelium TNFalpha + IL1beta	11.0
Primary Th2 rest	2.1	Small airway epithelium none	11.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	27.9
CD45RA CD4 lymphocyte act	36.9	Coronary artery SMC rest	34.9
CD45RO CD4 lymphocyte act	55.5	Coronary artery SMC TNFalpha + IL-1beta	41.5
CD8 lymphocyte act	11.1	Astrocytes rest	10.9
Secondary CD8 lymphocyte rest	5.2	Astrocytes TNFalpha + IL-1beta	10.0

Secondary CD8 lymphocyte act	4.5	KU-812 (Basophil) rest	63.3
CD4 lymphocyte none	4.3	KU-812 (Basophil) PMA/ionomycin	81.2
2ry Th1/Th2/Tr1_anti-CD95 CH11	4.7	CCD1106 (Keratinocytes) none	28.1
LAK cells rest	20.4	CCD1106 (Keratinocytes) TNFalpha + IL-1 beta	3.9
LAK cells IL-2	4.6	Liver cirrhosis	5.3
LAK cells IL-2+IL-12	1.6	NCI-H292 none	13.5
LAK cells IL-2+IFN gamma	9.1	NCI-H292 IL-4	20.6
LAK cells IL-2+ IL-18	3.9	NCI-H292 IL-9	21.6
LAK cells PMA/ionomycin	37.1	NCI-H292 IL-13	28.7
NK Cells IL-2 rest	12.8	NCI-H292 IFN gamma	14.5
Two Way MLR 3 day	27.9	HPAEC none	10.8
Two Way MLR 5 day	3.3	HPAEC TNF alpha + IL-1 beta	35.8
Two Way MLR 7 day	8.8	Lung fibroblast none	44.4
PBMC rest	5.4	Lung fibroblast TNF alpha + IL-1 beta	45.4
PBMC PWM	11.4	Lung fibroblast IL-4	12.5
PBMC PHA-L	12.4	Lung fibroblast IL-9	14.6
Ramos (B cell) none	20.6	Lung fibroblast IL-13	11.3
Ramos (B cell) ionomycin	53.2	Lung fibroblast IFN gamma	37.6
B lymphocytes PWM	4.9	Dermal fibroblast CCD1070 rest	24.8
B lymphocytes CD40L and IL-4	17.9	Dermal fibroblast CCD1070 TNF alpha	33.0
EOL-1 dbcAMP	38.4	Dermal fibroblast CCD1070 IL-1 beta	21.0
EOL-1 dbcAMP PMA/ionomycin	37.1	Dermal fibroblast IFN gamma	16.2
Dendritic cells none	24.0	Dermal fibroblast IL-4	56.6
Dendritic cells LPS	3.4	Dermal Fibroblasts rest	22.7
Dendritic cells anti-CD40	2.6	Neutrophils TNFa+LPS	1.5
Monocytes rest	8.8	Neutrophils rest	2.9
Monocytes LPS	41.5	Colon	5.4
Macrophages rest	11.6	Lung	1.1
Macrophages LPS	3.0	Thymus	5.6
HUVEC none	22.1	Kidney	50.0
HUVEC starved	35.8		

CNS_neurodegeneration_v1.0 Summary: Ag7248 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Low levels of expression of this gene in brain regions suggests that this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy,
 5 multiple sclerosis, schizophrenia and depression.

Panel 4.1D Summary: Ag7248 Highest expression of this gene is detected in lung microvascular endothelial cells (CT=32). Expression of this gene is down-regulated on activation of these endothelial cells by cytokines. Thus, this gene may play a role in the maintenance of the integrity of the microvasculature. Therefore, therapeutics designed for
 10 this putative protein could be beneficial for the treatment of diseases associated with damaged microvasculature including inflammatory diseases of lung, such as asthma, allergy, and chronic obstructive pulmonary diseases.

In addition, low to moderate levels of expression of this gene is also seen in lung and dermal fibroblasts, keratinocytes, basophils, coronary artery SMC, cytokine activated small
 15 airway epithelium, dermal microvascular EC, HUVEC, cytokine activated HPAEC, activated monocytes, eosinophils, Ramos B cells, two way MLR, activated LAK cells, and various types of activated T cells. Therefore, therapeutic modulation of this gene may be useful in the treatment of inflammatory and autoimmune diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and
 20 osteoarthritis.

V. CG141643-01:RIKEN 2010001CC9 protein-like protein.

Expression of gene CG141643-01 was assessed using the primer-probe set Ag5057, described in Table VA. Results of the RTQ-PCR runs are shown in Tables VB, VC and VD.

Table VA. Probe Name Ag5057

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcgtccaggaaccttcttc-3'	19	355	324
Probe	TET-5'- actgggtcctgctggcactagctct- 3'-TAMRA	25	386	325
Reverse	5'-caacggacaagagcaggtt-3'	19	415	326

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Table VB. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag5057, Run 219965745	Tissue Name	Rel. Exp.(%) Ag5057, Run 219965745
110967 COPD-F	7.0	112427 Match Control Psoriasis-F	80.7
110980 COPD-F	3.6	112418 Psoriasis-M	7.0
110968 COPD-M	12.7	112723 Match Control Psoriasis-M	5.0
110977 COPD-M	0.0	112419 Psoriasis-M	8.8
110989 Emphysema-F	30.1	112424 Match Control Psoriasis-M	25.0
110992 Emphysema-F	22.2	112420 Psoriasis-M	70.7
110993 Emphysema-F	11.1	112425 Match Control Psoriasis-M	48.3
110994 Emphysema-F	5.8	104689 (MF) OA Bone- Backus	7.0
110995 Emphysema-F	98.6	104690 (MF) Adj "Normal" Bone-Backus	8.1
110996 Emphysema-F	13.6	104691 (MF) OA Synovium-Backus	10.7
110997 Asthma-M	19.9	104692 (BA) OA Cartilage-Backus	10.4
111001 Asthma-F	8.2	104694 (BA) OA Bone- Backus	7.7
111002 Asthma-F	21.3	104695 (BA) Adj "Normal" Bone-Backus	8.8
111003 Atopic Asthma- F	25.5	104696 (BA) OA Synovium-Backus	3.0
111004 Atopic Asthma- F	87.1	104700 (SS) OA Bone- Backus	6.8
111005 Atopic Asthma- F	32.1	104701 (SS) Adj "Normal" Bone-Backus	10.7
111006 Atopic Asthma- F	14.1	104702 (SS) OA Synovium-Backus	9.6
111417 Allergy-M	33.2	117093 OA Cartilage Rep7	5.0
112347 Allergy-M	10.7	112672 OA Bone5	20.9
112349 Normal Lung-F	25.3	112673 OA Synovium5	6.4
112357 Normal Lung-F	30.1	112674 OA Synovial Fluid cells5	14.1
112354 Normal Lung- M	17.2	117100 OA Cartilage Rep14	8.0
112374 Crohns-F	10.7	112756 OA Bone9	23.0
112389 Match Control Crohns-F	9.5	112757 OA Synovium9	3.3
112375 Crohns-F	14.2	112758 OA Synovial Fluid Cells9	11.0

112732 Match Control Crohns-F	54.7	117125 RA Cartilage Rep2	2.9
112725 Crohns-M	11.8	113492 Bone2 RA	27.5
112387 Match Control Crohns-M	10.3	113493 Synovium2 RA	17.4
112378 Crohns-M	7.4	113494 Syn Fluid Cells RA	38.4
112390 Match Control Crohns-M	42.6	113499 Cartilage4 RA	49.3
112726 Crohns-M	32.3	113500 Bone4 RA	51.8
112731 Match Control Crohns-M	42.3	113501 Synovium4 RA	45.1
112380 Ulcer Col-F	12.6	113502 Syn Fluid Cells4 RA	34.4
112734 Match Control Ulcer Col-F	85.3	113495 Cartilage3 RA	13.8
112384 Ulcer Col-F	50.3	113496 Bone3 RA	23.8
112737 Match Control Ulcer Col-F	16.7	113497 Synovium3 RA	22.8
112386 Ulcer Col-F	2.6	113498 Syn Fluid Cells3 RA	24.5
112738 Match Control Ulcer Col-F	100.0	117106 Normal Cartilage Rep20	6.3
112381 Ulcer Col-M	3.5	113663 Bone3 Normal	5.8
112735 Match Control Ulcer Col-M	24.1	113664 Synovium3 Normal	7.5
112382 Ulcer Col-M	20.0	113665 Syn Fluid Cells3 Normal	7.1
112394 Match Control Ulcer Col-M	2.7	117107 Normal Cartilage Rep22	2.7
112383 Ulcer Col-M	23.2	113667 Bone4 Normal	8.2
112736 Match Control Ulcer Col-M	11.3	113668 Synovium4 Normal	14.7
112423 Psoriasis-F	11.5	113669 Syn Fluid Cells4 Normal	19.2

Table VC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag5057, Run 219514716	Tissue Name	Rel. Exp.(%) Ag5057, Run 219514716
Adipose	0.5	Renal ca. TK-10	1.6
Melanoma* Hs688(A).T	0.1	Bladder	12.9
Melanoma* Hs688(B).T	0.1	Gastric ca. (liver met.) NCI-N87	43.2
Melanoma* M14	0.4	Gastric ca. KATO III	100.0
Melanoma* LOXIMVI	0.2	Colon ca. SW-948	21.9
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	1.2

Squamous cell carcinoma SCC-4	15.8	Colon ca.* (SW480 met) SW620	0.4
Testis Pool	0.8	Colon ca. HT29	24.3
Prostate ca.* (bone met) PC-3	0.5	Colon ca. HCT-116	53.2
Prostate Pool	2.1	Colon ca. CaCo-2	26.2
Placenta	0.3	Colon cancer tissue	33.2
Uterus Pool	0.1	Colon ca. SW1116	14.1
Ovarian ca. OVCAR-3	1.7	Colon ca. Colo-205	29.5
Ovarian ca. SK-OV-3	3.3	Colon ca. SW-48	25.3
Ovarian ca. OVCAR-4	22.1	Colon Pool	0.5
Ovarian ca. OVCAR-5	24.1	Small Intestine Pool	1.5
Ovarian ca. IGROV-1	1.0	Stomach Pool	1.0
Ovarian ca. OVCAR-8	0.4	Bone Marrow Pool	0.1
Ovary	0.8	Fetal Heart	0.1
Breast ca. MCF-7	17.3	Heart Pool	0.2
Breast ca. MDA-MB-231	0.5	Lymph Node Pool	1.0
Breast ca. BT 549	0.5	Fetal Skeletal Muscle	0.1
Breast ca. T47D	51.1	Skeletal Muscle Pool	0.1
Breast ca. MDA-N	0.4	Spleen Pool	0.4
Breast Pool	1.2	Thymus Pool	1.8
Trachea	4.7	CNS cancer (glio/astro) U87-MG	0.8
Lung	0.9	CNS cancer (glio/astro) U-118-MG	1.0
Fetal Lung	1.6	CNS cancer (neuro;met) SK-N-AS	0.5
Lung ca. NCI-N417	0.2	CNS cancer (astro) SF-539	0.5
Lung ca. LX-1	30.4	CNS cancer (astro) SNB-75	0.6
Lung ca. NCI-H146	9.7	CNS cancer (glio) SNB-19	0.9
Lung ca. SHP-77	0.3	CNS cancer (glio) SF-295	2.9
Lung ca. A549	0.9	Brain (Amygdala) Pool	0.2
Lung ca. NCI-H526	6.3	Brain (cerebellum)	0.9
Lung ca. NCI-H23	1.3	Brain (fetal)	0.8
Lung ca. NCI-H460	1.1	Brain (Hippocampus) Pool	0.2
Lung ca. HOP-62	0.7	Cerebral Cortex Pool	0.2
Lung ca. NCI-H522	0.9	Brain (Substantia nigra) Pool	0.2
Liver	0.7	Brain (Thalamus) Pool	0.3
Fetal Liver	1.4	Brain (whole)	0.2
Liver ca. HepG2	1.0	Spinal Cord Pool	0.3

Kidney Pool	0.9	Adrenal Gland	0.8
Fetal Kidney	1.0	Pituitary gland Pool	1.3
Renal ca. 786-0	0.5	Salivary Gland	1.4
Renal ca. A498	0.1	Thyroid (female)	2.1
Renal ca. ACHN	0.5	Pancreatic ca. CAPAN2	40.3
Renal ca. UO-31	0.5	Pancreas Pool	3.3

Table VD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag5057, Run 220366655	Tissue Name	Rel. Exp.(%) Ag5057, Run 220366655
Secondary Th1 act	14.0	HUVEC IL-1beta	3.8
Secondary Th2 act	15.8	HUVEC IFN gamma	9.7
Secondary Tr1 act	1.4	HUVEC TNF alpha + IFN gamma	6.7
Secondary Th1 rest	3.8	HUVEC TNF alpha + IL4	2.4
Secondary Th2 rest	5.3	HUVEC IL-11	2.3
Secondary Tr1 rest	10.2	Lung Microvascular EC none	17.1
Primary Th1 act	2.3	Lung Microvascular EC TNFalpha + IL-1beta	4.9
Primary Th2 act	8.2	Microvascular Dermal EC none	0.0
Primary Tr1 act	9.7	Microvascular Dermal EC TNFalpha + IL-1beta	4.4
Primary Th1 rest	14.5	Bronchial epithelium TNFalpha + IL1beta	24.3
Primary Th2 rest	0.0	Small airway epithelium none	19.9
Primary Tr1 rest	8.3	Small airway epithelium TNFalpha + IL-1beta	100.0
CD45RA CD4 lymphocyte act	0.6	Coronary artery SMC rest	0.9
CD45RO CD4 lymphocyte act	17.3	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	17.3	Astrocytes rest	4.2
Secondary CD8 lymphocyte rest	5.6	Astrocytes TNFalpha + IL- 1beta	7.1
Secondary CD8 lymphocyte act	15.1	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	5.0	KU-812 (Basophil) PMA/ionomycin	3.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	7.3	CCD1106 (Keratinocytes) none	53.2
LAK cells rest	15.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	59.0
LAK cells IL-2	27.4	Liver cirrhosis	27.9
LAK cells IL-2+IL-12	7.7	NCI-H292 none	3.5

LAK cells IL-2+IFN gamma	9.6	NCI-H292 IL-4	11.8
LAK cells IL-2+ IL-18	6.3	NCI-H292 IL-9	3.7
LAK cells PMA/ionomycin	6.0	NCI-H292 IL-13	10.0
NK Cells IL-2 rest	20.2	NCI-H292 IFN gamma	20.3
Two Way MLR 3 day	12.2	HPAEC none	3.2
Two Way MLR 5 day	7.7	HPAEC TNF alpha + IL-1 beta	9.4
Two Way MLR 7 day	4.4	Lung fibroblast none	2.5
PBMC rest	2.4	Lung fibroblast TNF alpha + IL-1 beta	4.0
PBMC PWM	11.2	Lung fibroblast IL-4	4.3
PBMC PHA-L	9.5	Lung fibroblast IL-9	7.1
Ramos (B cell) none	5.8	Lung fibroblast IL-13	4.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	2.7
B lymphocytes PWM	4.2	Dermal fibroblast CCD1070 rest	4.5
B lymphocytes CD40L and IL-4	9.5	Dermal fibroblast CCD1070 TNF alpha	8.8
EOL-1 dbcAMP	5.0	Dermal fibroblast CCD1070 IL-1 beta	2.2
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.5
Dendritic cells none	17.8	Dermal fibroblast IL-4	2.4
Dendritic cells LPS	2.3	Dermal Fibroblasts rest	2.8
Dendritic cells anti-CD40	5.6	Neutrophils TNFa+LPS	2.4
Monocytes rest	7.6	Neutrophils rest	2.3
Monocytes LPS	13.2	Colon	39.2
Macrophages rest	23.7	Lung	16.5
Macrophages LPS	2.6	Thymus	19.1
HUVEC none	9.3	Kidney	44.8
HUVEC starved	13.8		

- AI_comprehensive panel_v1.0 Summary:** Ag5057 Highest expression of this gene is detected in a matched control for ulcerative colitis (CT=30.2). This gene shows a ubiquitous expression with moderate to low levels of expression in normal and diseased lung (COPD, emphysema and asthma), normal and diseased colon (Crohn's and ulcerative colitis), psoriasis, bone, cartilage, synovium and synovial fluids from normal and patients suffering from orthoarthritis and rheumatoid arthritis. Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

General_screening_panel_v1.4 Summary: Ag5057 This gene is expressed at a high to moderate level in pancreatic, gastric, colon cancer and some breast and ovarian cancer cell line with the highest expression seen in a gastric cancer cell line (KATO III, CT=26.33). It is also expressed at a low level in lung, CNS and prostate cancer cell lines as well as most of the normal tissues on this panel. Hence it may be used as a marker to differentiate cancer cells from normal tissue and therapeutic modulation of the gene product can be used for the treatment of these cancers.

In addition, low levels of expression of this gene is also seen in some regions of central nervous system including fetal brain, cerebellum, thalamus and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Panel 4.1D Summary: Ag5057 Highest expression of this gene is detected in TNF alpha and IL-1 beta treated small airway epithelium (CT=31.7). Expression of this gene is enhanced in cytokine treated small airway epithelium as compared to the resting cells (CT=34). Therefore, modulation of the expression or activity of the protein encoded by this transcript through the application of small molecule therapeutics may be useful in the treatment of asthma, COPD, and emphysema.

Moderate to low levels of expression of this gene is also seen in activated secondary polarized T cells, activated memory T cells, CD8 lymphocytes, resting and IL-2 treated LAK cells, IL-2 treated NK cells, dendritic cells, resting macrophage, activated monocytes, starved HUVEC cells, activated bronchial epithelium, keratinocytes, liver cirrhosis, activated NCI-H292 cells, and normal tissues represented by colon, lung, thymus and kidney. Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

W. CG142003-01: Plasma Protease C1 Inhibitor Precursor Protein-like Protein.

Expression of gene CG142003-01 was assessed using the primer-probe set Ag5686, described in Table WA. Note that CG142003-01 represents a full-length physical clone.

5 **Table WA. Probe Name Ag5686**

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-catcgcagaaacctgaagatc-3'	21	187	327
Probe	TET-5'- taccactgatgaacccaccacacaac -3'-TAMRA	26	225	328
Reverse	5'-cagccaccaaataacagctaa-3'	22	251	329

AI_comprehensive_panel_v1.0 Summary: Ag5686 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

General_screening_panel_v1.5 Summary: Ag5686 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

10 **Panel 4.1D Summary:** Ag5686 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

X. CG142023-01: 6230421J19Rik protein-like protein

Expression of gene CG142023-01 was assessed using the primer-probe set Ag7414, described in Table XA.

15 **Table XA. Probe Name Ag7414**

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaagagcatcgccaccat-3'	18	798	330
Probe	TET-5'- ccctgggctctatcatttactgtgt- 3'-TAMRA	25	887	331
Reverse	5'-gctttctggtctccatgaactt-3'	22	916	332

Y. CG142092-01: C4b-BINDING PROTEIN ALPHA CHAIN PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG142092-01 was assessed using the primer-probe set Ag6869, described in Table YA. Results of the RTQ-PCR runs are shown in Tables YB and YC. Note that CG142092-01 represents a full-length physical clone.

Table YA. Probe Name Ag6869

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tcacctacagctgtgaacaa-3'	20	585	333
Probe	TET-5'- caggcaaaagactcatgcagtgctctcc -3'-TAMRA	27	612	334
Reverse	5'-ttttcacatcctctgggttt-3'	20	640	335

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Table YB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6869, Run 278387610	Tissue Name	Rel. Exp.(%) Ag6869, Run 278387610
Adipose	0.0	Renal ca. TK-10	9.8
Melanoma* Hs688(A).T	0.0	Bladder	33.4
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	9.1
Placenta	0.0	Colon cancer tissue	2.0
Uterus Pool	0.3	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.9
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	2.8	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.6	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.2
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.2
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.5
Breast ca. MDA-N	0.0	Spleen Pool	0.0

Breast Pool	0.3	Thymus Pool	0.3
Trachea	0.6	CNS cancer (glio/astro) U87-MG	0.3
Lung	0.6	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	2.4	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	1.2	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.7
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	1.3	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.3
Liver	100.0	Brain (Thalamus) Pool	0.2
Fetal Liver	5.8	Brain (whole)	6.2
Liver ca. HepG2	16.2	Spinal Cord Pool	0.0
Kidney Pool	0.4	Adrenal Gland	0.0
Fetal Kidney	0.2	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	1.1

Table YC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6869, Run 310594482	Tissue Name	Rel. Exp.(%) Ag6869, Run 310594482
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0

Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0

EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	1.8
Macrophages rest	0.0	Lung	23.7
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

General screening panel v1.6 Summary: Ag6869 Highest expression of this gene is seen in liver (CT=30). In addition, this gene is expressed at much higher levels in adult liver when compared to expression in the fetal counterpart (CT=34). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

- 5 Low but significant levels of expression are also seen in cancer cell lines derived from liver, renal, and colon cancers, as well as in normal bladder and whole brain. This gene encodes a protein with homology to C4BP, a regulatory protein synthesized by the liver that is involved in the regulation of the classical pathway of complement and the natural anticoagulant pathway. Thus, the restricted pattern of expression of this protein, with
- 10 highest expression in the liver, is consistent with the its characterization as a novel C4BP.

- Panel 4.1D Summary:** Ag6869 Low expression of this gene is exclusively seen in liver cirrhosis sample (CT=34). The putative C4b-binding protein encoded for by this gene could potentially allow cells within the liver to respond to specific microenvironmental signals. Therefore, therapeutic modulation of this gene through the use of antibodies or
- 15 small molecule drug may potentially modulate liver function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the liver including liver cirrhosis and fibrosis.

Z. CG142092-02: C4b-binding protein alpha-chain precursor protein-like protein.

- 20 Expression of gene CG142092-02 was assessed using the primer-probe set Ag7037, described in Table ZA. Results of the RTQ-PCR runs are shown in Tables ZB and ZC.

Table ZA. Probe Name Ag7037

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gctgttcagaaggctgtgaac-3'	21	554	336
Probe	TET-5'- acaggcaaaagactcatgcagtgtctcc -3'-TAMRA	28	583	337
Reverse	5'-ggccattttcacatcctctg-3'	20	617	338

Table ZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag7037, Run 282263012	Tissue Name	Rel. Exp.(%) Ag7037, Run 282263012
AD 1 Hippo	0.0	Control (Path) 3 Temporal Ctx	0.0
AD 2 Hippo	7.5	Control (Path) 4 Temporal Ctx	37.9
AD 3 Hippo	3.7	AD 1 Occipital Ctx	6.8
AD 4 Hippo	0.0	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	63.3	AD 3 Occipital Ctx	0.0
AD 6 Hippo	46.7	AD 4 Occipital Ctx	0.0
Control 2 Hippo	0.0	AD 5 Occipital Ctx	4.1
Control 4 Hippo	2.8	AD 6 Occipital Ctx	18.4
Control (Path) 3 Hippo	13.0	Control 1 Occipital Ctx	4.4
AD 1 Temporal Ctx	21.6	Control 2 Occipital Ctx	29.9
AD 2 Temporal Ctx	11.7	Control 3 Occipital Ctx	11.0
AD 3 Temporal Ctx	0.0	Control 4 Occipital Ctx	16.2
AD 4 Temporal Ctx	21.3	Control (Path) 1 Occipital Ctx	40.3
AD 5 Inf Temporal Ctx	59.9	Control (Path) 2 Occipital Ctx	15.2
AD 5 Sup Temporal Ctx	28.9	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	49.0	Control (Path) 4 Occipital Ctx	14.9
AD 6 Sup Temporal Ctx	45.4	Control 1 Parietal Ctx	16.7
Control 1 Temporal Ctx	0.0	Control 2 Parietal Ctx	35.8
Control 2 Temporal Ctx	35.6	Control 3 Parietal Ctx	12.2
Control 3 Temporal Ctx	24.7	Control (Path) 1 Parietal Ctx	37.6
Control 4 Temporal Ctx	4.3	Control (Path) 2 Parietal Ctx	4.9
Control (Path) 1 Temporal Ctx	6.9	Control (Path) 3 Parietal Ctx	0.0
Control (Path) 2 Temporal Ctx	100.0	Control (Path) 4 Parietal Ctx	14.4

Table ZC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7037, Run 282263188	Tissue Name	Rel. Exp.(%) Ag7037, Run 282263188
Secondary Th1 act	0.0	HUVEC IL-1beta	0.1
Secondary Th2 act	0.0	HUVEC IFN gamma	0.3
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.5
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.1
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.3
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.2
Primary Th2 act	0.3	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.2
Two Way MLR 3 day	0.0	HPAEC none	0.0

Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.5
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.1
B lymphocytes CD40L and IL-4	0.1	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.1
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	1.7
Monocytes rest	0.0	Neutrophils rest	0.2
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	16.4
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.4
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag7037 This gene is expressed at low levels in the CNS. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurological disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

- 5 **Panel 4.1D Summary:** Ag7037 Highest expression of this gene is seen in liver cirrhosis (CT=29.6). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker of this condition. Furthermore, therapeutic modulation of the expression or function of this gene may reduce or inhibit fibrosis that occurs in liver cirrhosis.

10 **AA. CG142092-03: C4b-binding protein alpha chain precursor protein-like protein.**

Expression of gene CG142092-03 was assessed using the primer-probe set Ag7668, described in Table AAA.

Table AAA. Probe Name Ag7668

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tgtgggtcctccaccact-3'	18	286	339
Probe	TET-5'- tctcagtcaacgtaatatccatcggggc a-3'-TAMRA	29	315	340
Reverse	5'- gttcaatttccagagtagttccagt-3'	25	355	341

CNS_neurodegeneration_v1.0 Summary: Ag7668 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag7668 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AB. CG51117-03, CG51117-05, CG51117-06 and CG51117-07:

Nephronectin-like Protein

Expression of gene CG51117-03, CG51117-05, and CG51117-06 was assessed using the primer-probe sets Ag2505, Ag2667, Ag2767, Ag2831, Ag5113, Ag5124 and Ag7237, described in Tables ABA, ABB, ABC, ABD, ABE, ABF and ABG. Results of the RTQ-PCR runs are shown in Tables ABH, ABI, ABJ, ABK, ABL, ABM, ABN, ABO, ABP, ABQ, ABR and ABS. Note that Ag5113 is specific for CG51117-07 variant, and Ag5124 is specific for CG51117-06 variant.

Table ABA. Probe Name Ag2505

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaagaaggataccagggtagt-3'	22	1113	342
Probe	TET-5'- atgattgaaccttcaggtccaattca -3'-TAMRA	26	1164	343
Reverse	5'-ggtaccatttcccttgggtaca-3'	22	1190	344

Table ABB. Probe Name Ag2667

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcagagaatagccaggataagg-3'	22	434	345
Probe	TET-5'- caaccacgatgcaaacatggtgaat-3'-TAMRA	25	477	346

Reverse	5'-cacttgtttgcccagatac-3'	19	502	347
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Table ABC. Probe Name Ag2767

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcagagaatagccaggataagg-3'	22	434	348
Probe	TET-5'- caaccacgatgcaaacatggtgaat-3'-TAMRA	25	477	349
Reverse	5'-cacttgtttgcccagatac-3'	19	502	350

Table ABD. Probe Name Ag2831

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcagagaatagccaggataagg-3'	22	434	351
Probe	TET-5'- caaccacgatgcaaacatggtgaat-3'-TAMRA	25	477	352
Reverse	5'-cacttgtttgcccagatac-3'	19	502	353

Table ABE. Probe Name Ag5113

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtcagcctgtgtgccaa-3'	17	412	354
Probe	TET-5'- ccaaacaagtgcaagtgtcatcctgg-3'-TAMRA	26	459	355
Reverse	5'-gggatgtgctcgtcttga-3'	18	506	356

5

Table ABF. Probe Name Ag5124

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aggataaggtgccagctca-3'	19	447	357
Probe	TET-5'- ccaaacaagtgcaagtgtcatcctgg-3'-TAMRA	26	510	358
Reverse	5'-gggatgtgctcgtcttga-3'	18	557	359

Table ABG. Probe Name Ag7237

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgttcattccacggcaac-3'	19	1539	360

Probe	TET-5' - catcgtctgcactgactcctctttcta -3' - TAMRA	27	1588	361
Reverse	5' -gtgtaccagaacacctggatca- 3'	22	1625	362

Table ABH. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag2505, Run 248588456	Rel. Exp.(%) Ag2831, Run 244570250	Tissue Name	Rel. Exp.(%) Ag2505, Run 248588456	Rel. Exp.(%) Ag2831, Run 244570250
110967 COPD-F	15.3	9.3	112427 Match Control Psoriasis-F	16.7	18.9
110980 COPD-F	11.8	7.0	112418 Psoriasis-M	14.0	13.9
110968 COPD-M	8.9	5.8	112723 Match Control Psoriasis-M	0.2	0.2
110977 COPD-M	28.1	14.1	112419 Psoriasis-M	18.2	8.7
110989 Emphysema-F	9.6	12.2	112424 Match Control Psoriasis-M	6.8	6.7
110992 Emphysema-F	1.9	4.1	112420 Psoriasis-M	13.9	15.5
110993 Emphysema-F	7.7	9.3	112425 Match Control Psoriasis-M	13.6	16.6
110994 Emphysema-F	5.2	4.1	104689 (MF) OA Bone-Backus	25.3	38.4
110995 Emphysema-F	3.6	4.3	104690 (MF) Adj "Normal" Bone-Backus	27.9	21.2
110996 Emphysema-F	0.4	0.2	104691 (MF) OA Synovium-Backus	2.9	3.0
110997 Asthma-M	4.6	3.0	104692 (BA) OA Cartilage-Backus	0.0	0.0
111001 Asthma-F	2.3	5.0	104694 (BA) OA Bone-Backus	5.8	18.7
111002 Asthma-F	3.5	7.2	104695 (BA) Adj "Normal" Bone-Backus	14.1	19.8
111003 Atopic Asthma-F	22.5	22.2	104696 (BA) OA Synovium-Backus	2.3	3.6
111004 Atopic Asthma-F	10.4	11.4	104700 (SS) OA Bone-Backus	28.9	22.4

I11005 Atopic Asthma-F	7.3	9.4	104701 (SS) Adj "Normal" Bone-Backus	25.5	18.7
I11006 Atopic Asthma-F	1.6	1.4	104702 (SS) OA Synovium-Backus	11.7	7.1
I11417 Allergy-M	5.1	2.8	I17093 OA Cartilage Rep7	7.5	7.5
I12347 Allergy-M	1.4	0.2	I12672 OA Bone5	19.2	17.2
I12349 Normal Lung-F	0.7	0.2	I12673 OA Synovium5	6.4	3.8
I12357 Normal Lung-F	7.1	6.4	I12674 OA Synovial Fluid cells5	6.8	4.2
I12354 Normal Lung-M	7.6	6.0	I17100 OA Cartilage Rep14	1.9	2.1
I12374 Crohns-F	9.0	3.2	I12756 OA Bone9	26.4	31.6
I12389 Match Control Crohns-F	11.2	6.6	I12757 OA Synovium9	2.8	1.3
I12375 Crohns-F	10.2	6.0	I12758 OA Synovial Fluid Cells9	8.1	6.3
I12732 Match Control Crohns-F	1.2	2.1	I17125 RA Cartilage Rep2	14.8	9.2
I12725 Crohns-M	0.9	1.6	I13492 Bone2 RA	84.7	47.0
I12387 Match Control Crohns-M	11.4	13.0	I13493 Synovium2 RA	40.9	25.3
I12378 Crohns-M	1.3	2.0	I13494 Syn Fluid Cells RA	61.1	49.3
I12390 Match Control Crohns-M	16.7	4.3	I13499 Cartilage4 RA	90.1	73.2
I12726 Crohns-M	21.8	17.0	I13500 Bone4 RA	100.0	100.0
I12731 Match Control Crohns-M	15.3	6.3	I13501 Synovium4 RA	71.2	59.5
I12380 Ulcer Col-F	5.8	7.0	I13502 Syn Fluid Cells4 RA	48.6	37.9
I12734 Match Control Ulcer Col-F	3.7	5.0	I13495 Cartilage3 RA	77.9	47.0
I12384 Ulcer Col-F	19.2	15.0	I13496 Bone3 RA	92.0	41.8

112737 Match Control Ulcer Col-F	13.5	12.0	113497 Synovium3 RA	53.6	24.0
112386 Ulcer Col-F	8.4	6.0	113498 Syn Fluid Cells3 RA	98.6	57.0
112738 Match Control Ulcer Col-F	3.8	2.1	117106 Normal Cartilage Rep20	3.0	1.6
112381 Ulcer Col-M	5.0	9.9	113663 Bone3 Normal	2.0	0.7
112735 Match Control Ulcer Col-M	9.7	5.8	113664 Synovium3 Normal	0.5	0.4
112382 Ulcer Col-M	11.7	12.6	113665 Syn Fluid Cells3 Normal	1.6	1.4
112394 Match Control Ulcer Col-M	3.1	3.4	117107 Normal Cartilage Rep22	3.7	5.5
112383 Ulcer Col-M	5.1	13.7	113667 Bone4 Normal	4.3	6.0
112736 Match Control Ulcer Col-M	5.0	6.3	113668 Synovium4 Normal	9.1	7.4
112423 Psoriasis-F	14.0	10.3	113669 Syn Fluid Cells4 Normal	6.6	6.6

Table ABI. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag2505, Run 208123723	Rel. Exp.(%) Ag2505, Run 224116291	Rel. Exp.(%) Ag2667, Run 206955569	Rel. Exp.(%) Ag2767, Run 206985756	Rel. Exp.(%) Ag2831, Run 208699692	Rel. Exp.(%) Ag7237, Run 296423778
AD 1 Hippo	14.1	19.1	42.9	27.4	29.1	11.7
AD 2 Hippo	29.3	40.3	58.2	37.1	56.3	36.6
AD 3 Hippo	5.1	8.5	9.0	5.6	2.9	7.8
AD 4 Hippo	10.4	10.1	13.4	21.2	8.8	11.4
AD 5 Hippo	43.8	47.6	52.1	35.4	40.3	43.2
AD 6 Hippo	100.0	100.0	98.6	100.0	79.0	100.0
Control 2 Hippo	15.3	19.6	5.1	19.6	5.5	11.0
Control 4 Hippo	15.6	21.0	16.0	15.2	25.7	32.8
Control (Path) 3 Hippo	4.8	5.8	22.1	2.7	4.5	6.5
AD 1 Temporal Ctx	21.5	26.4	40.9	15.6	24.5	22.2

AD 2 Temporal Ctx	28.5	27.9	52.5	27.0	84.7	35.8
AD 3 Temporal Ctx	9.3	8.5	13.4	7.3	3.2	2.1
AD 4 Temporal Ctx	26.1	35.1	59.0	18.2	30.8	29.1
AD 5 Inf Temporal Ctx	28.9	33.9	39.5	27.0	49.3	37.1
AD 5 Sup Temporal Ctx	38.4	40.6	23.0	17.2	54.7	45.7
AD 6 Inf Temporal Ctx	83.5	96.6	100.0	66.4	100.0	94.0
AD 6 Sup Temporal Ctx	70.7	90.8	99.3	43.5	62.4	82.9
Control 1 Temporal Ctx	4.2	4.2	17.3	7.7	3.1	1.9
Control 2 Temporal Ctx	10.6	14.0	12.1	25.5	18.6	15.5
Control 3 Temporal Ctx	3.1	5.6	0.0	0.0	3.6	10.7
Control 3 Temporal Ctx	6.5	14.6	12.5	18.2	19.2	16.6
Control (Path) 1 Temporal Ctx	18.0	21.6	43.2	26.6	19.3	21.9
Control (Path) 2 Temporal Ctx	13.9	22.1	26.1	42.3	42.0	21.5
Control (Path) 3 Temporal Ctx	3.2	4.2	4.4	7.0	11.8	4.6
Control (Path) 4 Temporal Ctx	13.4	15.3	26.6	21.9	13.8	19.6
AD 1 Occipital Ctx	13.4	15.2	27.9	7.9	16.2	13.5
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	4.1	5.8	11.8	0.0	9.9	3.0
AD 4 Occipital Ctx	19.3	23.2	17.0	9.0	41.2	27.4
AD 5 Occipital Ctx	17.8	16.8	39.5	27.9	17.6	19.6
AD 6 Occipital Ctx	29.3	43.8	30.8	25.5	13.2	32.8
Control 1 Occipital Ctx	4.0	3.0	14.0	0.0	13.0	2.8

Control 2 Occipital Ctx	21.8	25.3	2.3	29.1	17.7	32.3
Control 3 Occipital Ctx	6.9	7.3	28.7	4.8	7.1	9.2
Control 4 Occipital Ctx	9.4	10.3	13.8	9.1	17.6	17.7
Control (Path) 1 Occipital Ctx	29.1	28.1	37.6	29.3	47.6	34.2
Control (Path) 2 Occipital Ctx	5.1	7.0	6.7	5.3	8.6	5.3
Control (Path) 3 Occipital Ctx	1.6	2.5	25.7	3.5	0.0	2.4
Control (Path) 4 Occipital Ctx	13.7	17.2	19.8	13.5	13.7	12.2
Control 1 Parietal Ctx	3.8	4.0	10.8	24.1	7.3	3.8
Control 2 Parietal Ctx	37.4	47.6	53.6	36.1	57.4	53.6
Control 3 Parietal Ctx	4.1	5.4	0.0	3.4	3.5	5.3
Control (Path) 1 Parietal Ctx	23.5	28.9	24.7	21.5	42.6	30.4
Control (Path) 2 Parietal Ctx	15.7	20.2	44.8	11.5	39.5	20.6
Control (Path) 3 Parietal Ctx	2.6	4.0	14.9	3.7	3.0	2.4
Control (Path) 4 Parietal Ctx	21.9	25.7	49.7	20.4	50.7	26.2

Table ABJ. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5113, Run 228738816	Rel. Exp.(%) Ag5124, Run 228745551	Tissue Name	Rel. Exp.(%) Ag5113, Run 228738816	Rel. Exp.(%) Ag5124, Run 228745551
Adipose	3.6	3.3	Renal ca. TK-10	0.0	0.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	1.2	2.4
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.1	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.1	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW-948	0.0	0.0
Melanoma* SK- MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0

Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	3.9	5.9	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.1	0.0	Colon ca. HCT-116	0.1	0.5
Prostate Pool	7.3	5.0	Colon ca. CaCo-2	0.0	0.0
Placenta	0.1	0.0	Colon cancer tissue	0.5	1.3
Uterus Pool	4.7	4.1	Colon ca. SW1116	0.0	0.4
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.1	0.0
Ovarian ca. SK-OV-3	0.2	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.1	0.0	Colon Pool	2.1	5.5
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	2.4	2.8
Ovarian ca. IGROV-1	0.0	1.4	Stomach Pool	2.0	3.2
Ovarian ca. OVCAR-8	0.3	0.0	Bone Marrow Pool	3.0	1.8
Ovary	0.5	2.5	Fetal Heart	0.2	0.0
Breast ca. MCF-7	0.2	0.6	Heart Pool	2.4	1.9
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	8.5	9.3
Breast ca. BT 549	0.3	1.4	Fetal Skeletal Muscle	1.4	2.1
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	1.1	1.7
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.3	0.0
Breast Pool	4.2	3.7	Thymus Pool	1.1	0.0
Trachea	6.0	4.2	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	3.2	2.3	CNS cancer (glio/astro) U-118-MG	0.0	0.9
Fetal Lung	100.0	100.0	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.3	0.5
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.6
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.2	1.0

Lung ca. SHP-77	0.0	0.0	CNS cancer (glio) SF-295	0.0	1.9
Lung ca. A549	0.0	0.0	Brain (Amygdala) Pool	0.0	0.0
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	0.0	0.0
Lung ca. NCI-H23	0.0	0.0	Brain (fetal)	0.2	0.5
Lung ca. NCI-H460	0.1	0.0	Brain (Hippocampus) Pool	0.5	0.8
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	0.3	0.0
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	0.1	0.0
Liver	0.0	0.0	Brain (Thalamus) Pool	0.0	0.0
Fetal Liver	0.2	0.0	Brain (whole)	0.3	0.5
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	0.0	0.4
Kidney Pool	13.2	8.2	Adrenal Gland	0.6	2.0
Fetal Kidney	0.3	1.5	Pituitary gland Pool	0.2	0.0
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.0	0.0
Renal ca. A498	0.0	0.0	Thyroid (female)	0.3	0.4
Renal ca. ACHN	1.3	0.4	Pancreatic ca. CAPAN2	0.0	0.0
Renal ca. UO-31	0.0	0.0	Pancreas Pool	1.7	3.8

Table ABK. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7237, Run 296433071	Tissue Name	Rel. Exp.(%) Ag7237, Run 296433071
Adipose	19.9	Renal ca. TK-10	2.4
Melanoma* Hs688(A).T	0.2	Bladder	19.2
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	45.7
Melanoma* M14	0.0	Gastric ca. KATO III	11.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	9.1
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.5
Squamous cell carcinoma SCC-4	1.9	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	5.0	Colon ca. HT29	12.4
Prostate ca.* (bone met) PC-3	0.3	Colon ca. HCT-116	10.0
Prostate Pool	44.1	Colon ca. CaCo-2	17.4
Placenta	1.0	Colon cancer tissue	5.9
Uterus Pool	2.0	Colon ca. SW1116	4.8
Ovarian ca. OVCAR-3	5.6	Colon ca. Colo-205	4.2

Ovarian ca. SK-OV-3	18.0	Colon ca. SW-48	10.1
Ovarian ca. OVCAR-4	0.0	Colon Pool	5.8
Ovarian ca. OVCAR-5	4.7	Small Intestine Pool	6.3
Ovarian ca. IGROV-1	10.9	Stomach Pool	4.3
Ovarian ca. OVCAR-8	0.9	Bone Marrow Pool	6.4
Ovary	2.3	Fetal Heart	6.0
Breast ca. MCF-7	71.7	Heart Pool	4.5
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	18.0
Breast ca. BT 549	12.2	Fetal Skeletal Muscle	12.8
Breast ca. T47D	6.2	Skeletal Muscle Pool	0.6
Breast ca. MDA-N	0.0	Spleen Pool	5.7
Breast Pool	7.5	Thymus Pool	6.9
Trachea	10.7	CNS cancer (glio/astro) U87-MG	0.0
Lung	2.4	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	100.0	CNS cancer (neuro;met) SK-N-AS	0.1
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	1.7
Lung ca. LX-1	5.2	CNS cancer (astro) SNB- 75	0.7
Lung ca. NCI-H146	7.9	CNS cancer (glio) SNB- 19	12.7
Lung ca. SHP-77	0.7	CNS cancer (glio) SF-295	0.2
Lung ca. A549	0.7	Brain (Amygdala) Pool	3.0
Lung ca. NCI-H526	0.3	Brain (cerebellum)	0.6
Lung ca. NCI-H23	4.5	Brain (fetal)	24.8
Lung ca. NCI-H460	0.5	Brain (Hippocampus) Pool	7.5
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	3.7
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.9
Liver	0.0	Brain (Thalamus) Pool	5.5
Fetal Liver	1.3	Brain (whole)	6.1
Liver ca. HepG2	2.7	Spinal Cord Pool	1.0
Kidney Pool	0.0	Adrenal Gland	3.1
Fetal Kidney	23.2	Pituitary gland Pool	5.8
Renal ca. 786-0	0.0	Salivary Gland	0.7
Renal ca. A498	0.0	Thyroid (female)	47.3
Renal ca. ACHN	47.6	Pancreatic ca. CAPAN2	0.7
Renal ca. UO-31	0.0	Pancreas Pool	9.6

Table ABL. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2505, Run 165531061	Rel. Exp.(%) Ag2667, Run 162554578	Rel. Exp.(%) Ag2767, Run 165527179	Rel. Exp.(%) Ag2831, Run 165517578
Liver adenocarcinoma	1.8	0.0	0.0	1.3
Pancreas	13.7	8.9	35.4	14.1
Pancreatic ca. CAPAN 2	1.5	2.0	0.0	2.0
Adrenal gland	3.6	2.9	2.8	4.6
Thyroid	100.0	52.5	100.0	67.8
Salivary gland	4.1	2.3	9.3	2.5
Pituitary gland	37.6	9.9	18.7	19.8
Brain (fetal)	44.1	6.8	40.9	28.5
Brain (whole)	9.3	0.6	11.2	0.0
Brain (amygdala)	8.1	4.4	8.2	2.6
Brain (cerebellum)	1.8	0.8	0.0	4.4
Brain (hippocampus)	10.2	1.6	6.4	2.2
Brain (substantia nigra)	29.3	3.7	12.5	11.0
Brain (thalamus)	3.6	1.9	8.7	7.2
Cerebral Cortex	7.7	8.8	3.8	1.3
Spinal cord	15.2	14.4	13.3	10.4
glio/astro U87-MG	0.0	0.0	0.0	0.0
glio/astro U-118-MG	0.0	0.0	0.0	0.0
astrocytoma SW1783	0.3	0.6	0.0	1.0
neuro*; met SK-N-AS	0.4	0.0	0.0	0.0
astrocytoma SF-539	1.8	1.2	2.5	1.2
astrocytoma SNB-75	2.7	0.6	0.0	2.0
glioma SNB-19	0.0	0.0	0.0	0.0
glioma U251	9.3	2.0	12.2	9.1
glioma SF-295	0.4	0.0	2.6	1.3
Heart (fetal)	10.0	24.7	9.6	7.4
Heart	3.1	0.0	2.4	2.4
Skeletal muscle (fetal)	12.8	66.4	7.7	1.3
Skeletal muscle	20.9	2.1	7.5	13.1
Bone marrow	1.2	1.9	4.5	0.9
Thymus	6.0	24.0	17.8	4.9
Spleen	6.7	5.0	19.8	9.2
Lymph node	6.7	1.4	5.4	2.6
Colorectal	23.5	19.3	6.5	9.9
Stomach	12.0	1.8	4.5	2.5
Small intestine	54.3	13.3	69.7	43.2
Colon ca. SW480	1.1	0.5	0.0	0.0
Colon ca.* SW620(SW480 met)	1.4	0.0	2.8	3.1
Colon ca. HT29	7.3	28.3	11.3	5.3

Colon ca. HCT-116	7.3	9.0	12.4	10.2
Colon ca. CaCo-2	10.7	29.7	19.6	11.1
Colon ca. tissue(ODO3866)	8.5	14.6	10.6	10.6
Colon ca. HCC-2998	2.9	6.3	19.8	2.9
Gastric ca.* (liver met) NCI-N87	71.7	49.7	95.3	100.0
Bladder	14.8	44.4	29.7	20.4
Trachea	21.9	13.9	18.6	5.5
Kidney	38.2	74.2	56.3	67.4
Kidney (fetal)	27.5	37.1	40.1	33.9
Renal ca. 786-0	0.0	0.0	0.0	0.0
Renal ca. A498	0.2	1.7	3.7	2.9
Renal ca. RXF 393	39.8	5.9	20.3	10.8
Renal ca. ACHN	51.1	6.8	20.2	7.2
Renal ca. UO-31	0.2	0.0	0.0	0.0
Renal ca. TK-10	0.0	0.0	0.0	0.0
Liver	1.4	0.7	0.0	3.5
Liver (fetal)	2.3	0.0	4.0	1.2
Liver ca. (hepatoblast) HepG2	11.8	4.7	19.5	10.8
Lung	75.3	46.0	91.4	84.1
Lung (fetal)	54.7	100.0	92.0	64.6
Lung ca. (small cell) LX-1	5.5	2.5	5.8	4.1
Lung ca. (small cell) NCI-H69	5.6	6.2	10.1	5.3
Lung ca. (s.cell var.) SHP-77	0.2	0.6	0.0	0.0
Lung ca. (large cell) NCI-H460	1.2	0.0	0.0	0.0
Lung ca. (non-sm. cell) A549	1.2	0.7	3.1	1.3
Lung ca. (non-s.cell) NCI-H23	3.2	4.7	8.2	4.5
Lung ca. (non-s.cell) HOP-62	0.0	0.0	0.0	0.0
Lung ca. (non-s.cl) NCI-H522	0.0	0.0	0.0	0.0
Lung ca. (squam.) SW 900	1.8	0.0	3.4	2.0
Lung ca. (squam.) NCI-H596	14.6	10.9	31.6	53.6
Mammary gland	11.9	4.9	23.8	17.4
Breast ca.* (pl.ef) MCF-7	89.5	92.7	84.1	80.1

Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0	0.0	0.0
Breast ca.* (pl.ef) T47D	24.7	7.6	20.3	9.9
Breast ca. BT-549	2.3	0.0	0.0	1.2
Breast ca. MDA-N	0.0	0.0	0.0	0.0
Ovary	3.5	20.3	8.5	4.9
Ovarian ca. OVCAR-3	6.4	2.6	8.2	4.5
Ovarian ca. OVCAR-4	0.0	0.0	0.0	0.0
Ovarian ca. OVCAR-5	0.0	0.0	0.0	0.0
Ovarian ca. OVCAR-8	0.2	1.0	0.0	0.0
Ovarian ca. IGROV-1	14.5	17.6	31.6	33.7
Ovarian ca.* (ascites) SK-OV-3	9.3	5.4	20.7	22.5
Uterus	27.7	3.5	39.0	46.3
Placenta	2.9	4.9	6.4	8.9
Prostate	25.0	8.8	16.7	16.7
Prostate ca.* (bone met)PC-3	0.0	0.0	0.0	0.0
Testis	2.5	0.7	4.4	2.7
Melanoma Hs688(A).T	0.0	0.0	0.0	0.0
Melanoma* (met) Hs688(B).T	0.0	0.0	0.0	0.0
Melanoma UACC-62	0.0	0.0	0.0	0.0
Melanoma M14	0.0	0.0	0.0	0.0
Melanoma LOX IMVI	0.0	0.0	0.0	0.0
Melanoma* (met) SK- MEL-5	0.0	0.0	0.0	0.0
Adipose	19.3	6.5	4.3	22.1

Table ABM. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag2831, Run 175063921	Tissue Name	Rel. Exp.(%) Ag2831, Run 175063921
Normal Colon	4.7	Kidney Margin (OD04348)	100.0
Colon cancer (OD06064)	24.7	Kidney malignant cancer (OD06204B)	0.0
Colon Margin (OD06064)	12.0	Kidney normal adjacent tissue (OD06204E)	7.0
Colon cancer (OD06159)	1.1	Kidney Cancer (OD04450-01)	1.2
Colon Margin (OD06159)	6.2	Kidney Margin (OD04450-03)	16.6
Colon cancer (OD06297- 04)	1.9	Kidney Cancer 8120613	1.8

Colon Margin (OD06297-05)	6.9	Kidney Margin 8120614	5.7
CC Gr.2 ascend colon (ODO3921)	0.4	Kidney Cancer 9010320	0.6
CC Margin (ODO3921)	2.7	Kidney Margin 9010321	2.6
Colon cancer metastasis (OD06104)	2.4	Kidney Cancer 8120607	6.2
Lung Margin (OD06104)	10.2	Kidney Margin 8120608	2.3
Colon mets to lung (OD04451-01)	7.0	Normal Uterus	13.4
Lung Margin (OD04451-02)	20.4	Uterine Cancer 064011	0.8
Normal Prostate	4.9	Normal Thyroid	6.1
Prostate Cancer (OD04410)	5.9	Thyroid Cancer 064010	28.5
Prostate Margin (OD04410)	8.3	Thyroid Cancer A302152	46.3
Normal Ovary	1.9	Thyroid Margin A302153	21.0
Ovarian cancer (OD06283-03)	1.2	Normal Breast	10.2
Ovarian Margin (OD06283-07)	3.6	Breast Cancer (OD04566)	1.5
Ovarian Cancer 064008	7.8	Breast Cancer 1024	4.6
Ovarian cancer (OD06145)	0.9	Breast Cancer (OD04590-01)	62.0
Ovarian Margin (OD06145)	0.9	Breast Cancer Mets (OD04590-03)	98.6
Ovarian cancer (OD06455-03)	0.0	Breast Cancer Metastasis (OD04655-05)	70.7
Ovarian Margin (OD06455-07)	7.3	Breast Cancer 064006	3.6
Normal Lung	14.2	Breast Cancer 9100266	3.4
Invasive poor diff. lung adeno (ODO4945-01)	1.5	Breast Margin 9100265	2.9
Lung Margin (ODO4945-03)	15.5	Breast Cancer A209073	1.7
Lung Malignant Cancer (OD03126)	4.2	Breast Margin A2090734	2.5
Lung Margin (OD03126)	8.3	Breast cancer (OD06083)	49.7
Lung Cancer (OD05014A)	5.4	Breast cancer node metastasis (OD06083)	64.2
Lung Margin (OD05014B)	41.5	Normal Liver	0.5
Lung cancer (OD06081)	3.8	Liver Cancer 1026	0.5
Lung Margin (OD06081)	37.6	Liver Cancer 1025	1.8
Lung Cancer (OD04237-01)	1.6	Liver Cancer 6004-T	0.0
Lung Margin (OD04237-02)	33.2	Liver Tissue 6004-N	1.3

Ocular Melanoma Metastasis	0.0	Liver Cancer 6005-T	0.5
Ocular Melanoma Margin (Liver)	0.0	Liver Tissue 6005-N	1.4
Melanoma Metastasis	0.0	Liver Cancer 064003	0.0
Melanoma Margin (Lung)	37.9	Normal Bladder	2.8
Normal Kidney	5.5	Bladder Cancer 1023	2.5
Kidney Ca, Nuclear grade 2 (OD04338)	26.6	Bladder Cancer A302173	6.2
Kidney Margin (OD04338)	0.9	Normal Stomach	2.8
Kidney Ca Nuclear grade 1/2 (OD04339)	2.0	Gastric Cancer 9060397	0.0
Kidney Margin (OD04339)	10.3	Stomach Margin 9060396	1.4
Kidney Ca, Clear cell type (OD04340)	4.5	Gastric Cancer 9060395	2.3
Kidney Margin (OD04340)	12.6	Stomach Margin 9060394	4.1
Kidney Ca, Nuclear grade 3 (OD04348)	1.4	Gastric Cancer 064005	5.7

Table ABN. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2667, Run 162558279	Rel. Exp.(%) Ag2767, Run 162555855	Rel. Exp.(%) Ag2831, Run 163578438	Tissue Name	Rel. Exp.(%) Ag2667, Run 162558279	Rel. Exp.(%) Ag2767, Run 162555855	Rel. Exp.(%) Ag2831, Run 163578438
Normal Colon	4.8	4.8	6.1	Kidney Margin 8120608	2.3	2.4	2.0
CC Well to Mod Diff (ODO3866)	1.1	0.8	0.9	Kidney Cancer 8120613	8.5	9.9	9.6
CC Margin (ODO3866)	0.8	1.2	1.5	Kidney Margin 8120614	3.0	3.2	2.8
CC Gr.2 rectosigmoid (ODO3868)	0.8	0.5	0.3	Kidney Cancer 9010320	1.0	1.6	0.9
CC Margin (ODO3868)	0.2	0.2	0.1	Kidney Margin 9010321	3.9	4.6	0.0
CC Mod Diff (ODO3920)	0.2	0.2	0.1	Normal Uterus	1.3	1.1	0.6
CC Margin (ODO3920)	1.0	0.7	0.9	Uterus Cancer 064011	1.6	1.1	1.4

CC Gr.2 ascend colon (ODO3921)	3.8	3.8	3.8	Normal Thyroid	13.9	13.7	10.4
CC Margin (ODO3921)	1.4	1.5	1.0	Thyroid Cancer 064010	33.2	35.1	36.9
CC from Partial Hepatectomy (ODO4309) Mets	6.5	5.6	6.1	Thyroid Cancer A302152	19.3	21.3	21.5
Liver Margin (ODO4309)	0.3	0.4	0.1	Thyroid Margin A302153	41.8	39.8	37.9
Colon mets to lung (OD04451-01)	1.5	1.6	1.2	Normal Breast	1.7	2.4	1.7
Lung Margin (OD04451-02)	3.1	4.0	3.3	Breast Cancer (OD04566)	2.0	2.2	2.5
Normal Prostate 6546-1	10.6	10.5	11.9	Breast Cancer (OD04590- 01)	68.3	69.7	64.2
Prostate Cancer (OD04410)	13.3	13.4	15.2	Breast Cancer Mets (OD04590- 03)	100.0	100.0	100.0
Prostate Margin (OD04410)	8.3	12.1	10.5	Breast Cancer Metastasis (OD04655- 05)	38.7	39.0	33.4
Prostate Cancer (OD04720-01)	2.2	1.7	1.6	Breast Cancer 064006	3.7	4.0	3.9
Prostate Margin (OD04720-02)	5.0	4.5	4.1	Breast Cancer 1024	2.7	2.1	2.7
Normal Lung 061010	15.0	17.3	13.5	Breast Cancer 9100266	2.6	2.3	2.9
Lung Met to Muscle (ODO4286)	0.5	0.5	0.3	Breast Margin 9100265	0.9	0.8	0.6
Muscle Margin (ODO4286)	0.1	0.1	0.0	Breast Cancer A209073	3.5	3.7	3.8
Lung Malignant Cancer (OD03126)	3.7	3.8	3.5	Breast Margin A209073	1.7	1.5	1.5
Lung Margin (OD03126)	15.1	20.4	15.5	Normal Liver	0.2	0.1	0.1

Lung Cancer (OD04404)	4.7	4.2	2.8	Liver Cancer 064003	0.0	0.1	0.2
Lung Margin (OD04404)	12.1	12.9	9.8	Liver Cancer 1025	0.1	0.1	0.0
Lung Cancer (OD04565)	0.6	0.7	0.4	Liver Cancer 1026	0.8	0.5	0.8
Lung Margin (OD04565)	9.9	8.4	8.6	Liver Cancer 6004-T	0.1	0.1	0.1
Lung Cancer (OD04237-01)	1.1	1.5	1.0	Liver Tissue 6004-N	0.8	0.9	0.9
Lung Margin (OD04237-02)	17.4	13.0	14.3	Liver Cancer 6005-T	0.4	0.7	0.5
Ocular Mel Met to Liver (ODO4310)	0.0	0.1	0.0	Liver Tissue 6005-N	0.1	0.1	0.1
Liver Margin (ODO4310)	0.2	0.2	0.3	Normal Bladder	3.5	3.8	4.2
Melanoma Mets to Lung (OD04321)	0.1	0.3	0.2	Bladder Cancer 1023	0.9	0.9	0.6
Lung Margin (OD04321)	21.3	20.7	19.5	Bladder Cancer A302173	3.8	4.6	4.4
Normal Kidney	14.9	18.4	15.2	Bladder Cancer (OD04718-01)	0.6	1.1	1.0
Kidney Ca, Nuclear grade 2 (OD04338)	0.9	1.2	0.6	Bladder Normal Adjacent (OD04718-03)	0.6	0.3	0.8
Kidney Margin (OD04338)	7.3	10.3	7.0	Normal Ovary	0.8	0.7	0.6
Kidney Ca Nuclear grade 1/2 (OD04339)	0.3	0.3	0.6	Ovarian Cancer 064008	7.2	9.6	8.8
Kidney Margin (OD04339)	14.8	11.7	14.6	Ovarian Cancer (OD04768-07)	0.2	0.2	0.1
Kidney Ca, Clear cell type (OD04340)	6.5	7.8	8.1	Ovary Margin (OD04768-08)	1.5	1.8	1.3
Kidney Margin (OD04340)	11.0	9.2	9.8	Normal Stomach	0.5	1.0	0.6
Kidney Ca, Nuclear grade 3 (OD04348)	1.1	0.6	1.1	Gastric Cancer 9060358	0.3	0.2	0.6

Kidney Margin (OD04348)	15.5	11.7	13.5	Stomach Margin 9060359	0.4	0.9	0.8
Kidney Cancer (OD04622-01)	1.7	1.2	1.6	Gastric Cancer 9060395	1.6	2.2	1.3
Kidney Margin (OD04622-03)	3.0	2.7	2.5	Stomach Margin 9060394	0.7	1.2	0.6
Kidney Cancer (OD04450-01)	0.1	0.2	0.3	Gastric Cancer 9060397	0.3	0.3	0.0
Kidney Margin (OD04450-03)	11.6	15.2	14.0	Stomach Margin 9060396	0.3	0.3	0.0
Kidney Cancer 8120607	2.6	2.6	2.9	Gastric Cancer 064005	11.7	16.5	11.6

Table ABO. Panel 3D

Tissue Name	Rel. Exp.(%) Ag2831, Run 164843468	Tissue Name	Rel. Exp.(%) Ag2831, Run 164843468
Daoy- Medulloblastoma	0.4	Ca Ski- Cervical epidermoid carcinoma (metastasis)	9.4
TE671- Medulloblastoma	3.7	ES-2- Ovarian clear cell carcinoma	0.0
D283 Med- Medulloblastoma	6.7	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.0	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	1.2	MEG-01- Chronic myelogenous leukemia (megakaryoblast)	0.7
SNB-78- Glioma	1.7	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	0.0	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	0.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	0.0	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	0.0	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.0	JM1- pre-B-cell lymphoma	0.0
Cerebellum	0.0	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	23.7	TF-1- Erythroleukemia	0.0

DMS-114- Small cell lung cancer	0.0	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	1.1	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	100.0	KU-812- Myelogenous leukemia	0.6
NCI-H526- Small cell lung cancer	5.6	769-P- Clear cell renal carcinoma	3.2
NCI-N417- Small cell lung cancer	0.8	Caki-2- Clear cell renal carcinoma	0.8
NCI-H82- Small cell lung cancer	0.0	SW 839- Clear cell renal carcinoma	0.9
NCI-H157- Squamous cell lung cancer (metastasis)	0.0	G401- Wilms' tumor	0.0
NCI-H1155- Large cell lung cancer	14.6	Hs766T- Pancreatic carcinoma (LN metastasis)	0.0
NCI-H1299- Large cell lung cancer	0.0	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.0
NCI-H727- Lung carcinoid	14.8	SU86.86- Pancreatic carcinoma (liver metastasis)	0.0
NCI-UMC-11- Lung carcinoid	84.1	BxPC-3- Pancreatic adenocarcinoma	0.0
LX-1- Small cell lung cancer	7.5	HPAC- Pancreatic adenocarcinoma	0.0
Colo-205- Colon cancer	18.7	MIA PaCa-2- Pancreatic carcinoma	0.0
KM12- Colon cancer	66.4	CFPAC-1- Pancreatic ductal adenocarcinoma	0.0
KM20L2- Colon cancer	8.4	PANC-1- Pancreatic epithelioid ductal carcinoma	0.6
NCI-H716- Colon cancer	23.2	T24- Bladder carcinoma (transitional cell)	0.0
SW-48- Colon adenocarcinoma	63.7	5637- Bladder carcinoma	0.0
SW1116- Colon adenocarcinoma	15.5	HT-1197- Bladder carcinoma	3.2
LS 174T- Colon adenocarcinoma	62.9	UM-UC-3- Bladder carcinoma (transitional cell)	0.0
SW-948- Colon adenocarcinoma	2.7	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	39.2	HT-1080- Fibrosarcoma	0.0
NCI-SNU-5- Gastric carcinoma	0.0	MG-63- Osteosarcoma	0.0
KATO III- Gastric carcinoma	33.0	SK-LMS-1- Leiomyosarcoma (vulva)	0.0

NCI-SNU-16- Gastric carcinoma	0.0	SJRH30- Rhabdomyosarcoma (met to bone marrow)	27.7
NCI-SNU-1- Gastric carcinoma	35.6	A431- Epidermoid carcinoma	17.8
RF-1- Gastric adenocarcinoma	0.0	WM266-4- Melanoma	10.0
RF-48- Gastric adenocarcinoma	0.7	DU 145- Prostate carcinoma (brain metastasis)	0.0
MKN-45- Gastric carcinoma	96.6	MDA-MB-468- Breast adenocarcinoma	2.7
NCI-N87- Gastric carcinoma	79.6	SCC-4- Squamous cell carcinoma of tongue	0.0
OVCAR-5- Ovarian carcinoma	0.0	SCC-9- Squamous cell carcinoma of tongue	0.0
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.0
HelaS3- Cervical adenocarcinoma	0.0	CAL 27- Squamous cell carcinoma of tongue	1.2

Table ABP. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag2831, Run 244570230	Rel. Exp.(%) Ag5124, Run 225784387	Tissue Name	Rel. Exp.(%) Ag2831, Run 244570230	Rel. Exp.(%) Ag5124, Run 225784387
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	9.0
Secondary Tr1 act	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.0	0.0	HUVEC IL-11	0.0	0.0
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	0.0	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0

Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	11.5	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	Coronary artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	0.0	Astrocytes rest	0.9	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	9.9	0.0
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	0.0	CCD1106 (Keratinocytes) none	0.8	0.0
LAK cells rest	0.0	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	4.5	0.0
LAK cells IL-2	0.0	0.0	Liver cirrhosis	14.9	19.9
LAK cells IL-2+IL- 12	0.0	0.0	NCI-H292 none	19.9	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	62.4	0.0
LAK cells IL-2+ IL- 18	0.0	0.0	NCI-H292 IL-9	57.8	0.0
LAK cells PMA/ionomycin	0.0	0.0	NCI-H292 IL-13	73.2	0.0
NK Cells IL-2 rest	0.0	0.0	NCI-H292 IFN gamma	21.0	0.0
Two Way MLR 3 day	0.0	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.0	0.0	HPAEC TNF alpha + IL-1 beta	3.6	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	17.0	0.0
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	9.7	48.3
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	6.7	0.0
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	1.6	17.1
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	21.3	26.2
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	1.3	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	0.0

EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	0.0	0.0
Dendritic cells none	0.0	0.0	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	0.0	0.0	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti- CD40	0.0	0.0	Neutrophils TNFa+LPS	0.0	0.0
Monocytes rest	0.0	0.0	Neutrophils rest	0.0	0.0
Monocytes LPS	0.0	0.0	Colon	2.2	8.7
Macrophages rest	0.0	0.0	Lung	2.1	100.0
Macrophages LPS	0.0	0.0	Thymus	1.8	0.0
HUVEC none	0.0	0.0	Kidney	100.0	36.9
HUVEC starved	0.0	0.0			

Table ABQ. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2505, Run 164318134	Rel. Exp.(%) Ag2667, Run 158912431	Rel. Exp.(%) Ag2767, Run 162015289	Rel. Exp.(%) Ag2831, Run 162350949
Secondary Th1 act	0.0	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0	0.0
Secondary Tr1 act	0.2	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	0.4
Primary Th1 act	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.0	0.0	0.0
Primary Tr1 act	0.1	0.0	0.0	0.0
Primary Th1 rest	0.1	0.0	0.0	0.4
Primary Th2 rest	0.0	0.0	0.0	0.0
Primary Tr1 rest	0.1	0.0	0.3	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	0.0	0.0
CD8 lymphocyte act	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	0.0	0.0	0.0

LAK cells rest	0.0	0.0	0.0	0.0
LAK cells IL-2	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	0.0	0.0	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	0.0	0.0
Two Way MLR 3 day	0.0	0.0	0.0	0.0
Two Way MLR 5 day	0.0	0.0	0.0	0.0
Two Way MLR 7 day	0.0	0.0	0.0	0.0
PBMC rest	0.0	0.0	0.0	0.0
PBMC PWM	0.1	0.0	0.0	0.0
PBMC PHA-L	0.0	0.6	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.3	0.0	0.0
B lymphocytes PWM	0.2	0.3	0.9	0.7
B lymphocytes CD40L and IL-4	0.1	0.7	0.0	0.0
EOL-1 dbcAMP	0.0	0.0	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0	0.0
Dendritic cells none	0.1	0.0	0.0	0.3
Dendritic cells LPS	0.0	0.0	0.0	0.0
Dendritic cells anti-CD40	0.0	0.0	0.0	0.0
Monocytes rest	0.0	0.0	0.0	0.0
Monocytes LPS	0.0	0.0	0.0	0.0
Macrophages rest	0.0	0.0	0.3	0.0
Macrophages LPS	0.0	0.0	0.0	0.0
HUVEC none	0.0	0.0	0.0	0.0
HUVEC starved	0.3	0.0	0.0	0.0
HUVEC IL-1beta	0.2	0.3	0.0	0.0
HUVEC IFN gamma	0.1	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.7
HUVEC TNF alpha + IL4	0.1	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.3	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0

Microvascular Dermal EC TNFalpha + IL-1beta	0.2	0.0	1.4	0.0
Bronchial epithelium TNFalpha + IL1beta	2.0	0.0	1.2	0.0
Small airway epithelium none	0.5	0.0	0.0	0.4
Small airway epithelium TNFalpha + IL-1beta	19.6	10.4	11.7	8.4
Coronary artery SMC rest	0.0	0.0	0.0	0.0
Coronary artery SMC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Astrocytes rest	2.0	2.6	1.9	2.3
Astrocytes TNFalpha + IL-1beta	2.0	4.6	8.2	4.4
KU-812 (Basophil) rest	0.0	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.3	0.0	0.0
CCD1106 (Keratinocytes) none	0.4	0.4	0.8	0.6
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.3	0.0	2.0	1.5
Liver cirrhosis	7.5	3.4	8.0	4.7
Lupus kidney	13.3	6.5	12.2	5.4
NCI-H292 none	21.8	11.0	14.9	15.5
NCI-H292 IL-4	42.0	36.1	43.5	44.4
NCI-H292 IL-9	41.8	48.3	32.8	28.1
NCI-H292 IL-13	20.9	17.2	30.4	21.6
NCI-H292 IFN gamma	14.4	12.9	14.6	10.2
HPAEC none	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.5	0.9	1.1	1.0
Lung fibroblast none	4.5	2.4	2.6	4.5
Lung fibroblast TNF alpha + IL-1 beta	0.3	0.2	0.0	0.0
Lung fibroblast IL-4	14.6	6.3	9.0	8.8
Lung fibroblast IL-9	3.9	1.0	8.6	2.9
Lung fibroblast IL-13	8.7	5.6	5.9	3.5
Lung fibroblast IFN gamma	14.9	3.8	6.7	4.5
Dermal fibroblast CCD1070 rest	0.0	0.0	0.0	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	0.0	0.0	0.0
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0	0.0	0.0

Dermal fibroblast IFN gamma	0.0	0.0	0.0	0.0
Dermal fibroblast IL-4	0.2	0.8	0.8	0.0
IBD Colitis 2	0.3	0.0	0.4	0.4
IBD Crohn's	9.9	4.1	2.7	3.6
Colon	41.2	20.9	27.5	20.0
Lung	61.6	35.1	34.6	35.4
Thymus	100.0	100.0	100.0	100.0
Kidney	21.3	13.9	14.9	14.0

Table ABR. Panel 5 Islet.

Tissue Name	Rel. Exp.(%) Ag2505, Run 248045752	Tissue Name	Rel. Exp.(%) Ag2505, Run 248045752
97457_Patient-02go_adipose	32.3	94709_Donor 2 AM - A_adipose	0.0
97476_Patient-07sk_skeletal muscle	8.2	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-07ut_uterus	31.4	94711_Donor 2 AM - C_adipose	0.0
97478_Patient-07pl_placenta	3.5	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	9.5	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	90.1	94714_Donor 2 AD - C_adipose	0.0
97483_Patient-08pl_placenta	7.4	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	1.4	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	78.5	94730_Donor 3 AM - A_adipose	0.0
97488_Patient-09pl_placenta	0.6	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	66.0	94732_Donor 3 AM - C_adipose	0.2
97493_Patient-10pl_placenta	3.1	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	28.3	94734_Donor 3 AD - B_adipose	0.0
97496_Patient-11sk_skeletal muscle	5.8	94735_Donor 3 AD - C_adipose	0.0
97497_Patient-11ut_uterus	35.4	77138_Liver_HepG2untreated	21.2
97498_Patient-11pl_placenta	2.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	35.1	81735_Small Intestine	36.9

97501_Patient-12sk_skeletal muscle	9.9	72409_Kidney_Proximal Convoluted Tubule	4.6
97502_Patient-12ut_uterus	100.0	82685_Small intestine_Duodenum	27.0
97503_Patient-12pl_placenta	4.1	90650_Adrenal_Adrenocortical adenoma	0.3
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	7.2
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	10.7
94723_Donor 2 U - C_Mesenchymal Stem Cells	0.0	73139_Uterus_Uterine smooth muscle cells	0.0

Table ABS. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag2505, Run 267145080	Rel. Exp.(%) Ag5113, Run 260280405	Rel. Exp.(%) Ag5124, Run 259936347
Colon cancer 1	7.7	3.7	9.3
Colon NAT 1	2.5	1.3	3.6
Colon cancer 2	26.4	0.9	9.5
Colon NAT 2	8.4	2.8	0.0
Colon cancer 3	38.2	5.1	20.0
Colon NAT 3	16.7	14.0	18.6
Colon malignant cancer 4	69.7	1.9	20.3
Colon NAT 4	8.7	8.7	4.4
Lung cancer 1	7.2	2.4	5.3
Lung NAT 1	8.0	6.0	16.5
Lung cancer 2	26.1	8.4	67.8
Lung NAT 2	17.4	15.2	69.3
Squamous cell carcinoma 3	19.6	12.8	76.8
Lung NAT 3	8.3	2.6	0.0
Metastatic melanoma 1	14.5	11.5	36.1
Melanoma 2	1.1	0.0	0.0
Melanoma 3	2.5	0.8	1.4
Metastatic melanoma 4	13.5	7.3	100.0
Metastatic melanoma 5	12.6	11.0	99.3
Bladder cancer 1	1.0	2.0	0.0
Bladder NAT 1	0.0	0.0	0.0
Bladder cancer 2	2.4	3.5	6.0

Bladder NAT 2	0.3	0.5	0.0
Bladder NAT 3	0.7	0.0	0.0
Bladder NAT 4	1.5	0.0	12.5
Prostate adenocarcinoma 1	100.0	100.0	0.0
Prostate adenocarcinoma 2	12.9	5.6	2.8
Prostate adenocarcinoma 3	15.1	1.7	6.8
Prostate adenocarcinoma 4	15.9	2.1	18.2
Prostate NAT 5	14.7	2.3	0.0
Prostate adenocarcinoma 6	13.1	2.0	9.2
Prostate adenocarcinoma 7	16.2	8.1	35.6
Prostate adenocarcinoma 8	4.5	2.3	0.0
Prostate adenocarcinoma 9	33.4	21.0	69.3
Prostate NAT 10	7.7	0.9	0.0
Kidney cancer 1	9.6	1.1	18.0
Kidney NAT 1	33.4	4.0	27.4
Kidney cancer 2	19.8	6.0	65.1
Kidney NAT 2	64.6	10.2	31.6
Kidney cancer 3	7.1	1.6	2.2
Kidney NAT 3	29.7	1.7	12.7
Kidney cancer 4	8.5	5.2	12.8
Kidney NAT 4	7.9	2.1	26.6

AI_comprehensive_panel_v1.0 Summary: Ag2505/Ag2831 Two experiments with different probes and primer sets are in excellent agreement, with highest expression of this gene seen in rheumatoid arthritis bone (CT=27-29). This gene shows ubiquitous expression, but expression of this gene is higher in bone, synovium, cartilage and synovial fluid from RA patients as compared to expression in samples from OA patients, normal and diseased lung. Expression of this gene is downregulated in Crohn's samples as compared to the corresponding control samples. This gene encode a putative novel adhesion molecule which is homologous to mouse POEM (preosteoblast epidermal growth factor-like repeat protein with meprin) or nephronectin. Murine nephronectin may function in multiple biological processes including development of the kidney (1) and bone (2) and contribute to liver and lung fibrosis (3). Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory diseases such as rheumatoid and

osteoarthritis, Inflammatory bowel disease, COPD, asthma, psoriasis, liver and lung fibrosis.

References:

1. Miner JH. J Cell Biol 2001 Jul 23;154(2):257-9, PMID: 11470814.
- 5 2. Morimura N *et al.*, 2001, J. Biol. Chem. 2000 Nov 9;276(45):42172-42181, PMID: 11546798.
3. Levine *et al.*, 2000, Am J Pathol 2000 Jun;156(6):1927-35, PMID: 10854216.

CNS_neurodegeneration_v1.0

Summary: Ag2505/Ag2667/Ag2767/Ag2831/Ag7237 Six experiments with three different
10 probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. This gene is found to be upregulated in the temporal cortex of Alzheimer's disease patients. This gene codes for a homolog of mouse POEM (Nephronectin short isoform), a cell adhesion molecule with EGF domains. Alpha secretase activity, which is generally believed to be a beneficial
15 processing alternative to beta secretase, is increased by EGF in neuronal cells (1). This suggests the increased expression of this gene observed here is a compensatory action in the brain to counter the mechanisms of Alzheimer's Disease. Therefore, the protein encoded by this gene may be a potential therapeutic agent for the treatment of Alzheimer's disease and other neurodegenerative diseases.

20 EGF is also known to facilitate long term potentiation (LTP) in the hippocampus, a process thought to underlie learning and memory (2). Therefore, this gene may have utility in treating disorders of memory, such as neurodegenerative diseases and aging, when used alone or in combination with other growth factors such as bFGF.

In addition, EGF supports the growth and differentiation of dopaminergic neurons
25 (3), which are selectively vulnerable to loss in Parkinson's disease. Therefore, this gene product may have utility in treating Parkinson's Disease.

Ag5113 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

References:

- 30 1. Slack BE, Breu J, Muchnicki L, Wurtman RJ, 1997, Biochem J 327 (Pt 1):245-9.

2. Abe K, Ishiyama J, Saito H, 1992, Brain Res 593(2):335-8.

3. Storch A, Paul G, Csete M, Boehm BO, Carvey PM, Kupsch A, Schwarz J, 2001, Exp Neurol 170(2):317-25.

General_screening_panel_v1.5 Summary: Ag5113/Ag5124 Highest expression
5 of this gene is detected in fetal lung (CT=29). Low but significant expression of this gene is
also seen in tissues with metabolic function including adipose, pancreas, and gastrointestinal
tract. See panel 1.3 for further discussion of this gene.

General_screening_panel_v1.6 Summary: Ag7237 Highest expression of this
gene is detected in fetal lung (CT=27). Expression of this gene is higher in fetal (CTs=27-
10 33) as compared to corresponding adult lung, kidney, liver and skeletal muscle tissues
(CT=32-40). Therefore, expression of this gene may be used to distinguish between these
fetal and adult tissues. In addition, the relative overexpression of this gene in fetal tissue
suggests that the protein product may enhance growth or development of these tissues in the
fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic
15 modulation of the protein encoded by this gene could be useful in treatment of lung, liver,
kidney and muscle related diseases.

Moderate to low levels of expression of this gene is also seen in cancer cell lines
derived from squamous cell carcinoma, brain, colon, renal, lung, breast, and ovarian
cancers. Therefore, expression of this gene may be useful as diagnostic marker for detection
20 of these cancers. Furthermore, therapeutic modulation of this gene may be useful in the
treatment of squamous cell carcinoma, brain, colon, renal, lung, breast, and ovarian cancers.

Moderate to low levels of expression of this gene is also seen in tissues with
metabolic/endocrine functions and also in all the regions of brain. See panel 1.3D for further
discussion of this gene.

Panel 1.3D Summary: Ag2505/Ag2667/Ag2767/Ag2831 Four experiments with
25 two different probes and primer sets are in good agreement. Highest expression of this gene
is detected in the thyroid and fetal lung (CTs=29-31). Moderate to low levels of expression
of this gene is also seen in other tissues with metabolic/endocrine functions, including
skeletal muscle, fetal skeletal muscle, small intestine, stomach, pancreas, adipose and fetal
30 heart. Very low levels are also seen in heart and placenta. Nephronectin is the ligand for the
alpha8beta1 integrin as evidenced by two independent sets of published data (1,4). Integrins

are known to mediate development and organogenesis (5,6). Nephronectin can bind integrins including alpha5beta3, alpha5beta5, alpha5beta6 and alpha4beta7, but not alpha4beta1, alpha3beta1, alpha2beta1 or alpha1beta1. Nephronectin interacts with integrins via the RGD sequence, but RGD alone is not sufficient for binding, the MAM domain is
5 also required (2). MAM domains are thought to have an adhesive function. Thus, modulation of the expression or activity of this gene product by protein or antibody therapeutics may be an effective therapeutic for disorders involving alpha8beta1 integrin signaling including inflammatory diseases.

Obesity has also been linked as an inflammatory condition (7) and thus humanized
10 antibodies may also be therapeutically relevant in treating this condition and related complications such as type II diabetes.

Overall, this gene is expressed at a low to moderate level in the normal tissues on this panel. Furthermore, the brain, prostate, lung and colon cancer cell lines show a very low level of expression compared to the normal organs. This suggests that this molecule can
15 potentially be used as a therapeutic inhibitor for these cancers.

Moderate to low levels of expression is seen in all the regions of the central nervous system including substantia nigra, hippocampus, cortex, amygdala, thalamus and spinal cord. POEM is a ligand for alpha8beta1 integrin, which in turn promotes attachment, cell spreading, and neurite outgrowth on fibronectin (8). See CNS_neurodegeneration_v1.0 for
20 discussion of this gene in the central nervous system.

Reference:

4. Brandenberger R *et al.*, 2001, J Cell Biol 154(2):447-58, PMID: 11470831.
5. Schwartz *et al.*, 1995, Annu. Rev. Cell Dev. Biol. 11, 549-599, PMID: 8689569.
6. Clark and Brugge, 1995, Science 268, 233-239, PMID: 7716514.
- 25 7. Das UN, 2001, Nutrition 17(11-12):953-66, PMID: 11744348.
8. Muller *et al.*, 1995, Mol Biol Cell 6(4):433-48, PMID: 7626807

Panel 2.2 Summary: Ag2831 Highest expression of this gene is detected in kidney (CT=30.3). Expression of this gene is down regulated in kidney, lung and colon cancer as compared to the corresponding normal adjacent tissue. Conversely, increased expression of
30 this gene is seen in breast cancer samples. Therefore, expression of this gene may be used to

distinguish between cancer and normal kidney, lung, colon and breast. In addition, therapeutic modulation of this gene or its protein product in the form of protein therapeutic or through the use of antibodies may be useful in the treatment of kidney, lung, colon and breast cancer.

5 **Panel 2D Summary:** Ag2667/Ag2767/Ag2831 Three experiments with same probe and primer sets are in excellent agreement, with highest expression of this gene in metastatic breast cancer sample (CTs=26). Expression of this gene in this panel correlates with the expression pattern seen in panel 2.2. See panel 2.2 for further discussion of this gene.

10 **Panel 3D Summary:** Ag2831 Highest expression of this gene is detected in a small cell lung cancer NCI-H146 cell line (CT=29.7). Moderate to low levels of expression of this gene is also seen in cancer cell lines derived from epidermoid carcinoma, rhabdomyosarcoma, gastric, colon and small cell lung cancers. Therefore, expression of this gene may be used as diagnostic marker for detection of these cancers. Furthermore,
15 therapeutic modulation of this gene or its protein product through the use of antibodies may be useful in the treatment of these cancers.

Panel 4.1D Summary: Ag2831 Highest expression of this gene is detected in kidney (CT=31.3). In addition, moderate to low levels of expression of this gene is mainly seen in lung fibroblasts, and mucoepidermoid NCI-H292 cells. Expression of this gene is
20 upregulated in cytokine treated NCI-H292 cells, small airway epithelium and astrocytes. This expression pattern correlates with the expression observed in panel 4D. See panel 4D and AI panel for further discussion of this gene.

 Ag5113/Ag5124 Highest expression of this gene is seen in lung (CT=33). Low levels of expression of this gene is also seen in kidney and IL-4 treated lung fibroblasts.

25 **Panel 4D Summary:** Ag 2505 Highest expression of this transcript is found in the thymus and the lung(CTs=27-28). Consistent with this lung expression, this transcript is found in the pulmonary mucoepidermoid cell line H292 and is up-regulated upon treatment with the Th2 cytokines IL4 and IL9. This gene is also expressed at lower levels in lung fibroblasts treated with IL4. This transcript profile suggests that modulation of the
30 expression or activity of this gene product by protein or antibody therapeutics may be

beneficial for the treatment of inflammatory lung diseases such as asthma, emphysema and chronic obstructive pulmonary diseases.

Furthermore, therapeutics designed with the protein encoded for by this transcript could be important for maintaining or restoring normal function of thymus during
5 inflammation.

Panel 5 Islet Summary: Ag2505 Highest expression of this gene is detected in uterus (CT=30). Moderate expression of this gene is also seen in adipose and skeletal muscle of gestational diabetic patients requiring and not requiring daily injections of insulin. This gene is also expressed in samples derived from pregnant and a nondiabetic, but
10 overweight patient. In addition, this gene is also expressed in islet beta cells (those that are insulin producing) and small intestine. Therefore, therapeutic modulation of this gene may be useful in the treatment of metabolically related diseases including obesity, Type I and Type II diabetes.

general oncology screening panel_v_2.4 Summary: Ag2505 Highest expression of this gene is detected in prostate cancer (CT=27.7). Moderate to low levels of expression
15 of this gene is seen in both normal and cancer samples derived from colon, lung, prostate and kidney. As Consistent with panels 2.2 and 2D, expression of this gene is downregulated in kidney cancer as compared to normal kidney. But higher expression of this gene is seen in colon cancer as compared to corresponding normal adjacent sample. Therefore,
20 expression of this gene may be used to distinguish between cancer and normal kidney and colon tissue. See panel 1.3, 1.6, 2.2 for further discussion of this gene.

Ag5113/Ag5124 Highest expression of this gene is seen in metastatic melanoma and prostate cancer (CTs=31-33.7). Significant expression of this gene is seen in cancer samples derived from kidney, lung, and prostate cancers.

25 **AC. CG51264-01, CG51264-06 and CG51264-07: ST7-LIKE PROTEIN (17941787).**

Expression of gene CG51264-01, CG51264-06 and CG51264-07 was assessed using the primer-probe set Ag7547, described in Table ACA. Results of the RTQ-PCR runs are shown in Table ACB.

30 Table ACA. Probe Name Ag7547

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agcattgggatgtacttgaagc-3'	23	1592	363
Probe	TET-5'- ctgtgtttcaaatgatcttctttcaaac a-3'-TAMRA	29	1630	364
Reverse	5'-ttctgcttccactcttgacaa-3'	21	1659	365

Table ACB. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag7547, Run 308743747	Tissue Name	Rel. Exp.(%) Ag7547, Run 308743747
97457_Patient-02go_adipose	3.5	94709_Donor 2 AM - A_adipose	23.3
97476_Patient-07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	23.0
97477_Patient-07ut_uterus	6.1	94711_Donor 2 AM - C_adipose	16.4
97478_Patient-07pl_placenta	1.0	94712_Donor 2 AD - A_adipose	43.5
99167_Bayer Patient 1	4.8	94713_Donor 2 AD - B_adipose	66.0
97482_Patient-08ut_uterus	3.7	94714_Donor 2 AD - C_adipose	47.0
97483_Patient-08pl_placenta	1.4	94742_Donor 3 U - A_Mesenchymal Stem Cells	21.9
97486_Patient-09sk_skeletal muscle	7.3	94743_Donor 3 U - B_Mesenchymal Stem Cells	27.7
97487_Patient-09ut_uterus	4.6	94730_Donor 3 AM - A_adipose	41.2
97488_Patient-09pl_placenta	0.8	94731_Donor 3 AM - B_adipose	43.5
97492_Patient-10ut_uterus	8.0	94732_Donor 3 AM - C_adipose	47.0
97493_Patient-10pl_placenta	3.3	94733_Donor 3 AD - A_adipose	82.4
97495_Patient-11go_adipose	1.7	94734_Donor 3 AD - B_adipose	100.0
97496_Patient-11sk_skeletal muscle	5.9	94735_Donor 3 AD - C_adipose	31.9
97497_Patient-11ut_uterus	14.4	77138_Liver_HepG2untreated	4.5
97498_Patient-11pl_placenta	1.1	73556_Heart_Cardiac stromal cells (primary)	0.5
97500_Patient-12go_adipose	3.7	81735_Small Intestine	4.8
97501_Patient-12sk_skeletal muscle	14.2	72409_Kidney_Proximal Convoluted Tubule	15.5

97502_Patient-12ut_uterus	18.2	82685_Small intestine_Duodenum	3.1
97503_Patient-12pl_placenta	3.0	90650_Adrenal_Adrenocortical adenoma	0.8
94721_Donor 2 U - A_Mesenchymal Stem Cells	30.1	72410_Kidney_HRCE	49.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	39.2	72411_Kidney_HRE	9.5
94723_Donor 2 U - C_Mesenchymal Stem Cells	51.1	73139_Uterus_Uterine smooth muscle cells	23.0

Panel 5 Islet Summary: Ag7547 Highest expression of this gene is detected in differentiated adipose tissue. Moderate levels of expression of this gene is mesenchymal stem cells, midway differentiated and differentiated adipose tissue. Low to moderate levels of expression of this gene is also detected in uterine smooth muscle, skeletal muscle from diabetic patient on insulin and kidney. Therefore, therapeutic modulation of this gene may be useful in the treatment of metabolic related diseases such as obesity, and diabetes.

AD. CG51264-03, and CG51264-04: (17941787-31) ST7-LIKE

PROTEIN.

Expression of gene CG51264-03 and CG51264-04 was assessed using the primer-probe sets Ag2725 and Ag2727, described in Tables ADA and ADB.

Table ADA. Probe Name Ag2725

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgcaactaccagaatcattgc-3'	22	1415	366
Probe	TET-5'- tggcaaacagaacccatctacttggt -3'-TAMRA	26	1442	367
Reverse	5'-tgcaaggggatttaatgctact-3'	22	1469	368

Table ADB. Probe Name Ag2727

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgcaactaccagaatcattgc-3'	22	1415	369
Probe	TET-5'- tggcaaacagaacccatctacttggt -3'-TAMRA	26	1442	370

Reverse	5'-tgcaaggggattttaatgctact-3'	22	1469	371
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AE. CG52423-01: PV1-LIKE PROTEIN (3544179_EXT).

Expression of gene CG52423-01 was assessed using the primer-probe sets Ag1039, Ag1537, Ag760 and Ag4932, described in Tables AEA, AEB, AEC and AED. Results of the RTQ-PCR runs are shown in Tables AEE, AEF, AEG, AEH, AEI, AEJ, AEK, AEL, AEM and AEN.

Table AEA. Probe Name Ag1039

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaggagcaactgcaaaagg-3'	20	753	372
Probe	TET-5'- ctgcccctggacaaggacaagttt-3'-TAMRA	24	786	373
Reverse	5'- acaggttacgaaggtccatctc-3'	22	810	374

Table AEB. Probe Name Ag1537

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaggagctggaagagaagaaga-3'	22	1197	375
Probe	TET-5'- atcagaaactcagccctggacacctg-3'-TAMRA	26	1251	376
Reverse	5'-gctgcgacttggtcttgat-3'	19	1278	377

Table AEC. Probe Name Ag760

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-caccatgacaacgacacctata-3'	22	1924	378
Probe	TET-5'- atatggcaccaacatcacatgcacg-3'-TAMRA	25	1947	379
Reverse	5'-tgggtagaaagtgtgtgtgaaa-3'	22	1979	380

Table AED. Probe Name Ag4932

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aatgcagagatcaattcaagga-3'	22	535	381

Probe	TET-5'- aacaagagctgcgatgccttgctctt -3'-TAMRA	26	561	382
Reverse	5'-tcttcaccttctgattcagcat- 3'	22	588	383

Table AEE. Ardais Panel v.1.0

Tissue Name	Rel. Exp.(%) Ag1537, Run 267680189	Tissue Name	Rel. Exp.(%) Ag1537, Run 267680189
136799_Lung cancer(362)	23.8	136787_lung cancer(356)	8.1
136800_Lung NAT(363)	15.6	136788_lung NAT(357)	52.5
136813_Lung cancer(372)	45.4	136806_Lung cancer(36B)	35.6
136814_Lung NAT(373)	14.4	136807_Lung NAT(36C)	18.8
136815_Lung cancer(374)	39.2	136789_lung cancer(358)	65.1
136816_Lung NAT(375)	100.0	136802_Lung cancer(365)	49.3
136791_Lung cancer(35A)	22.5	136803_Lung cancer(368)	24.5
136795_Lung cancer(35E)	35.4	136804_Lung cancer(369)	38.2
136797_Lung cancer(360)	22.4	136811_Lung cancer(370)	14.9
136794_lung NAT(35D)	14.3	136810_Lung NAT(36F)	31.4
136818_Lung NAT(377)	33.0		

Table AEF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1537, Run 266937073	Rel. Exp.(%) Ag4932, Run 269217367	Tissue Name	Rel. Exp.(%) Ag1537, Run 266937073	Rel. Exp.(%) Ag4932, Run 269217367
AD 1 Hippo	13.1	9.5	Control (Path) 3 Temporal Ctx	4.2	0.0
AD 2 Hippo	14.2	22.1	Control (Path) 4 Temporal Ctx	1.5	5.7
AD 3 Hippo	0.0	3.4	AD 1 Occipital Ctx	5.9	6.8
AD 4 Hippo	3.5	1.9	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 Hippo	23.3	25.7	AD 3 Occipital Ctx	0.0	1.6
AD 6 Hippo	16.6	29.5	AD 4 Occipital Ctx	5.4	4.2
Control 2 Hippo	43.8	28.1	AD 5 Occipital Ctx	25.2	18.8
Control 4 Hippo	100.0	56.6	AD 6 Occipital Ctx	4.3	6.9

Control (Path) 3 Hippo	49.3	100.0	Control 1 Occipital Ctx	0.0	0.0
AD 1 Temporal Ctx	11.5	8.3	Control 2 Occipital Ctx	19.3	14.0
AD 2 Temporal Ctx	28.5	25.3	Control 3 Occipital Ctx	23.5	8.2
AD 3 Temporal Ctx	1.7	0.9	Control 4 Occipital Ctx	3.3	4.1
AD 4 Temporal Ctx	3.8	11.7	Control (Path) 1 Occipital Ctx	15.4	13.5
AD 5 Inf Temporal Ctx	31.0	36.3	Control (Path) 2 Occipital Ctx	7.9	1.1
AD 5 Sup Temporal Ctx	67.8	96.6	Control (Path) 3 Occipital Ctx	0.0	1.0
AD 6 Inf Temporal Ctx	23.7	38.2	Control (Path) 4 Occipital Ctx	0.0	9.0
AD 6 Sup Temporal Ctx	13.3	22.4	Control 1 Parietal Ctx	3.4	0.8
Control 1 Temporal Ctx	0.0	6.3	Control 2 Parietal Ctx	23.7	22.2
Control 2 Temporal Ctx	34.2	28.7	Control 3 Parietal Ctx	4.0	0.0
Control 3 Temporal Ctx	12.9	13.4	Control (Path) 1 Parietal Ctx	28.3	14.0
Control 3 Temporal Ctx	13.0	6.8	Control (Path) 2 Parietal Ctx	5.0	10.0
Control (Path) 1 Temporal Ctx	43.5	26.1	Control (Path) 3 Parietal Ctx	0.0	1.2
Control (Path) 2 Temporal Ctx	12.2	10.0	Control (Path) 4 Parietal Ctx	16.3	12.2

Table AEG. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag4932, Run 228843451	Tissue Name	Rel. Exp.(%) Ag4932, Run 228843451
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	86.5
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	4.5
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca. * (SW480 met) SW620	0.0
Testis Pool	10.7	Colon ca. HT29	0.0
Prostate ca. * (bone met) PC-3	0.0	Colon ca. HCT-116	0.0

Prostate Pool	14.7	Colon ca. CaCo-2	0.0
Placenta	42.6	Colon cancer tissue	51.1
Uterus Pool	53.6	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	89.5
Ovarian ca. OVCAR-5	0.2	Small Intestine Pool	11.7
Ovarian ca. IGROV-1	0.0	Stomach Pool	37.9
Ovarian ca. OVCAR-8	0.1	Bone Marrow Pool	46.0
Ovary	11.1	Fetal Heart	15.1
Breast ca. MCF-7	0.0	Heart Pool	22.2
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	66.9
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	23.2
Breast ca. T47D	0.0	Skeletal Muscle Pool	32.5
Breast ca. MDA-N	0.0	Spleen Pool	100.0
Breast Pool	62.4	Thymus Pool	30.6
Trachea	47.3	CNS cancer (glio/astro) U87-MG	0.0
Lung	4.3	CNS cancer (glio/astro) U-118-MG	0.1
Fetal Lung	17.2	CNS cancer (neuro;met) SK-N-AS	0.1
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.7
Lung ca. A549	0.0	Brain (Amygdala) Pool	1.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	2.0
Lung ca. NCI-H23	0.0	Brain (fetal)	2.6
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	2.1
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	1.3
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.5
Liver	1.2	Brain (Thalamus) Pool	2.5
Fetal Liver	44.1	Brain (whole)	3.8
Liver ca. HepG2	0.0	Spinal Cord Pool	1.9
Kidney Pool	55.1	Adrenal Gland	55.1
Fetal Kidney	73.2	Pituitary gland Pool	10.3
Renal ca. 786-0	0.0	Salivary Gland	20.7
Renal ca. A498	0.1	Thyroid (female)	70.7
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0

Renal ca. UO-31	0.0	Pancreas Pool	53.6
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Table AEH. Oncology_cell_line_screening_panel_v3.2

Tissue Name	Rel. Exp.(%) Ag1537 Run 267177 741	Tissue Name	Rel. Exp.(%) Ag1537, Run 2671777 41
94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	0.0	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	0.2
94906_TE671_Medulloblastoma/Cerebellum_sscDNA	0.0	94955_ES-2_Ovarian clear cell carcinoma_sscDNA	0.0
94907_D283_Med_Medulloblastoma/Cerebellum_sscDNA	0.0	94957_Ramos/6h stim_Stimulated with PMA/ionomycin 6h_sscDNA	0.0
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	0.5	94958_Ramos/14h stim_Stimulated with PMA/ionomycin 14h_sscDNA	0.0
94909_XF-498_CNS_sscDNA	0.0	94962_MEG-01_Chronic myelogenous leukemia (megakaryoblast)_sscDNA	0.7
94910_SNB-78_CNS/glioma_sscDNA	0.0	94963_Raji_Burkitt's lymphoma_sscDNA	0.0
94911_SF-268_CNS/glioblastoma_sscDNA	0.0	94964_Daudi_Burkitt's lymphoma_sscDNA	0.8
94912_T98G_Glioblastoma_sscDNA	0.0	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	1.3
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.0	94968_CA46_Burkitt's lymphoma_sscDNA	0.2
94913_SF-295_CNS/glioblastoma_sscDNA	0.0	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.0
132565_NT2 pool_sscDNA	0.1	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	0.0
94914_Cerebellum_sscDNA	0.2	94973_Jurkat_T cell leukemia_sscDNA	0.0
96777_Cerebellum_sscDNA	0.3	94974_TF-1_Erythroleukemia_sscDNA	100.0
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	0.0	94975_HUT 78_T-cell lymphoma_sscDNA	0.0
94917_DMS-114_Small cell lung cancer_sscDNA	0.0	94977_U937_Histiocytic lymphoma_sscDNA	0.0
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94980_KU-812_Myelogenous leukemia_sscDNA	28.9
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94981_769-P_Clear cell renal carcinoma_sscDNA	0.1

94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94983_Caki-2_Clear cell renal carcinoma_sscDNA	0.0
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94984_SW 839_Clear cell renal carcinoma_sscDNA	0.0
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94986_G401_Wilms' tumor_sscDNA	0.0
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.0	126768_293 cells_sscDNA	0.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	0.0	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	0.6
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	0.0	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	0.0
94927_NCI-H727_Lung carcinoid_sscDNA	0.0	94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	0.0
94928_NCI-UMC-11_Lung carcinoid_sscDNA	0.0	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.0
94929_LX-1_Small cell lung cancer_sscDNA	0.0	94991_HPAC_Pancreatic adenocarcinoma_sscDNA	0.0
94930_Colo-205_Colon cancer_sscDNA	0.0	94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	0.0
94931_KM12_Colon cancer_sscDNA	0.0	94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	0.1
94932_KM20L2_Colon cancer_sscDNA	0.0	94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	0.0
94933_NCI-H716_Colon cancer_sscDNA	0.0	94996_T24_Bladder carcinoma (transitional cell)_sscDNA	0.1
94935_SW-48_Colon adenocarcinoma_sscDNA	0.0	94997_5637_Bladder carcinoma_sscDNA	0.0
94936_SW1116_Colon adenocarcinoma_sscDNA	0.0	94998_HT-1197_Bladder carcinoma_sscDNA	0.0
94937_LS 174T_Colon adenocarcinoma_sscDNA	0.0	94999_UM-UC-3_Bladder carcinoma (transitional cell)_sscDNA	0.0
94938_SW-948_Colon adenocarcinoma_sscDNA	0.0	95000_A204_Rhabdomyosarcoma_sscDNA	0.0
94939_SW-480_Colon adenocarcinoma_sscDNA	0.0	95001_HT-1080_Fibrosarcoma_sscDNA	0.0
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	0.0	95002_MG-63_Osteosarcoma (bone)_sscDNA	0.0
112197_KATO III_Stomach_sscDNA	0.0	95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	0.2
94943_NCI-SNU-16_Gastric carcinoma_sscDNA	0.0	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	0.0
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	0.0	95005_A431_Epidermoid carcinoma_sscDNA	0.0

94946_RF-1_Gastric adenocarcinoma_sscDNA	0.0	95007_WM266-4_Melanoma_sscDNA	0.0
94947_RF-48_Gastric adenocarcinoma_sscDNA	0.1	112195_DU 145_Prostate_sscDNA	0.0
96778_MKN-45_Gastric carcinoma_sscDNA	0.0	95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	0.0
94949_NCI-N87_Gastric carcinoma_sscDNA	0.0	112196_SSC-4_Tongue_sscDNA	0.0
94951_OVCAR-5_Ovarian carcinoma_sscDNA	0.0	112194_SSC-9_Tongue_sscDNA	0.0
94952_RL95-2_Uterine carcinoma_sscDNA	0.0	112191_SSC-15_Tongue_sscDNA	0.0
94953_HelaS3_Cervical adenocarcinoma_sscDNA	0.0	95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	0.0

Table AEI. Panel 1.2

Tissue Name	Rel. Exp.(%) Ag1537, Run 142331743	Rel. Exp.(%) Ag760, Run 114246835	Tissue Name	Rel. Exp.(%) Ag1537, Run 142331743	Rel. Exp.(%) Ag760, Run 114246835
Endothelial cells	2.5	1.3	Renal ca. 786-0	0.0	0.0
Heart (Fetal)	17.6	2.3	Renal ca. A498	0.1	0.1
Pancreas	35.4	74.2	Renal ca. RXF 393	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. ACHN	0.0	0.0
Adrenal Gland	37.4	19.1	Renal ca. UO-31	0.0	0.0
Thyroid	14.9	100.0	Renal ca. TK-10	0.0	0.0
Salivary gland	34.6	15.8	Liver	2.1	1.6
Pituitary gland	2.1	27.4	Liver (fetal)	4.4	4.0
Brain (fetal)	0.1	0.7	Liver ca. (hepatoblast) HepG2	0.0	0.1
Brain (whole)	0.2	0.5	Lung	1.0	4.1
Brain (amygdala)	0.3	0.3	Lung (fetal)	0.3	2.1
Brain (cerebellum)	0.1	0.1	Lung ca. (small cell) LX-1	0.0	0.0
Brain (hippocampus)	0.8	0.7	Lung ca. (small cell) NCI-H69	0.0	0.0
Brain (thalamus)	0.6	0.4	Lung ca. (s.cell var.) SHP-77	0.0	0.0
Cerebral Cortex	0.8	0.3	Lung ca. (large cell) NCI-H460	0.0	0.0
Spinal cord	0.1	0.6	Lung ca. (non-sm. cell) A549	0.0	0.0
glio/astro U87-MG	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	0.0	0.0

glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cell) HOP-62	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
neuro*; met SK-N- AS	0.0	0.0	Lung ca. (squam.) SW 900	0.0	0.0
astrocytoma SF-539	0.0	0.0	Lung ca. (squam.) NCI-H596	0.0	0.0
astrocytoma SNB-75	0.0	0.0	Mammary gland	14.8	19.3
glioma SNB-19	0.0	0.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0
glioma U251	0.1	0.2	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
glioma SF-295	0.1	0.1	Breast ca.* (pl. ef) T47D	0.1	0.0
Heart	50.3	17.0	Breast ca. BT-549	0.0	0.0
Skeletal Muscle	18.2	16.0	Breast ca. MDA-N	2.2	1.2
Bone marrow	2.7	1.4	Ovary	3.0	0.8
Thymus	0.9	2.8	Ovarian ca. OVCAR-3	0.0	0.0
Spleen	29.1	30.8	Ovarian ca. OVCAR-4	0.0	0.0
Lymph node	2.7	14.4	Ovarian ca. OVCAR-5	0.1	0.1
Colorectal Tissue	2.3	1.1	Ovarian ca. OVCAR-8	0.2	0.1
Stomach	11.5	33.2	Ovarian ca. IGROV- 1	0.0	0.0
Small intestine	52.5	41.5	Ovarian ca. (ascites) SK-OV-3	0.0	0.0
Colon ca. SW480	0.0	0.0	Uterus	9.2	12.8
Colon ca.* SW620 (SW480 met)	0.0	0.0	Placenta	3.1	7.3
Colon ca. HT29	0.0	0.0	Prostate	19.5	12.3
Colon ca. HCT-116	0.0	0.0	Prostate ca.* (bone met) PC-3	0.0	0.0
Colon ca. CaCo-2	0.0	0.0	Testis	0.2	1.4
Colon ca. Tissue (ODO3866)	1.7	1.4	Melanoma Hs688(A).T	0.0	0.0
Colon ca. HCC-2998	0.0	0.0	Melanoma* (met) Hs688(B).T	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.9	0.7	Melanoma UACC- 62	0.0	0.0
Bladder	52.5	13.1	Melanoma M14	0.0	0.0
Trachea	2.1	9.6	Melanoma LOX IMVI	0.0	0.0

Kidney	100.0	22.4	Melanoma* (met) SK-MEL-5	0.0	0.0
Kidney (fetal)	23.8	31.9			

Table AEJ. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag760, Run 165678100	Tissue Name	Rel. Exp.(%) Ag760, Run 165678100
Liver adenocarcinoma	0.0	Kidney (fetal)	33.4
Pancreas	43.8	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.2
Adrenal gland	21.5	Renal ca. RXF 393	0.0
Thyroid	79.6	Renal ca. ACHN	0.0
Salivary gland	13.9	Renal ca. UO-31	0.0
Pituitary gland	13.4	Renal ca. TK-10	0.0
Brain (fetal)	0.7	Liver	1.9
Brain (whole)	0.9	Liver (fetal)	12.4
Brain (amygdala)	1.6	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	0.4	Lung	15.3
Brain (hippocampus)	1.8	Lung (fetal)	6.1
Brain (substantia nigra)	2.3	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	2.7	Lung ca. (small cell) NCI- H69	0.0
Cerebral Cortex	0.7	Lung ca. (s.cell var.) SHP- 77	0.0
Spinal cord	1.7	Lung ca. (large cell) NCI- H460	0.4
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
glio/astro U-118-MG	0.1	Lung ca. (non-s.cell) NCI- H23	0.0
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI- H522	0.0
astrocytoma SF-539	0.1	Lung ca. (squam.) SW 900	0.0
astrocytoma SNB-75	0.0	Lung ca. (squam.) NCI- H596	0.0
glioma SNB-19	0.0	Mammary gland	26.8
glioma U251	0.7	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA- MB-231	0.0

Heart (fetal)	6.9	Breast ca.* (pl.ef) T47D	0.0
Heart	11.0	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	19.5	Breast ca. MDA-N	0.2
Skeletal muscle	9.9	Ovary	1.8
Bone marrow	7.9	Ovarian ca. OVCAR-3	0.1
Thymus	6.9	Ovarian ca. OVCAR-4	0.0
Spleen	90.8	Ovarian ca. OVCAR-5	0.0
Lymph node	73.7	Ovarian ca. OVCAR-8	0.0
Colorectal	7.9	Ovarian ca. IGROV-1	0.0
Stomach	65.5	Ovarian ca.* (ascites) SK-OV-3	0.1
Small intestine	100.0	Uterus	87.7
Colon ca. SW480	0.0	Placenta	6.4
Colon ca.* SW620(SW480 met)	0.0	Prostate	11.3
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	2.1
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	24.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	1.7	Melanoma M14	0.0
Bladder	17.1	Melanoma LOX IMVI	0.0
Trachea	27.0	Melanoma* (met) SK-MEL-5	0.0
Kidney	18.2	Adipose	26.6

Table AEK. Panel 2D

Tissue Name	Rel. Exp.(%) Ag1537, Run 145017308	Tissue Name	Rel. Exp.(%) Ag1537, Run 145017308
Normal Colon	12.3	Kidney Margin 8120608	23.5
CC Well to Mod Diff (ODO3866)	10.7	Kidney Cancer 8120613	21.5
CC Margin (ODO3866)	12.2	Kidney Margin 8120614	12.3
CC Gr.2 rectosigmoid (ODO3868)	3.2	Kidney Cancer 9010320	34.4
CC Margin (ODO3868)	0.8	Kidney Margin 9010321	27.7
CC Mod Diff (ODO3920)	3.4	Normal Uterus	9.3
CC Margin (ODO3920)	2.2	Uterus Cancer 064011	6.4

CC Gr.2 ascend colon (ODO3921)	13.4	Normal Thyroid	84.1
CC Margin (ODO3921)	5.8	Thyroid Cancer 064010	20.6
CC from Partial Hepatectomy (ODO4309) Mets	9.6	Thyroid Cancer A302152	15.2
Liver Margin (ODO4309)	0.6	Thyroid Margin A302153	21.3
Colon mets to lung (OD04451-01)	5.5	Normal Breast	22.1
Lung Margin (OD04451-02)	0.8	Breast Cancer (OD04566)	8.4
Normal Prostate 6546-1	14.1	Breast Cancer (OD04590-01)	21.0
Prostate Cancer (OD04410)	8.8	Breast Cancer Mets (OD04590-03)	27.7
Prostate Margin (OD04410)	6.9	Breast Cancer Metastasis (OD04655-05)	9.1
Prostate Cancer (OD04720-01)	3.1	Breast Cancer 064006	10.1
Prostate Margin (OD04720-02)	10.3	Breast Cancer 1024	7.1
Normal Lung 061010	11.8	Breast Cancer 9100266	10.4
Lung Met to Muscle (ODO4286)	6.4	Breast Margin 9100265	7.4
Muscle Margin (ODO4286)	9.9	Breast Cancer A209073	27.4
Lung Malignant Cancer (OD03126)	19.3	Breast Margin A209073	8.7
Lung Margin (OD03126)	3.3	Normal Liver	1.1
Lung Cancer (OD04404)	5.2	Liver Cancer 064003	6.5
Lung Margin (OD04404)	25.3	Liver Cancer 1025	0.7
Lung Cancer (OD04565)	3.4	Liver Cancer 1026	8.1
Lung Margin (OD04565)	3.1	Liver Cancer 6004-T	1.9
Lung Cancer (OD04237-01)	11.0	Liver Tissue 6004-N	3.6
Lung Margin (OD04237-02)	18.2	Liver Cancer 6005-T	9.3
Ocular Mel Met to Liver (ODO4310)	0.7	Liver Tissue 6005-N	0.6

Liver Margin (OD04310)	1.7	Normal Bladder	14.1
Melanoma Mets to Lung (OD04321)	3.9	Bladder Cancer 1023	4.5
Lung Margin (OD04321)	3.7	Bladder Cancer A302173	3.6
Normal Kidney	40.6	Bladder Cancer (OD04718-01)	7.4
Kidney Ca, Nuclear grade 2 (OD04338)	5.7	Bladder Normal Adjacent (OD04718-03)	15.2
Kidney Margin (OD04338)	11.1	Normal Ovary	1.4
Kidney Ca Nuclear grade 1/2 (OD04339)	2.5	Ovarian Cancer 064008	6.5
Kidney Margin (OD04339)	17.6	Ovarian Cancer (OD04768-07)	1.6
Kidney Ca, Clear cell type (OD04340)	100.0	Ovary Margin (OD04768-08)	9.2
Kidney Margin (OD04340)	22.7	Normal Stomach	13.5
Kidney Ca, Nuclear grade 3 (OD04348)	55.1	Gastric Cancer 9060358	2.8
Kidney Margin (OD04348)	19.9	Stomach Margin 9060359	12.6
Kidney Cancer (OD04622-01)	25.0	Gastric Cancer 9060395	20.6
Kidney Margin (OD04622-03)	7.4	Stomach Margin 9060394	7.5
Kidney Cancer (OD04450-01)	1.3	Gastric Cancer 9060397	10.0
Kidney Margin (OD04450-03)	9.2	Stomach Margin 9060396	3.2
Kidney Cancer 8120607	9.2	Gastric Cancer 064005	6.7

Table AEL. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4932, Run 223597251	Tissue Name	Rel. Exp.(%) Ag4932, Run 223597251
Secondary Th1 act	0.1	HUVEC IL-1beta	5.6
Secondary Th2 act	0.4	HUVEC IFN gamma	40.6
Secondary Tr1 act	0.1	HUVEC TNF alpha + IFN gamma	4.6

Secondary Th1 rest	0.1	HUVEC TNF alpha + IL4	5.0
Secondary Th2 rest	0.0	HUVEC IL-11	8.7
Secondary Tr1 rest	0.0	Lung Microvascular EC none	66.4
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	30.4
Primary Th2 act	0.0	Microvascular Dermal EC none	43.5
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	17.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.3
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	1.2	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.2	Coronary artery SMC TNFalpha + IL-1beta	1.1
CD8 lymphocyte act	0.1	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.4	Astrocytes TNFalpha + IL- 1beta	0.2
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	27.0
CD4 lymphocyte none	0.3	KU-812 (Basophil) PMA/ionomycin	28.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.1	Liver cirrhosis	20.6
LAK cells IL-2+IL-12	0.2	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.5	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.2	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.2	NCI-H292 IL-13	0.1
NK Cells IL-2 rest	0.2	NCI-H292 IFN gamma	0.0

Two Way MLR 3 day	2.7	HPAEC none	1.8
Two Way MLR 5 day	1.3	HPAEC TNF alpha + IL-1 beta	1.5
Two Way MLR 7 day	0.1	Lung fibroblast none	0.4
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.6
PBMC PWM	0.0	Lung fibroblast IL-4	0.2
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.4
Ramos (B cell) ionomycin	0.1	Lung fibroblast IFN gamma	0.2
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.5	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.1	Dermal fibroblast IFN gamma	1.1
Dendritic cells none	0.1	Dermal fibroblast IL-4	0.4
Dendritic cells LPS	1.7	Dermal Fibroblasts rest	0.7
Dendritic cells anti-CD40	0.9	Neutrophils TNFa+LPS	0.4
Monocytes rest	0.6	Neutrophils rest	0.3
Monocytes LPS	0.1	Colon	19.3
Macrophages rest	0.0	Lung	100.0
Macrophages LPS	0.1	Thymus	48.0
HUVEC none	1.9	Kidney	68.8
HUVEC starved	8.4		

Table AEM. Panel 4D

Tissue Name	Rel. Exp.(%) Ag760, Run 145803954	Tissue Name	Rel. Exp.(%) Ag760, Run 145803954
Secondary Th1 act	0.0	HUVEC IL-1beta	3.4
Secondary Th2 act	0.1	HUVEC IFN gamma	36.6

Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	4.0
Secondary Th1 rest	0.1	HUVEC TNF alpha + IL4	3.4
Secondary Th2 rest	0.0	HUVEC IL-11	5.5
Secondary Tr1 rest	0.0	Lung Microvascular EC none	47.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	22.8
Primary Th2 act	0.0	Microvascular Dermal EC none	40.1
Primary Tr1 act	0.1	Microvascular Dermal EC TNFalpha + IL-1beta	17.9
Primary Th1 rest	0.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.6	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.2	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	24.3
CD4 lymphocyte none	0.3	KU-812 (Basophil) PMA/ionomycin	29.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.1	Liver cirrhosis	19.5
LAK cells IL-2+IL-12	0.0	Lupus kidney	34.4
LAK cells IL-2+IFN gamma	1.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.7	NCI-H292 IL-4	0.0

LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.4	NCI-H292 IL-13	0.0
Two Way MLR 3 day	3.5	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	1.3	HPAEC none	0.9
Two Way MLR 7 day	0.1	HPAEC TNF alpha + IL-1 beta	0.7
PBMC rest	0.1	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.1	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.1	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.3	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.1
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	2.3	Dermal fibroblast IL-4	0.1
Dendritic cells anti-CD40	0.0	IBD Colitis 2	1.5
Monocytes rest	0.8	IBD Crohn's	9.0
Monocytes LPS	0.0	Colon	40.3
Macrophages rest	0.0	Lung	100.0
Macrophages LPS	0.6	Thymus	95.3
HUVEC none	3.8	Kidney	59.9
HUVEC starved	16.8		

Table AEN. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag1537, Run 266930996	Rel. Exp.(%) Ag760, Run 262228031	Tissue Name	Rel. Exp.(%) Ag1537, Run 266930996	Rel. Exp.(%) Ag760, Run 262228031
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Colon cancer 1	11.4	4.8	Bladder cancer NAT 2	0.6	0.4
Colon cancer NAT 1	9.4	1.7	Bladder cancer NAT 3	0.8	0.2
Colon cancer 2	4.1	3.9	Bladder cancer NAT 4	4.2	2.3
Colon cancer NAT 2	4.1	1.8	Prostate adenocarcinoma 1	2.1	2.9
Colon cancer 3	10.4	4.8	Prostate adenocarcinoma 2	1.2	0.5
Colon cancer NAT 3	7.6	1.2	Prostate adenocarcinoma 3	2.1	1.0
Colon malignant cancer 4	9.7	4.0	Prostate adenocarcinoma 4	6.0	3.3
Colon normal adjacent tissue 4	3.4	2.3	Prostate cancer NAT 5	3.0	1.1
Lung cancer 1	4.8	3.6	Prostate adenocarcinoma 6	1.3	0.5
Lung NAT 1	0.7	0.5	Prostate adenocarcinoma 7	1.2	0.7
Lung cancer 2	5.6	3.9	Prostate adenocarcinoma 8	1.2	0.4
Lung NAT 2	0.1	0.1	Prostate adenocarcinoma 9	4.8	2.7
Squamous cell carcinoma 3	5.4	2.4	Prostate cancer NAT 10	0.6	0.5
Lung NAT 3	0.7	0.3	Kidney cancer 1	90.1	100.0
metastatic melanoma 1	1.5	1.1	Kidney NAT 1	5.0	3.5
Melanoma 2	4.0	2.6	Kidney cancer 2	60.3	55.1
Melanoma 3	3.8	1.2	Kidney NAT 2	9.8	6.0
metastatic melanoma 4	2.2	0.9	Kidney cancer 3	30.8	39.5
metastatic melanoma 5	4.6	1.5	Kidney NAT 3	5.4	1.2
Bladder cancer 1	1.0	0.6	Kidney cancer 4	100.0	29.9
Bladder cancer NAT 1	0.0	0.0	Kidney NAT 4	6.7	1.6

Bladder cancer 2	4.4	2.1			
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Ardais Panel v.1.0 Summary: Ag1537 Highest expression of this gene is detected in normal lung sample (CT=26.7). In addition, high to moderate levels of expression is seen in both cancer and normal lung samples. Therefore, therapeutic modulation of the PV1 protein (PLVAP) encoded by this gene may be useful in the treatment of certain subtypes of lung cancer.

CNS_neurodegeneration_v1.0 Summary: Ag1537/Ag4932 Two experiments with different probe and primer sets are in good agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.5 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.5 Summary: Ag4932 Highest expression of this gene is detected in spleen (CT=26). In addition, high expression of this gene is also detected in tissues with metabolic/endocrine functions including pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. The PV-1-like protein is a plasma membrane protein with an extracellular domain. The extracellular domain of this protein makes it a potential antibody target for the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Moderate levels of expression of this gene is also seen in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene also shows high expression in colon cancer tissue, with moderate levels of expression in a gastric NCI-N87 cell line. Therefore, therapeutic modulation of this gene may be useful in the treatment of colon and gastric cancers.

HASS Panel v1.0 Summary: Ag1537 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Oncology_cell_line_screening_panel_v3.2 Summary: Ag1537 Highest expression of this gene is detected in TF-1 erythroleukemia cells (CT=28.6). Moderate levels of expression of this gene is restricted to erythroleukemia and myelogenous leukemia. Therefore, expression of this gene may be used to distinguish these leukemia samples from
5 other samples in the panel and also, as marker to detect the presence of these leukemia. In addition, therapeutic modulation of this gene or its protein product may be useful in the treatment of erythroleukemia and myelogenous leukemia.

Panel 1.2 Summary: Ag760/Ag1537 Results from two experiments using different probe/primer sets are in reasonable agreement with highest expression of this gene in
10 thyroid and kidney (CTs=20-21.6). Expression of this gene seems to be restricted to normal tissue and it is low or undetectable in cancer cell lines. Thus, expression of this gene could be used to distinguish between normal tissues and cultured cancer cell lines.

In addition, expression of this gene is high (CT<27) in a wide range of metabolic tissues including pancreas, adrenal gland, thyroid, pituitary, adult and fetal heart, skeletal
15 muscle and adult and fetal liver. Also, moderate levels of expression is seen in in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. This expression pattern is consistent to that seen in panel 1.5. See panel 1.5 for further discussion of this gene.

Panel 1.3D Summary: Ag760 Expression of this gene is highest in small intestine
20 (CT = 26). The expression pattern is similar to that observed in Panel 1.5 and 1.2. See panel 1.5 for and panel 1.2 for further discussion of this gene.

Panel 2D Summary: Ag1537 Expression of this gene is highest in a kidney cancer (OD04340) sample (CT=25). Overall, this gene is widely expressed across this panel with high to moderate expression in both normal and adjacent cancer tissue. However, this gene
25 is more highly expressed in kidney cancer tissue than in adjacent normal tissue, consistent with expression pattern seen in panel 2.4. Therefore, this gene could be used to distinguish kidney cancers from normal kidney tissue. In addition, therapeutic modulation of this gene, through the use of small molecule drugs or antibodies, might be of benefit in the treatment of kidney cancer.

Panel 4.1D Summary: Ag4932 Highest expression of this gene is detected in lung
30 (CT=28.5). In addition, moderate levels of expression of this gene is also seen in endothelial

cells, basophils and normal tissues represented by colon, thymus and kidney. This gene codes for a variant of PV-1, a component of the endothelial fenestral and stomatal diaphragms. Expression of this gene is consistent with the pattern already reported for PV-1 (Stan *et al.*, 1999, Proc. Natl. Acad. Sci. USA 96:13203-13207, PMID: 10557298; Stan *et al.*, 2001, Genomics 72(3):304-13, PMID: 11401446). Antibodies raised against the PV-1 encoded by this gene could prevent transendothelial trafficking of inflammatory cells to different tissues sites and therefore have a potential use for treatment of inflammatory diseases including delayed type hypersensitivity, asthma, emphysema, rheumatoid arthritis and inflammatory bowel disease.

10 Moderate levels of expression of this gene is also seen in liver cirrhosis samples. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Panel 4D Summary: Ag760 Expression of this gene is highest in lung and thymus (CTs=26.3). High expression of this gene is also seen in normal kidney and colon with more moderate expression in endothelial cells and basophils. Expression of this gene is consistent with the pattern seen in panel 4.1D and also, with the published report (Stan *et al.*, 1999, Proc. Natl. Acad. Sci. USA 96:13203-13207, PMID: 10557298; Stan *et al.*, 2001, Genomics 72(3):304-13, PMID: 11401446). See panel 4.1D for further discussion of this gene.

general oncology screening panel_v_2.4 Summary: Ag1537/Ag760 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in a kidney cancer sample (CTs=22.6-25). Significant expression of this gene is seen in melanoma, colon, lung, prostate, bladder and kidney cancer as well as normal tissue samples. Expression of this gene is higher in kidney cancer as compared to corresponding normal control samples. Therefore, expression of this gene may be used to distinguish kidney cancer from normal tissue and also as a marker to detect kidney cancer. Furthermore, therapeutic modulation of this gene or its protein product through the use of antibodies or small molecule drug may be useful in the treatment of melanoma, kidney, colon, lung and prostate cancers.

AF. CG52919-01: SEZ-6-like protein(7520500).

Expression of gene CG52919-01 was assessed using the primer-probe set Ag2806, described in Table AFA. Results of the RTQ-PCR runs are shown in Tables AFB, AFC, AFD and AFE.

Table AFA. Probe Name Ag2806

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgatgaggagaccaccacta-3'	22	835	384
Probe	TET-5'-atcatcaccaccaccatcaccacagt-3'-TAMRA	26	865	385
Reverse	5'-caggtagctgacctggtgtct-3'	21	893	386

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Table AFB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag2806, Run 206976054	Tissue Name	Rel. Exp.(%) Ag2806, Run 206976054
AD 1 Hippo	10.4	Control (Path) 3 Temporal Ctx	4.7
AD 2 Hippo	15.1	Control (Path) 4 Temporal Ctx	32.8
AD 3 Hippo	4.1	AD 1 Occipital Ctx	11.5
AD 4 Hippo	4.6	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	0.0	AD 3 Occipital Ctx	5.5
AD 6 Hippo	19.6	AD 4 Occipital Ctx	18.9
Control 2 Hippo	25.5	AD 5 Occipital Ctx	12.1
Control 4 Hippo	12.0	AD 6 Occipital Ctx	31.6
Control (Path) 3 Hippo	0.7	Control 1 Occipital Ctx	2.9
AD 1 Temporal Ctx	7.7	Control 2 Occipital Ctx	57.8
AD 2 Temporal Ctx	12.0	Control 3 Occipital Ctx	13.5
AD 3 Temporal Ctx	11.1	Control 4 Occipital Ctx	4.0
AD 4 Temporal Ctx	19.5	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	87.7	Control (Path) 2 Occipital Ctx	13.8

AD 5 Sup Temporal Ctx	52.9	Control (Path) 3 Occipital Ctx	0.9
AD 6 Inf Temporal Ctx	16.4	Control (Path) 4 Occipital Ctx	14.8
AD 6 Sup Temporal Ctx	31.0	Control 1 Parietal Ctx	13.1
Control 1 Temporal Ctx	13.5	Control 2 Parietal Ctx	45.4
Control 2 Temporal Ctx	16.5	Control 3 Parietal Ctx	9.6
Control 3 Temporal Ctx	12.5	Control (Path) 1 Parietal Ctx	53.2
Control 4 Temporal Ctx	19.5	Control (Path) 2 Parietal Ctx	22.7
Control (Path) 1 Temporal Ctx	49.7	Control (Path) 3 Parietal Ctx	0.6
Control (Path) 2 Temporal Ctx	36.3	Control (Path) 4 Parietal Ctx	31.4

Table AFC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2806, Run 165519991	Tissue Name	Rel. Exp.(%) Ag2806, Run 165519991
Liver adenocarcinoma	2.5	Kidney (fetal)	4.8
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.0
Adrenal gland	0.0	Renal ca. RXF 393	0.0
Thyroid	0.0	Renal ca. ACHN	0.0
Salivary gland	1.5	Renal ca. UO-31	0.0
Pituitary gland	6.0	Renal ca. TK-10	0.0
Brain (fetal)	47.0	Liver	0.0
Brain (whole)	17.7	Liver (fetal)	0.0
Brain (amygdala)	22.4	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	100.0	Lung	0.0
Brain (hippocampus)	47.3	Lung (fetal)	2.3
Brain (substantia nigra)	6.5	Lung ca. (small cell) LX-1	0.0

Brain (thalamus)	39.5	Lung ca. (small cell) NCI-H69	11.8
Cerebral Cortex	25.0	Lung ca. (s.cell var.) SHP-77	19.9
Spinal cord	5.9	Lung ca. (large cell) NCI-H460	0.0
glio/astro U87-MG	3.5	Lung ca. (non-sm. cell) A549	0.0
glio/astro U-118-MG	6.3	Lung ca. (non-s.cell) NCI-H23	5.0
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	2.3	Lung ca. (non-s.cl) NCI-H522	3.4
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.7
astrocytoma SNB-75	4.1	Lung ca. (squam.) NCI-H596	84.7
glioma SNB-19	1.1	Mammary gland	0.0
glioma U251	8.0	Breast ca.* (pl.ef) MCF-7	1.5
glioma SF-295	2.0	Breast ca.* (pl.ef) MDA-MB-231	1.0
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.0
Heart	0.0	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	3.8	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	6.7	Ovarian ca. OVCAR-3	3.8
Thymus	3.7	Ovarian ca. OVCAR-4	2.4
Spleen	5.5	Ovarian ca. OVCAR-5	0.0
Lymph node	11.4	Ovarian ca. OVCAR-8	2.0
Colorectal	2.3	Ovarian ca. IGROV-1	0.0
Stomach	2.3	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	8.7	Uterus	2.9
Colon ca. SW480	0.0	Placenta	3.6

Colon ca.* SW620(SW480 met)	0.0	Prostate	3.5
Colon ca. HT29	1.8	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	3.8
Colon ca. CaCo-2	1.8	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	2.2	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	5.1	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	0.3	Melanoma M14	3.8
Bladder	5.0	Melanoma LOX IMVI	0.0
Trachea	3.4	Melanoma* (met) SK- MEL-5	0.0
Kidney	0.0	Adipose	3.2

Table AFD. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2806, Run 163577806	Tissue Name	Rel. Exp.(%) Ag2806, Run 163577806
Normal Colon	1.2	Kidney Margin 8120608	0.2
CC Well to Mod Diff (ODO3866)	0.0	Kidney Cancer 8120613	0.0
CC Margin (ODO3866)	0.0	Kidney Margin 8120614	0.3
CC Gr.2 rectosigmoid (ODO3868)	0.1	Kidney Cancer 9010320	0.4
CC Margin (ODO3868)	0.1	Kidney Margin 9010321	0.2
CC Mod Diff (ODO3920)	0.3	Normal Uterus	0.4
CC Margin (ODO3920)	0.4	Uterus Cancer 064011	0.7
CC Gr.2 ascend colon (ODO3921)	0.5	Normal Thyroid	0.1
CC Margin (ODO3921)	0.1	Thyroid Cancer 064010	0.0
CC from Partial Hepatectomy (ODO4309) Mets	0.3	Thyroid Cancer A302152	0.2
Liver Margin (ODO4309)	0.0	Thyroid Margin A302153	0.1

Colon mets to lung (OD04451-01)	0.2	Normal Breast	0.4
Lung Margin (OD04451-02)	0.2	Breast Cancer (OD04566)	100.0
Normal Prostate 6546-1	1.4	Breast Cancer (OD04590-01)	0.2
Prostate Cancer (OD04410)	0.5	Breast Cancer Mets (OD04590-03)	0.3
Prostate Margin (OD04410)	0.9	Breast Cancer Metastasis (OD04655-05)	0.1
Prostate Cancer (OD04720-01)	1.0	Breast Cancer 064006	0.1
Prostate Margin (OD04720-02)	0.6	Breast Cancer 1024	0.7
Normal Lung 061010	0.9	Breast Cancer 9100266	0.1
Lung Met to Muscle (ODO4286)	0.0	Breast Margin 9100265	0.1
Muscle Margin (ODO4286)	0.2	Breast Cancer A209073	0.3
Lung Malignant Cancer (OD03126)	0.1	Breast Margin A209073	0.3
Lung Margin (OD03126)	0.3	Normal Liver	0.1
Lung Cancer (OD04404)	0.1	Liver Cancer 064003	0.0
Lung Margin (OD04404)	0.3	Liver Cancer 1025	0.1
Lung Cancer (OD04565)	0.1	Liver Cancer 1026	0.3
Lung Margin (OD04565)	0.3	Liver Cancer 6004-T	0.1
Lung Cancer (OD04237-01)	0.2	Liver Tissue 6004-N	0.2
Lung Margin (OD04237-02)	0.2	Liver Cancer 6005-T	0.2
Ocular Mel Met to Liver (ODO4310)	0.1	Liver Tissue 6005-N	0.0
Liver Margin (ODO4310)	0.0	Normal Bladder	0.2
Melanoma Mets to Lung (OD04321)	0.0	Bladder Cancer 1023	0.2
Lung Margin (OD04321)	0.4	Bladder Cancer A302173	0.2
Normal Kidney	0.3	Bladder Cancer (OD04718-01)	0.1

Kidney Ca, Nuclear grade 2 (OD04338)	0.4	Bladder Normal Adjacent (OD04718-03)	0.5
Kidney Margin (OD04338)	85.3	Normal Ovary	0.1
Kidney Ca Nuclear grade 1/2 (OD04339)	0.2	Ovarian Cancer 064008	0.2
Kidney Margin (OD04339)	0.2	Ovarian Cancer (OD04768-07)	0.1
Kidney Ca, Clear cell type (OD04340)	0.1	Ovary Margin (OD04768-08)	0.1
Kidney Margin (OD04340)	0.2	Normal Stomach	0.8
Kidney Ca, Nuclear grade 3 (OD04348)	0.0	Gastric Cancer 9060358	0.1
Kidney Margin (OD04348)	0.3	Stomach Margin 9060359	0.1
Kidney Cancer (OD04622-01)	0.1	Gastric Cancer 9060395	0.3
Kidney Margin (OD04622-03)	0.0	Stomach Margin 9060394	0.5
Kidney Cancer (OD04450-01)	0.2	Gastric Cancer 9060397	0.1
Kidney Margin (OD04450-03)	0.2	Stomach Margin 9060396	0.1
Kidney Cancer 8120607	0.0	Gastric Cancer 064005	0.2

Table AFE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2806, Run 162330998	Tissue Name	Rel. Exp.(%) Ag2806, Run 162330998
Secondary Th1 act	20.3	HUVEC IL-1beta	0.0
Secondary Th2 act	5.1	HUVEC IFN gamma	21.9
Secondary Tr1 act	9.7	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	21.9	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	34.6	HUVEC IL-11	5.6
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	11.2	Lung Microvascular EC TNFalpha + IL-1beta	0.0

Primary Th2 act	13.2	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	12.8
Primary Th1 rest	37.6	Bronchial epithelium TNFalpha + IL1beta	12.1
Primary Th2 rest	10.0	Small airway epithelium none	0.0
Primary Tr1 rest	2.3	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	11.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	11.8	Coronary artery SMC TNFalpha + IL-1beta	4.4
CD8 lymphocyte act	46.7	Astrocytes rest	12.8
Secondary CD8 lymphocyte rest	44.4	Astrocytes TNFalpha + IL-1beta	11.3
Secondary CD8 lymphocyte act	10.2	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	43.2	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	54.7	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	13.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	17.1	Liver cirrhosis	96.6
LAK cells IL-2+IL-12	17.4	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	70.2	NCI-H292 none	22.8
LAK cells IL-2+ IL-18	2.5	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	5.0	NCI-H292 IL-9	23.2
NK Cells IL-2 rest	21.0	NCI-H292 IL-13	32.1
Two Way MLR 3 day	43.5	NCI-H292 IFN gamma	11.4
Two Way MLR 5 day	18.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	7.2	Lung fibroblast none	0.0

PBMC PWM	48.3	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	76.8	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	12.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	28.7	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	100.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	21.2	Dermal fibroblast CCD1070 TNF alpha	85.3
EOL-1 dbcAMP PMA/ionomycin	50.7	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	15.3	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	32.3	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	31.4	IBD Colitis 2	12.1
Monocytes rest	52.5	IBD Crohn's	5.6
Monocytes LPS	42.3	Colon	94.0
Macrophages rest	11.0	Lung	27.7
Macrophages LPS	0.0	Thymus	34.6
HUVEC none	0.0	Kidney	78.5
HUVEC starved	11.7		

CNS_neurodegeneration_v1.0 Summary: Ag2806 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.3D

5 for a discussion of this gene in treatment of central nervous system disorders.

Panel 1.3D Summary: Ag2806 Highest expression of this gene is detected in brain cerebellum (CT=31.2). Moderate levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may

10 be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for a homolog of mouse seizure related protein, SEZ-6. Mouse SEZ-6 was first isolated from cerebrum cortex-derived cells treated with pentylentetrazole (PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also
 5 play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in three lung cancer cell lines. Therefore, expression of this gene may be used as diagnostic marker to detect lung cancer and also, modulation of this gene or its protein product through the use of antibody or protein therapeutics, may be useful in the treatment of lung cancer.

10 **Panel 2D Summary:** Ag2806 Highest expression of this gene is detected in breast cancer and normal kidney (CTs=26). Low levels of expression of this gene is also seen in breast, prostate, colon, uterine and kidney cancer. Therefore, therapeutic modulation of this gene product through the use of antibodies may be useful in the treatment of these cancers.

Panel 4D Summary: Ag2806 Highest expression of this gene is detected in CD40L
 15 and IL-4 treated B lymphocytes (CT=34). Low but significant levels of expression of this gene is also seen in TNF alpha treated dermal fibroblasts, IL-2+IFN gamma treated LAK cells, PHA-L treated PBMC cells, liver cirrhosis and normal tissue represented by colon and kidney. Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory diseases such as lupus erythematosus, Crohn's disease,
 20 ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis and liver cirrhosis.

AG. , CG52919-02, CG52919-03 and CG52919-04: SEZ-6-like protein (7520500-54-1).

Expression of gene CG52919-02, CG52919-03 and CG52919-04 was assessed using
 25 the primer-probe sets Ag2795, Ag2807, Ag90 and Ag7017, described in Tables AGA, AGB, AGC and AGD. Results of the RTQ-PCR runs are shown in Tables AGE, AGF, AGG, AGH, AGI, AGJ, AGK, AGL, AGM and AGN.

Table AGA. Probe Name Ag2795

Primers	Sequences	Length	Start Position	SEQ ID No
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Forward	5'-cctacaaccgcattaccataga-3'	22	1670	387
Probe	TET-5'- tcagcgtttgacaatccaacttacga-3'-TAMRA	26	1693	388
Reverse	5'-cccacctagatggagacttcac-3'	22	1739	389

Table AGB. Probe Name Ag2807

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctacaaccgcattaccataga-3'	22	1670	390
Probe	TET-5'- tcagcgtttgacaatccaacttacga-3'-TAMRA	26	1693	391
Reverse	5'-cccacctagatggagacttcac-3'	22	1739	392

Table AGC. Probe Name Ag90

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttggcctggactgcttcttc-3'	20	977	393
Probe	TET-5'- catctctgtctacctggctatggcgtg-3'-TAMRA	28	999	394
Reverse	5'-aggctgatattctggaccttgatt-3'	24	1029	395

Table AGD. Probe Name Ag7017

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtttgacaatccaacttacgagac-3'	24	1698	396
Probe	TET-5'- cctagatggagacttcattctctcgtc-3'-TAMRA	30	1727	397
Reverse	5'-caagctctgagttgacttcctagac-3'	25	1765	398

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Table AGE. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag2795, Run 255324382	Tissue Name	Rel. Exp.(%) Ag2795, Run 255324382
110967 COPD-F	0.0	112427 Match Control Psoriasis-F	0.1
110980 COPD-F	0.0	112418 Psoriasis-M	0.0
110968 COPD-M	0.0	112723 Match Control Psoriasis-M	0.0
110977 COPD-M	0.1	112419 Psoriasis-M	0.0
110989 Emphysema-F	0.0	112424 Match Control Psoriasis-M	0.1
110992 Emphysema-F	0.0	112420 Psoriasis-M	0.1
110993 Emphysema-F	0.0	112425 Match Control Psoriasis-M	0.1
110994 Emphysema-F	0.0	104689 (MF) OA Bone- Backus	0.1
110995 Emphysema-F	0.2	104690 (MF) Adj "Normal" Bone-Backus	0.3
110996 Emphysema-F	0.0	104691 (MF) OA Synovium-Backus	0.0
110997 Asthma-M	0.0	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	0.1	104694 (BA) OA Bone- Backus	0.1
111002 Asthma-F	0.0	104695 (BA) Adj "Normal" Bone-Backus	0.0
111003 Atopic Asthma- F	0.0	104696 (BA) OA Synovium-Backus	0.0
111004 Atopic Asthma- F	0.0	104700 (SS) OA Bone- Backus	0.0
111005 Atopic Asthma- F	0.0	104701 (SS) Adj "Normal" Bone-Backus	0.0
111006 Atopic Asthma- F	0.0	104702 (SS) OA Synovium-Backus	0.0
111417 Allergy-M	0.0	117093 OA Cartilage Rep7	0.0
112347 Allergy-M	0.0	112672 OA Bone5	0.0
112349 Normal Lung-F	0.0	112673 OA Synovium5	0.0

112357 Normal Lung-F	0.1	112674 OA Synovial Fluid cells5	0.0
112354 Normal Lung-M	0.0	117100 OA Cartilage Rep14	0.0
112374 Crohns-F	0.0	112756 OA Bone9	100.0
112389 Match Control Crohns-F	0.0	112757 OA Synovium9	0.0
112375 Crohns-F	0.2	112758 OA Synovial Fluid Cells9	0.0
112732 Match Control Crohns-F	0.0	117125 RA Cartilage Rep2	0.1
112725 Crohns-M	0.0	113492 Bone2 RA	0.0
112387 Match Control Crohns-M	0.0	113493 Synovium2 RA	0.0
112378 Crohns-M	0.0	113494 Syn Fluid Cells RA	0.0
112390 Match Control Crohns-M	0.2	113499 Cartilage4 RA	0.0
112726 Crohns-M	0.1	113500 Bone4 RA	0.2
112731 Match Control Crohns-M	0.1	113501 Synovium4 RA	0.0
112380 Ulcer Col-F	0.1	113502 Syn Fluid Cells4 RA	0.0
112734 Match Control Ulcer Col-F	0.1	113495 Cartilage3 RA	0.0
112384 Ulcer Col-F	0.4	113496 Bone3 RA	0.3
112737 Match Control Ulcer Col-F	0.0	113497 Synovium3 RA	0.2
112386 Ulcer Col-F	0.0	113498 Syn Fluid Cells3 RA	0.0
112738 Match Control Ulcer Col-F	0.0	117106 Normal Cartilage Rep20	0.0
112381 Ulcer Col-M	0.0	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	0.7	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	0.0	113665 Syn Fluid Cells3 Normal	0.0

112394 Match Control Ulcer Col-M	0.0	117107 Normal Cartilage Rep22	0.0
112383 Ulcer Col-M	0.1	113667 Bone4 Normal	0.0
112736 Match Control Ulcer Col-M	0.0	113668 Synovium4 Normal	0.0
112423 Psoriasis-F	0.1	113669 Syn Fluid Cells4 Normal	0.0

Table AGF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag2795, Run 20697605 2	Rel. Exp.(%) Ag2807, Run 20648228 2	Rel. Exp.(%) Ag7017, Run 279032451	Tissue Name	Rel. Exp.(%) Ag2795, Run 206976052	Rel. Exp.(%) Ag2807, Run 206482282	Rel. Exp.(%) Ag7017, Run 27903245 1
AD 1 Hippo	13.4	14.6	10.6	Control (Path) 3 Temporal Ctx	3.5	2.4	3.9
AD 2 Hippo	66.4	80.1	62.4	Control (Path) 4 Temporal Ctx	25.2	28.1	23.3
AD 3 Hippo	7.5	6.0	7.3	AD 1 Occipital Ctx	6.7	7.9	9.3
AD 4 Hippo	7.4	11.1	9.5	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	0.0	77.4	61.6	AD 3 Occipital Ctx	1.8	1.7	2.6
AD 6 Hippo	53.6	49.7	46.0	AD 4 Occipital Ctx	19.9	20.9	21.0
Control 2 Hippo	49.7	48.3	51.8	AD 5 Occipital Ctx	7.9	9.8	5.6
Control 4 Hippo	6.6	8.1	7.3	AD 6 Occipital Ctx	54.3	66.4	50.3
Control (Path) 3 Hippo	2.0	2.4	0.0	Control 1 Occipital Ctx	1.3	2.2	1.8

AD 1 Temporal Ctx	6.8	6.9	9.3	Control 2 Occipital Ctx	60.7	69.3	97.3
AD 2 Temporal Ctx	27.9	34.4	25.7	Control 3 Occipital Ctx	14.2	16.3	13.4
AD 3 Temporal Ctx	4.1	2.3	6.5	Control 4 Occipital Ctx	3.4	2.9	3.4
AD 4 Temporal Ctx	19.1	20.7	21.2	Control (Path) 1 Occipital Ctx	100.0	100.0	79.6
AD 5 Inf Temporal Ctx	59.5	69.3	100.0	Control (Path) 2 Occipital Ctx	8.5	7.6	6.6
AD 5 Sup Temporal Ctx	46.0	45.7	39.5	Control (Path) 3 Occipital Ctx	0.7	1.2	1.7
AD 6 Inf Temporal Ctx	18.9	26.2	21.5	Control (Path) 4 Occipital Ctx	10.0	11.0	10.6
AD 6 Sup Temporal Ctx	20.9	21.2	22.2	Control 1 Parietal Ctx	6.4	5.0	3.5
Control 1 Temporal Ctx	3.1	2.5	3.9	Control 2 Parietal Ctx	22.8	26.2	24.7
Control 2 Temporal Ctx	48.3	56.6	52.5	Control 3 Parietal Ctx	14.9	20.0	20.4
Control 3 Temporal Ctx	12.6	15.4	14.7	Control (Path) 1 Parietal Ctx	74.2	92.7	84.7
Control 4 Temporal Ctx	5.9	8.5	6.7	Control (Path) 2 Parietal Ctx	20.3	20.4	20.0
Control (Path) 1 Temporal Ctx	74.7	81.2	71.2	Control (Path) 3 Parietal Ctx	1.4	1.3	2.9
Control (Path) 2 Temporal Ctx	29.1	40.1	30.4	Control (Path) 4 Parietal Ctx	30.8	40.1	38.2

Table AGG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7017, Run 279032445	Tissue Name	Rel. Exp.(%) Ag7017, Run 279032445
Adipose	0.1	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.1
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.1
Testis Pool	0.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.2	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.1	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.1	Small Intestine Pool	0.1
Ovarian ca. IGROV-1	0.8	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.3	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0

Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.1	CNS cancer (neuro;met) SK-N-AS	0.2
Lung ca. NCI-N417	4.3	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	0.1
Lung ca. NCI-H146	36.9	CNS cancer (glio) SNB- 19	0.6
Lung ca. SHP-77	28.5	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	9.7
Lung ca. NCI-H526	27.9	Brain (cerebellum)	84.7
Lung ca. NCI-H23	0.1	Brain (fetal)	100.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	12.8
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	11.1
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	6.4
Liver	0.0	Brain (Thalamus) Pool	19.5
Fetal Liver	0.0	Brain (whole)	22.7
Liver ca. HepG2	0.0	Spinal Cord Pool	2.1
Kidney Pool	0.0	Adrenal Gland	0.1
Fetal Kidney	0.0	Pituitary gland Pool	1.8
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.1	Pancreas Pool	0.0

Table AGH. HASS Panel v1.0

Tissue Name	Rel. Exp.(%) Ag2795, Run 268787250	Tissue Name	Rel. Exp.(%) Ag2795, Run 268787250
MCF-7 C1	0.2	U87-MG F1 (B)	0.0

MCF-7 C2	0.0	U87-MG F2	0.0
MCF-7 C3	0.4	U87-MG F3	0.0
MCF-7 C4	0.0	U87-MG F4	0.2
MCF-7 C5	0.2	U87-MG F5	0.0
MCF-7 C6	0.5	U87-MG F6	0.0
MCF-7 C7	0.4	U87-MG F7	0.1
MCF-7 C9	0.2	U87-MG F8	0.1
MCF-7 C10	0.1	U87-MG F9	0.0
MCF-7 C11	0.0	U87-MG F10	0.0
MCF-7 C12	0.2	U87-MG F11	0.0
MCF-7 C13	0.3	U87-MG F12	0.0
MCF-7 C15	0.2	U87-MG F13	0.0
MCF-7 C16	0.3	U87-MG F14	0.0
MCF-7 C17	0.4	U87-MG F15	0.1
T24 D1	0.0	U87-MG F16	0.0
T24 D2	0.1	U87-MG F17	0.0
T24 D3	0.0	LnCAP A1	0.2
T24 D4	0.0	LnCAP A2	0.5
T24 D5	0.1	LnCAP A3	0.2
T24 D6	0.0	LnCAP A4	0.9
T24 D7	0.0	LnCAP A5	0.1
T24 D9	0.0	LnCAP A6	0.3
T24 D10	0.0	LnCAP A7	0.4
T24 D11	0.0	LnCAP A8	0.2
T24 D12	0.0	LnCAP A9	0.0
T24 D13	0.0	LnCAP A10	0.3
T24 D15	0.0	LnCAP A11	0.9
T24 D16	0.0	LnCAP A12	0.0
T24 D17	0.0	LnCAP A13	0.0
CAPaN B1	0.0	LnCAP A14	0.0
CAPaN B2	0.0	LnCAP A15	0.1

CAPaN B3	0.0	LnCAP A16	0.9
CAPaN B4	0.0	LnCAP A17	0.2
CAPaN B5	0.0	Primary Astrocytes	1.0
CAPaN B6	0.0	Primary Renal Proximal Tubule Epithelial cell A2	0.0
CAPaN B7	0.0	Primary melanocytes A5	0.0
CAPaN B8	0.0	126443 - 341 medullo	0.0
CAPaN B9	0.1	126444 - 487 medullo	0.1
CAPaN B10	0.0	126445 - 425 medullo	0.5
CAPaN B11	0.1	126446 - 690 medullo	100.0
CAPaN B12	0.0	126447 - 54 adult glioma	0.3
CAPaN B13	0.0	126448 - 245 adult glioma	0.1
CAPaN B14	0.0	126449 - 317 adult glioma	3.7
CAPaN B15	0.0	126450 - 212 glioma	30.8
CAPaN B16	0.0	126451 - 456 glioma	50.0
CAPaN B17	0.0		

Table AGI. Oncology_cell_line_screening_panel_v3.2

Tissue Name	Rel. Exp.(%) Ag2795, Run 2714006 11	Tissue Name	Rel. Exp.(%) Ag2795 , Run 271400 611
94905_Daoy_Medulloblastoma/Cerebellu m_sscDNA	0.0	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	0.0
94906_TE671_Medulloblastom/Cerebellu m_sscDNA	0.0	94955_ES-2_Ovarian clear cell carcinoma_sscDNA	0.0
94907_D283 Med_Medulloblastoma/Cerebellum_sscDN A	7.2	94957_Ramos/6h stim_ Stimulated with PMA/ionomycin 6h_sscDNA	0.0
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	0.0	94958_Ramos/14h stim_ Stimulated with PMA/ionomycin 14h_sscDNA	0.0
94909_XF-498_CNS_sscDNA	0.2	94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	0.0

94910_SNB-78_CNS/glioma_sscDNA	0.0	94963_Raji_Burkitt's lymphoma_sscDNA	0.0
94911_SF-268_CNS/glioblastoma_sscDNA	0.0	94964_Daudi_Burkitt's lymphoma_sscDNA	0.0
94912_T98G_Glioblastoma_sscDNA	0.0	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	0.0
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.6	94968_CA46_Burkitt's lymphoma_sscDNA	0.0
94913_SF-295_CNS/glioblastoma_sscDNA	0.0	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.0
132565_NT2 pool_sscDNA	0.0	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	0.0
94914_Cerebellum_sscDNA	14.9	94973_Jurkat_T cell leukemia_sscDNA	0.0
96777_Cerebellum_sscDNA	15.2	94974_TF-1_Erythroleukemia_sscDNA	0.0
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	0.0	94975_HUT 78_T-cell lymphoma_sscDNA	0.0
94917_DMS-114_Small cell lung cancer_sscDNA	0.0	94977_U937_Histiocytic lymphoma_sscDNA	0.0
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	100.0	94980_KU-812_Myelogenous leukemia_sscDNA	0.0
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	36.6	94981_769-P_Clear cell renal carcinoma_sscDNA	0.0
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	33.0	94983_Caki-2_Clear cell renal carcinoma_sscDNA	0.0
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	5.1	94984_SW 839_Clear cell renal carcinoma_sscDNA	0.0
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	6.9	94986_G401_Wilms' tumor_sscDNA	0.0
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.0	126768_293 cells_sscDNA	0.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	7.3	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	0.0
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	0.0	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	0.0
94927_NCI-H727_Lung carcinoid_sscDNA	3.1	94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	0.0

94928_NCI-UMC-11_Lung carcinoid_sscDNA	7.5	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.0
94929_LX-1_Small cell lung cancer_sscDNA	0.0	94991_HPAC_Pancreatic adenocarcinoma_sscDNA	0.0
94930_Colo-205_Colon cancer_sscDNA	0.0	94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	0.0
94931_KM12_Colon cancer_sscDNA	0.0	94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	0.0
94932_KM20L2_Colon cancer_sscDNA	0.0	94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	0.0
94933_NCI-H716_Colon cancer_sscDNA	3.6	94996_T24_Bladder carcinoma (transitional cell)_sscDNA	0.0
94935_SW-48_Colon adenocarcinoma_sscDNA	0.0	94997_5637_Bladder carcinoma_sscDNA	0.0
94936_SW1116_Colon adenocarcinoma_sscDNA	0.0	94998_HT-1197_Bladder carcinoma_sscDNA	0.0
94937_LS 174T_Colon adenocarcinoma_sscDNA	0.0	94999_UM-UC-3_Bladder carcinoma (transitional cell)_sscDNA	0.0
94938_SW-948_Colon adenocarcinoma_sscDNA	0.0	95000_A204_Rhabdomyosarcoma_s scDNA	0.0
94939_SW-480_Colon adenocarcinoma_sscDNA	0.0	95001_HT- 1080_Fibrosarcoma_sscDNA	0.0
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	0.0	95002_MG-63_Osteosarcoma (bone)_sscDNA	0.0
112197_KATO III_Stomach_sscDNA	0.0	95003_SK-LMS- 1_Leiomyosarcoma (vulva)_sscDNA	0.0
94943_NCI-SNU-16_Gastric carcinoma_sscDNA	0.0	95004_SJRH30_Rhabdomyosarcom a (met to bone marrow)_sscDNA	0.8
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	0.0	95005_A431_Epidermoid carcinoma_sscDNA	0.0
94946_RF-1_Gastric adenocarcinoma_sscDNA	0.0	95007_WM266- 4_Melanoma_sscDNA	0.0
94947_RF-48_Gastric adenocarcinoma_sscDNA	0.0	112195_DU 145_Prostate_sscDNA	0.0
96778_MKN-45_Gastric carcinoma_sscDNA	0.0	95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	0.0
94949_NCI-N87_Gastric carcinoma_sscDNA	0.0	112196_SSC-4_Tongue_sscDNA	0.0

94951_OVCAR-5_Ovarian carcinoma_sscDNA	0.0	112194_SSC-9_Tongue_sscDNA	0.0
94952_RL95-2_Uterine carcinoma_sscDNA	0.0	112191_SSC-15_Tongue_sscDNA	0.0
94953_HelaS3_Cervical adenocarcinoma_sscDNA	0.0	95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	0.0

Table AGJ. Panel 1

Tissue Name	Rel. Exp.(%) Ag90, Run 87586258	Tissue Name	Rel. Exp.(%) Ag90, Run 87586258
Endothelial cells	0.0	Renal ca. 786-0	0.0
Endothelial cells (treated)	0.0	Renal ca. A498	0.0
Pancreas	0.1	Renal ca. RXF 393	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. ACHN	0.0
Adrenal gland	0.0	Renal ca. UO-31	0.0
Thyroid	0.0	Renal ca. TK-10	0.0
Salivary gland	0.0	Liver	0.0
Pituitary gland	0.0	Liver (fetal)	0.0
Brain (fetal)	37.1	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	22.5	Lung	0.0
Brain (amygdala)	24.8	Lung (fetal)	0.0
Brain (cerebellum)	100.0	Lung ca. (small cell) LX-1	0.0
Brain (hippocampus)	29.5	Lung ca. (small cell) NCI-H69	33.7
Brain (substantia nigra)	7.6	Lung ca. (s.cell var.) SHP-77	0.0
Brain (thalamus)	13.7	Lung ca. (large cell) NCI-H460	0.0
Brain (hypothalamus)	7.7	Lung ca. (non-sm. cell) A549	0.0
Spinal cord	1.4	Lung ca. (non-s.cell) NCI-H23	0.0

glio/astro U87-MG	0.0	Lung ca. (non-s.cell) HOP-62	0.0
glio/astro U-118-MG	0.0	Lung ca. (non-s.cl) NCI- H522	0.0
astrocytoma SW1783	0.0	Lung ca. (squam.) SW 900	0.0
neuro*; met SK-N-AS	0.4	Lung ca. (squam.) NCI- H596	20.0
astrocytoma SF-539	0.0	Mammary gland	0.1
astrocytoma SNB-75	0.0	Breast ca.* (pl.ef) MCF-7	0.0
glioma SNB-19	1.8	Breast ca.* (pl.ef) MDA- MB-231	0.0
glioma U251	0.4	Breast ca.* (pl. ef) T47D	0.0
glioma SF-295	0.0	Breast ca. BT-549	0.0
Heart	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.1	Ovarian ca. OVCAR-4	0.0
Spleen	0.0	Ovarian ca. OVCAR-5	0.0
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colon (ascending)	0.1	Ovarian ca. IGROV-1	0.0
Stomach	0.1	Ovarian ca. (ascites) SK- OV-3	0.0
Small intestine	0.3	Uterus	0.0
Colon ca. SW480	0.0	Placenta	0.0
Colon ca.* SW620 (SW480 met)	0.0	Prostate	0.0
Colon ca. HT29	0.0	Prostate ca.* (bone met) PC-3	0.0
Colon ca. HCT-116	0.0	Testis	1.3
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca. * (liver met) NCI-N87	0.0	Melanoma M14	0.0

Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.0	Melanoma SK-MEL-28	0.0
Kidney (fetal)	0.0		

Table AGK. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2795, Run 165643063	Rel. Exp.(%) Ag2807, Run 165528058	Tissue Name	Rel. Exp.(%) Ag2795, Run 165643063	Rel. Exp.(%) Ag2807, Run 165528058
Liver adenocarcinoma	0.0	0.0	Kidney (fetal)	0.0	0.0
Pancreas	0.0	0.2	Renal ca. 786-0	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. A498	0.3	0.3
Adrenal gland	0.0	0.3	Renal ca. RXF 393	0.0	0.0
Thyroid	0.0	0.0	Renal ca. ACHN	0.0	0.0
Salivary gland	0.0	0.0	Renal ca. UO-31	0.0	0.0
Pituitary gland	6.8	6.9	Renal ca. TK-10	0.0	0.0
Brain (fetal)	100.0	100.0	Liver	0.2	0.0
Brain (whole)	51.4	56.3	Liver (fetal)	0.0	0.0
Brain (amygdala)	77.4	78.5	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (cerebellum)	58.6	79.0	Lung	0.0	0.0
Brain (hippocampus)	49.0	53.2	Lung (fetal)	0.1	0.2
Brain (substantia nigra)	9.7	13.5	Lung ca. (small cell) LX-1	0.0	0.0
Brain (thalamus)	46.7	63.7	Lung ca. (small cell) NCI-H69	41.5	92.7
Cerebral Cortex	37.9	32.5	Lung ca. (s.cell var.) SHP-77	34.4	25.2
Spinal cord	5.9	4.1	Lung ca. (large cell) NCI-H460	0.3	0.0

glio/astro U87-MG	0.0	0.0	Lung ca. (non-sm. cell) A549	0.0	0.0
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	0.1	0.0
astrocytoma SW1783	0.0	0.1	Lung ca. (non-s.cell) HOP-62	0.0	0.0
neuro*; met SK-N-AS	0.4	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
astrocytoma SF-539	0.0	0.0	Lung ca. (squam.) SW 900	0.0	0.0
astrocytoma SNB-75	0.0	0.0	Lung ca. (squam.) NCI-H596	70.2	58.2
glioma SNB-19	1.2	2.5	Mammary gland	0.4	1.1
glioma U251	3.5	4.2	Breast ca.* (pl.ef) MCF-7	0.0	0.0
glioma SF-295	0.0	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
Heart (fetal)	0.0	0.0	Breast ca.* (pl.ef) T47D	0.0	0.0
Heart	0.1	0.0	Breast ca. BT-549	0.0	0.0
Skeletal muscle (fetal)	0.4	0.0	Breast ca. MDA-N	0.0	0.0
Skeletal muscle	0.0	0.0	Ovary	0.0	0.0
Bone marrow	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.2
Thymus	0.0	0.0	Ovarian ca. OVCAR-4	0.1	0.0
Spleen	0.5	0.0	Ovarian ca. OVCAR-5	0.0	0.0
Lymph node	0.1	0.1	Ovarian ca. OVCAR-8	0.0	0.0
Colorectal	0.0	0.0	Ovarian ca. IGROV-1	0.0	0.0
Stomach	0.0	0.0	Ovarian ca.* (ascites) SK-OV-3	0.2	0.0
Small intestine	0.6	1.0	Uterus	0.0	0.1
Colon ca. SW480	0.0	0.0	Placenta	0.1	0.2

Colon ca.* SW620(SW480 met)	0.0	0.0	Prostate	0.0	0.0
Colon ca. HT29	0.0	0.0	Prostate ca.* (bone met)PC-3	0.0	0.0
Colon ca. HCT-116	0.3	0.0	Testis	0.4	0.3
Colon ca. CaCo-2	0.0	0.0	Melanoma Hs688(A).T	0.0	0.0
Colon ca. tissue(ODO3866)	0.0	0.0	Melanoma* (met) Hs688(B).T	0.1	0.0
Colon ca. HCC-2998	0.0	0.0	Melanoma UACC- 62	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.4	0.1	Melanoma M14	0.0	0.0
Bladder	0.4	0.1	Melanoma LOX IMVI	0.0	0.0
Trachea	0.1	0.1	Melanoma* (met) SK-MEL-5	0.0	0.1
Kidney	0.0	0.0	Adipose	0.1	0.0

Table AGL. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2795, Run 163577802	Rel. Exp.(%) Ag2807, Run 162598819	Tissue Name	Rel. Exp.(%) Ag2795, Run 163577802	Rel. Exp.(%) Ag2807, Run 162598819
Normal Colon	6.3	13.2	Kidney Margin 8120608	0.0	3.8
CC Well to Mod Diff (ODO3866)	0.0	0.0	Kidney Cancer 8120613	0.5	0.0
CC Margin (ODO3866)	1.7	5.9	Kidney Margin 8120614	2.5	1.5
CC Gr.2 rectosigmoid (ODO3868)	0.0	0.0	Kidney Cancer 9010320	0.0	0.7
CC Margin (ODO3868)	0.0	2.9	Kidney Margin 9010321	1.7	1.7
CC Mod Diff (ODO3920)	0.0	0.7	Normal Uterus	0.0	1.0
CC Margin (ODO3920)	0.6	1.4	Uterus Cancer 064011	1.5	0.8

CC Gr.2 ascend colon (ODO3921)	0.0	3.4	Normal Thyroid	1.3	0.3
CC Margin (ODO3921)	1.0	2.3	Thyroid Cancer 064010	1.6	0.0
CC from Partial Hepatectomy (ODO4309) Mets	0.0	0.4	Thyroid Cancer A302152	1.3	0.2
Liver Margin (ODO4309)	0.0	0.4	Thyroid Margin A302153	0.0	0.0
Colon mets to lung (OD04451-01)	0.0	2.9	Normal Breast	0.7	1.7
Lung Margin (OD04451-02)	1.1	4.5	Breast Cancer (OD04566)	0.0	0.3
Normal Prostate 6546-1	6.7	9.8	Breast Cancer (OD04590-01)	0.9	1.3
Prostate Cancer (OD04410)	2.3	3.4	Breast Cancer Mets (OD04590- 03)	0.6	1.8
Prostate Margin (OD04410)	1.6	3.3	Breast Cancer Metastasis (OD04655-05)	1.0	0.8
Prostate Cancer (OD04720-01)	1.2	2.6	Breast Cancer 064006	0.0	0.0
Prostate Margin (OD04720-02)	9.0	7.2	Breast Cancer 1024	0.0	1.5
Normal Lung 061010	2.1	2.6	Breast Cancer 9100266	0.3	1.2
Lung Met to Muscle (ODO4286)	0.0	0.0	Breast Margin 9100265	0.0	1.7
Muscle Margin (ODO4286)	0.7	0.0	Breast Cancer A209073	0.3	0.0
Lung Malignant Cancer (OD03126)	0.0	0.0	Breast Margin A209073	0.0	0.0
Lung Margin (OD03126)	0.5	0.5	Normal Liver	0.0	0.4
Lung Cancer (OD04404)	0.0	0.0	Liver Cancer 064003	0.0	0.0
Lung Margin (OD04404)	0.0	1.5	Liver Cancer 1025	0.0	0.0

Lung Cancer (OD04565)	0.0	0.3	Liver Cancer 1026	100.0	100.0
Lung Margin (OD04565)	0.0	1.7	Liver Cancer 6004-T	0.0	0.0
Lung Cancer (OD04237-01)	20.4	13.2	Liver Tissue 6004-N	0.0	0.0
Lung Margin (OD04237-02)	1.3	0.9	Liver Cancer 6005-T	80.1	64.6
Ocular Mel Met to Liver (ODO4310)	0.0	2.6	Liver Tissue 6005-N	0.0	0.0
Liver Margin (ODO4310)	0.0	0.0	Normal Bladder	7.2	7.4
Melanoma Mets to Lung (OD04321)	0.0	0.0	Bladder Cancer 1023	0.4	0.0
Lung Margin (OD04321)	1.6	2.9	Bladder Cancer A302173	1.3	2.8
Normal Kidney	1.1	1.0	Bladder Cancer (OD04718-01)	0.0	0.4
Kidney Ca, Nuclear grade 2 (OD04338)	1.2	1.2	Bladder Normal Adjacent (OD04718-03)	0.7	0.4
Kidney Margin (OD04338)	0.5	1.1	Normal Ovary	0.0	0.0
Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	0.5	Ovarian Cancer 064008	0.0	0.7
Kidney Margin (OD04339)	0.5	0.9	Ovarian Cancer (OD04768-07)	0.4	1.1
Kidney Ca, Clear cell type (OD04340)	0.0	0.5	Ovary Margin (OD04768-08)	0.0	0.0
Kidney Margin (OD04340)	1.0	0.3	Normal Stomach	1.2	2.6
Kidney Ca, Nuclear grade 3 (OD04348)	0.0	0.9	Gastric Cancer 9060358	0.0	0.0
Kidney Margin (OD04348)	0.3	0.8	Stomach Margin 9060359	0.4	1.4
Kidney Cancer (OD04622-01)	0.0	0.9	Gastric Cancer 9060395	0.4	0.5
Kidney Margin (OD04622-03)	0.0	0.0	Stomach Margin 9060394	0.6	2.0

Kidney Cancer (OD04450-01)	0.0	1.2	Gastric Cancer 9060397	1.4	0.8
Kidney Margin (OD04450-03)	0.3	0.4	Stomach Margin 9060396	6.0	1.9
Kidney Cancer 8120607	0.0	0.0	Gastric Cancer 064005	3.4	1.6

Table AGM. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag7017, Run 279031713	Tissue Name	Rel. Exp.(%) Ag7017, Run 279031713
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	2.1	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	42.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	15.5

Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	5.3
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	5.5	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	13.6	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0

Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	100.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	14.3	Colon	6.8
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	4.1
HUVEC starved	0.0		

Table AGN. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2807, Run 165806333	Tissue Name	Rel. Exp.(%) Ag2807, Run 165806333
Secondary Th1 act	1.2	HUVEC IL-1beta	0.0
Secondary Th2 act	1.1	HUVEC IFN gamma	2.1
Secondary Tr1 act	2.7	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	1.9	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	2.4	HUVEC IL-11	0.9
Secondary Tr1 rest	0.0	Lung Microvascular EC none	1.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1 beta	0.0
Primary Th2 act	1.2	Microvascular Dermal EC none	1.9
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1 beta	0.0
Primary Th1 rest	6.1	Bronchial epithelium TNFalpha + IL1 beta	0.0
Primary Th2 rest	2.7	Small airway epithelium none	3.9
Primary Tr1 rest	1.1	Small airway epithelium TNFalpha + IL-1 beta	3.6
CD45RA CD4 lymphocyte act	4.0	Coronary artery SMC rest	0.8
CD45RO CD4 lymphocyte act	4.5	Coronary artery SMC TNFalpha + IL-1 beta	0.0
CD8 lymphocyte act	3.2	Astrocytes rest	100.0

Secondary CD8 lymphocyte rest	2.1	Astrocytes TNFalpha + IL-1beta	84.1
Secondary CD8 lymphocyte act	1.6	KU-812 (Basophil) rest	4.6
CD4 lymphocyte none	1.2	KU-812 (Basophil) PMA/ionomycin	1.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	5.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	4.1	Liver cirrhosis	1.1
LAK cells IL-2+IL-12	2.6	Lupus kidney	1.6
LAK cells IL-2+IFN gamma	3.8	NCI-H292 none	6.1
LAK cells IL-2+ IL-18	1.0	NCI-H292 IL-4	2.5
LAK cells PMA/ionomycin	1.2	NCI-H292 IL-9	2.1
NK Cells IL-2 rest	2.1	NCI-H292 IL-13	2.8
Two Way MLR 3 day	3.8	NCI-H292 IFN gamma	1.0
Two Way MLR 5 day	2.6	HPAEC none	0.0
Two Way MLR 7 day	3.6	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	1.9	Lung fibroblast none	1.3
PBMC PWM	1.3	Lung fibroblast TNF alpha + IL-1 beta	1.6
PBMC PHA-L	0.0	Lung fibroblast IL-4	2.5
Ramos (B cell) none	6.0	Lung fibroblast IL-9	2.8
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	1.3
B lymphocytes PWM	0.9	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	9.0	Dermal fibroblast CCD1070 rest	2.1
EOL-1 dbcAMP	5.6	Dermal fibroblast CCD1070 TNF alpha	4.4
EOL-1 dbcAMP PMA/ionomycin	14.8	Dermal fibroblast CCD1070 IL-1 beta	0.8
Dendritic cells none	4.3	Dermal fibroblast IFN gamma	1.5

Dendritic cells LPS	5.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	5.1	IBD Colitis 2	6.3
Monocytes rest	5.4	IBD Crohn's	0.0
Monocytes LPS	4.4	Colon	58.2
Macrophages rest	1.6	Lung	3.4
Macrophages LPS	0.0	Thymus	8.8
HUVEC none	1.2	Kidney	31.6
HUVEC starved	0.9		

AI_comprehensive_panel_v1.0 Summary: Ag2795 High expression of this gene is mostly restricted to orthoarthritis (OA) bone (CT=28). Thus, expression of this gene may be used to distinguish OA bone from other samples used in this panel. In addition, therapeutic modulation of this gene product may be useful in the treatment of orthoarthritis.

- 5 **CNS_neurodegeneration_v1.0 Summary:** Ag2795/Ag2807/Ag7017 Three experiments with two different probes and primer sets are in very good agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this
- 10 experiment. See Panel 1.3D for a discussion of this gene in treatment of central nervous system disorders.

- 15 **General_screening_panel_v1.6 Summary:** Ag7017 Highest expression of this gene is detected in brain cerebellum (CT=25.3). High to moderate levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore,
- therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

- 20 This gene codes for a homolog of mouse seizure related protein, SEZ-6. Mouse SEZ-6 was first isolated from cerebrum cortex-derived cells treated with pentylenetetrazole (PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in four lung cancer cell lines and a ovarian cancer cell line. Therefore, expression of this gene may be used as diagnostic marker to detect lung cancer and also, modulation of this gene or its protein product through the use of antibody or protein therapeutics, may be useful in the treatment of lung and ovarian cancers.

HASS Panel v1.0 Summary: Ag7017 Highest expression of this gene is detected in a medulloblastoma (CT=28). In addition, moderate levels of expression of this gene is also seen in glioma samples. Therefore, therapeutic modulation of this gene may be useful in the treatment of brain cancer.

Oncology_cell_line_screening_panel_v3.2 Summary: Ag2795 Highest expression of this gene is detected in small lung cancer DMS-79 cell line (CT=26.5). Moderate to low levels of expression of this gene is also seen in number of cell lines derived from lung, colon, bone and brain cancers. Therefore, expression of this gene may be used as marker to detect these cancers. In addition, therapeutic modulation of this gene through the use of antibodies or small molecule drug may be useful in the treatment of lung, colon, bone and brain cancers.

Panel 1 Summary: Ag90 Highest expression of this gene is detected in brain cerebellum (CT=25). High levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. In addition, moderate levels of expression of this gene is also seen in two lung cancer cell lines and a glioma cell line. See panel 1.3D for further discussion of this gene.

Panel 1.3D Summary: Ag2795/Ag2807 Two experiments with same probe and primer sets are in excellent agreement with highest expression of this gene detected fetal brain (CTs=27-28.5). Moderate levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for a homolog of mouse seizure related protein, SEZ-6. Mouse SEZ-6 was first isolated from cerebrum cortex-derived cells treated with pentylentetrazole

(PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in three
5 lung cancer cell lines and two of the glioma cell lines. Therefore, expression of this gene may be used as diagnostic marker to detect lung cancer and glioma. Furthermore, modulation of this gene or its protein product through the use of antibody or protein therapeutics, may be useful in the treatment of lung cancer and glioma.

Panel 2D Summary: Ag2795/Ag2807 Two experiments with same probe and
10 primer sets are in excellent agreement with highest expression of this gene detected in liver cancer 1026 sample (CTs=31.3). In addition, moderate to low levels of expression of this gene is also seen in a lung cancer and a liver cancer (6005-T). Expression of this gene is higher in cancer as compared to corresponding adjacent normal tissue (CTs>37). Thus, expression of this gene may be used to distinguish between normal and cancer samples and
15 as diagnostic marker to detect lung and liver cancer. In addition, therapeutic modulation of this gene through the use of antibodies may be useful in the treatment of these cancers.

Panel 4.1D Summary: Ag7017 Low levels of expression of this gene is restricted to TNF alpha and LPS stimulated neutrophils (CT=34.4). Therefore, expression of this gene may be used to distinguish this sample from other samples in the panel. This expression
20 profile suggest that the protein encoded by this gene is produced by activated neutrophils but not by resting neutrophils. Therefore, therapeutic modulation of this gene product through the use of antibodies or small molecule drug may reduce activation of these inflammatory cells and be useful to reduce or eliminate the symptoms in patients with Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary
25 disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis. In addition, small molecule or antibody antagonists of this gene product may be effective in increasing the immune response in patients with AIDS or other immunodeficiencies.

Panel 4D Summary: Ag2807 Highest expression of this gene is detected in astrocytes (CTs=33). Thus expression of this gene may be used to distinguish astrocytes
30 from other samples in this panel. In addition, low but significant levels of expression of this gene is also seen in normal tissue represented by colon and kidney. Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory

diseases affecting brain, colon and kidney such as lupus erythematosus, Crohn's disease, and ulcerative colitis.

general oncology screening panel_v_2.4 Summary: Ag2795 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

**AH. CG52919-05 and CG52919-06: SEZ-6-Like Protein
(7520500-54-4).**

Expression of gene CG52919-05 and CG52919-06 was assessed using the primer-probe sets Ag2796, Ag90 and Ag124, described in Tables AHA, AHB and AHC. Results of the RTQ-PCR runs are shown in Tables AHD, AHE, AHF and AHG. Note that probe-primer sets Ag2796 and Ag124 are specific for the CG52919-05 variant. Also, Note that CG52919-06 represents a full-length physical clone.

Table AHA. Probe Name Ag2796

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctacaaccgcattaccataga-3'	22	1670	399
Probe	TET-5'-tcagcggtttgacaatccaacttacga-3'-TAMRA	26	1693	400
Reverse	5'-gtctcctgcaaaggaaagagat-3'	22	1725	401

Table AHB. Probe Name Ag90

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttggcctggactgcttcttc-3'	20	977	402
Probe	TET-5'-catctctgtctaccctggctatggcgtg-3'-TAMRA	28	999	403
Reverse	5'-aggctgatattctggaccttgatt-3'	24	1029	404

Table AHC. Probe Name Ag124

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cgccctacaaccgcat-3'	17	1666	405

Probe	TET-5' - ccatagagtcagcgtttgacaatccaactt acg-3' - TAMRA	33	1685	406
Reverse	5' - ctgcaaaggaaagagatccagtc-3'	23	1719	407

Table AHD. Panel I

Tissue Name	Rel. Exp.(%) Ag124, Run 87587871	Rel. Exp.(%) Ag90, Run 87586258	Tissue Name	Rel. Exp.(%) Ag124, Run 87587871	Rel. Exp.(%) Ag90, Run 87586258
Endothelial cells	0.0	0.0	Renal ca. 786-0	0.0	0.0
Endothelial cells (treated)	0.0	0.0	Renal ca. A498	0.0	0.0
Pancreas	0.1	0.1	Renal ca. RXF 393	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. ACHN	0.0	0.0
Adrenal gland	0.0	0.0	Renal ca. UO-31	0.0	0.0
Thyroid	0.0	0.0	Renal ca. TK-10	0.0	0.0
Salivary gland	0.0	0.0	Liver	0.0	0.0
Pituitary gland	0.0	0.0	Liver (fetal)	0.0	0.0
Brain (fetal)	25.3	37.1	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (whole)	24.0	22.5	Lung	0.0	0.0
Brain (amygdala)	26.2	24.8	Lung (fetal)	0.0	0.0
Brain (cerebellum)	100.0	100.0	Lung ca. (small cell) LX-1	0.0	0.0
Brain (hippocampus)	21.6	29.5	Lung ca. (small cell) NCI-H69	43.5	33.7
Brain (substantia nigra)	7.7	7.6	Lung ca. (s.cell var.) SHP-77	0.0	0.0
Brain (thalamus)	20.0	13.7	Lung ca. (large cell) NCI-H460	0.0	0.0
Brain (hypothalamus)	8.4	7.7	Lung ca. (non-sm. cell) A549	0.0	0.0
Spinal cord	1.8	1.4	Lung ca. (non-s.cell) NCI-H23	0.0	0.0

glio/astro U87-MG	0.0	0.0	Lung ca. (non-s.cell) HOP-62	0.0	0.0
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (squam.) SW 900	0.0	0.0
neuro*; met SK-N- AS	0.0	0.4	Lung ca. (squam.) NCI-H596	26.8	20.0
astrocytoma SF-539	0.0	0.0	Mammary gland	0.0	0.1
astrocytoma SNB-75	0.0	0.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0
glioma SNB-19	2.1	1.8	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
glioma U251	0.5	0.4	Breast ca.* (pl. ef) T47D	0.0	0.0
glioma SF-295	0.0	0.0	Breast ca. BT-549	0.0	0.0
Heart	0.0	0.0	Breast ca. MDA-N	0.0	0.0
Skeletal muscle	0.0	0.0	Ovary	0.0	0.0
Bone marrow	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.0
Thymus	0.0	0.1	Ovarian ca. OVCAR-4	0.0	0.0
Spleen	0.0	0.0	Ovarian ca. OVCAR-5	0.0	0.0
Lymph node	0.0	0.0	Ovarian ca. OVCAR-8	0.0	0.0
Colon (ascending)	0.0	0.1	Ovarian ca. IGROV- 1	0.0	0.0
Stomach	0.0	0.1	Ovarian ca. (ascites) SK-OV-3	0.0	0.0
Small intestine	0.5	0.3	Uterus	0.0	0.0
Colon ca. SW480	0.0	0.0	Placenta	0.0	0.0
Colon ca.* SW620 (SW480 met)	0.0	0.0	Prostate	0.0	0.0
Colon ca. HT29	0.0	0.0	Prostate ca.* (bone met) PC-3	0.0	0.0
Colon ca. HCT-116	0.0	0.0	Testis	1.0	1.3

Colon ca. CaCo-2	0.0	0.0	Melanoma Hs688(A).T	0.0	0.0
Colon ca. HCT-15	0.0	0.0	Melanoma* (met) Hs688(B).T	0.0	0.0
Colon ca. HCC-2998	0.0	0.0	Melanoma UACC-62	0.0	0.0
Gastric ca. * (liver met) NCI-N87	0.0	0.0	Melanoma M14	0.0	0.0
Bladder	0.0	0.0	Melanoma LOX IMVI	0.0	0.0
Trachea	0.0	0.0	Melanoma* (met) SK-MEL-5	0.0	0.0
Kidney	0.0	0.0	Melanoma SK-MEL-28	0.0	0.0
Kidney (fetal)	0.0	0.0			

Table AHE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2796, Run 165527192	Tissue Name	Rel. Exp.(%) Ag2796, Run 165527192
Liver adenocarcinoma	0.0	Kidney (fetal)	0.0
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.4
Adrenal gland	0.2	Renal ca. RXF 393	0.0
Thyroid	0.0	Renal ca. ACHN	0.2
Salivary gland	0.0	Renal ca. UO-31	0.0
Pituitary gland	10.0	Renal ca. TK-10	0.0
Brain (fetal)	100.0	Liver	0.0
Brain (whole)	65.1	Liver (fetal)	0.0
Brain (amygdala)	76.8	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	76.8	Lung	0.0
Brain (hippocampus)	51.4	Lung (fetal)	0.0
Brain (substantia nigra)	11.7	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	70.2	Lung ca. (small cell) NCI-H69	23.8

Cerebral Cortex	37.9	Lung ca. (s.cell var.) SHP-77	21.6
Spinal cord	3.5	Lung ca. (large cell) NCI-H460	0.6
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
glio/astro U-118-MG	0.1	Lung ca. (non-s.cell) NCI-H23	0.0
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.4	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.1
astrocytoma SNB-75	0.0	Lung ca. (squam.) NCI-H596	35.8
glioma SNB-19	3.2	Mammary gland	0.0
glioma U251	4.3	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.1
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.0
Heart	0.0	Breast ca. BT-549	0.1
Skeletal muscle (fetal)	2.3	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.0	Ovarian ca. OVCAR-4	0.0
Spleen	0.1	Ovarian ca. OVCAR-5	0.1
Lymph node	0.3	Ovarian ca. OVCAR-8	0.0
Colorectal	0.0	Ovarian ca. IGROV-1	0.0
Stomach	0.1	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	0.6	Uterus	0.1
Colon ca. SW480	0.0	Placenta	1.9
Colon ca.* SW620(SW480 met)	0.0	Prostate	0.0

Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	3.3	Testis	2.0
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma M14	0.0
Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.0	Adipose	0.0

Table AHF. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2796, Run 162570140	Tissue Name	Rel. Exp.(%) Ag2796, Run 162570140
Normal Colon	26.6	Kidney Margin 8120608	0.0
CC Well to Mod Diff (ODO3866)	0.0	Kidney Cancer 8120613	0.0
CC Margin (ODO3866)	4.2	Kidney Margin 8120614	1.7
CC Gr.2 rectosigmoid (ODO3868)	0.0	Kidney Cancer 9010320	3.5
CC Margin (ODO3868)	0.7	Kidney Margin 9010321	3.7
CC Mod Diff (ODO3920)	0.0	Normal Uterus	3.7
CC Margin (ODO3920)	13.1	Uterus Cancer 064011	6.0
CC Gr.2 ascend colon (ODO3921)	4.8	Normal Thyroid	0.0
CC Margin (ODO3921)	5.1	Thyroid Cancer 064010	0.0
CC from Partial Hepatectomy (ODO4309) Mets	8.5	Thyroid Cancer A302152	3.5
Liver Margin (ODO4309)	0.0	Thyroid Margin A302153	0.0
Colon mets to lung (OD04451-01)	0.0	Normal Breast	4.5

Lung Margin (OD04451-02)	1.1	Breast Cancer (OD04566)	1.8
Normal Prostate 6546-1	17.6	Breast Cancer (OD04590-01)	3.0
Prostate Cancer (OD04410)	12.3	Breast Cancer Mets (OD04590-03)	6.3
Prostate Margin (OD04410)	6.2	Breast Cancer Metastasis (OD04655-05)	9.2
Prostate Cancer (OD04720-01)	11.5	Breast Cancer 064006	2.3
Prostate Margin (OD04720-02)	18.3	Breast Cancer 1024	4.3
Normal Lung 061010	2.0	Breast Cancer 9100266	4.1
Lung Met to Muscle (ODO4286)	0.0	Breast Margin 9100265	0.0
Muscle Margin (ODO4286)	0.7	Breast Cancer A209073	3.0
Lung Malignant Cancer (OD03126)	1.0	Breast Margin A209073	0.7
Lung Margin (OD03126)	2.1	Normal Liver	0.0
Lung Cancer (OD04404)	1.8	Liver Cancer 064003	0.0
Lung Margin (OD04404)	2.1	Liver Cancer 1025	3.7
Lung Cancer (OD04565)	5.6	Liver Cancer 1026	95.9
Lung Margin (OD04565)	0.0	Liver Cancer 6004-T	0.0
Lung Cancer (OD04237-01)	48.0	Liver Tissue 6004-N	7.2
Lung Margin (OD04237-02)	0.0	Liver Cancer 6005-T	100.0
Ocular Mel Met to Liver (ODO4310)	2.8	Liver Tissue 6005-N	0.0
Liver Margin (ODO4310)	0.0	Normal Bladder	8.8
Melanoma Mets to Lung (OD04321)	1.3	Bladder Cancer 1023	0.0
Lung Margin (OD04321)	21.6	Bladder Cancer A302173	1.5
Normal Kidney	6.9	Bladder Cancer (OD04718-01)	1.8
Kidney Ca, Nuclear grade 2 (OD04338)	6.4	Bladder Normal Adjacent (OD04718-03)	2.8
Kidney Margin (OD04338)	2.0	Normal Ovary	4.9

Kidney Ca Nuclear grade 1/2 (OD04339)	0.9	Ovarian Cancer 064008	3.6
Kidney Margin (OD04339)	3.0	Ovarian Cancer (OD04768-07)	2.5
Kidney Ca, Clear cell type (OD04340)	3.0	Ovary Margin (OD04768-08)	0.0
Kidney Margin (OD04340)	1.3	Normal Stomach	3.7
Kidney Ca, Nuclear grade 3 (OD04348)	0.7	Gastric Cancer 9060358	0.6
Kidney Margin (OD04348)	2.5	Stomach Margin 9060359	4.8
Kidney Cancer (OD04622-01)	0.8	Gastric Cancer 9060395	1.8
Kidney Margin (OD04622-03)	0.0	Stomach Margin 9060394	1.0
Kidney Cancer (OD04450-01)	3.9	Gastric Cancer 9060397	0.0
Kidney Margin (OD04450-03)	2.2	Stomach Margin 9060396	1.0
Kidney Cancer 8120607	0.8	Gastric Cancer 064005	5.3

Table AHG. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2796, Run 162292586	Tissue Name	Rel. Exp.(%) Ag2796, Run 162292586
Secondary Th1 act	4.3	HUVEC IL-1beta	0.0
Secondary Th2 act	8.9	HUVEC IFN gamma	8.1
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	4.7
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	4.2
Secondary Tr1 rest	4.7	Lung Microvascular EC none	3.7
Primary Th1 act	6.2	Lung Microvascular EC TNFalpha + IL-1beta	3.7
Primary Th2 act	0.0	Microvascular Dermal EC none	9.9
Primary Tr1 act	4.0	Microvascular Dermal EC TNFalpha + IL-1beta	4.2

Primary Th1 rest	4.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	8.2	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	6.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	8.4	Astrocytes rest	34.9
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	42.3
Secondary CD8 lymphocyte act	9.5	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	14.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	14.5	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	16.8	Liver cirrhosis	3.8
LAK cells IL-2+IL-12	3.8	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	3.9	NCI-H292 none	30.6
LAK cells IL-2+ IL-18	21.8	NCI-H292 IL-4	15.3
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	30.1
NK Cells IL-2 rest	15.4	NCI-H292 IL-13	18.2
Two Way MLR 3 day	18.8	NCI-H292 IFN gamma	8.3
Two Way MLR 5 day	7.9	HPAEC none	0.0
Two Way MLR 7 day	3.1	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	6.1	Lung fibroblast none	11.2
PBMC PWM	20.4	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	6.5	Lung fibroblast IL-4	7.5

Ramos (B cell) none	3.3	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	23.0	Lung fibroblast IL-13	4.2
B lymphocytes PWM	35.6	Lung fibroblast IFN gamma	9.5
B lymphocytes CD40L and IL-4	70.7	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	7.4	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	51.1	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	10.6	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	20.9	Dermal fibroblast IL-4	8.9
Dendritic cells anti-CD40	9.8	IBD Colitis 2	0.0
Monocytes rest	9.3	IBD Crohn's	0.0
Monocytes LPS	9.6	Colon	100.0
Macrophages rest	4.6	Lung	17.2
Macrophages LPS	5.4	Thymus	20.3
HUVEC none	11.3	Kidney	33.0
HUVEC starved	18.4		

Panel 1 Summary: Ag90/Ag2796 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in brain cerebellum (CT=25-26). High levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. In addition, moderate levels of expression of this gene is also seen in two lung cancer cell lines and a glioma cell line. See panel 1.3D for further discussion of this gene.

Panel 1.3D Summary: Ag2796 Highest expression of this gene is detected in fetal brain (CT=28.7). Moderate levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for a homolog of mouse seizure related protein, SEZ-6. Mouse SEZ-6 was first isolated from cerebrum cortex-derived cells treated with pentylentetrazole (PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also
5 play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in three lung cancer cell lines, two of the glioma cell lines and a colon cancer cell line. Therefore, expression of this gene may be used as diagnostic marker to detect lung, colon and brain cancers. Furthermore, modulation of this gene or its protein product through the use of
10 antibody or protein therapeutics, may be useful in the treatment of lung, colon and brain cancers.

Significant expression is also detected in fetal skeletal muscle. This gene is expressed at much higher levels in fetal (CT = 34.1) when compared to adult skeletal muscle (CT = 40). This observation suggests that expression of this gene can be used to
15 distinguish fetal from adult skeletal muscle. In addition, the relative overexpression of this gene in fetal skeletal muscle suggests that the protein product may enhance muscular growth or development in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the SEZ-6 encoded by this gene could be useful in treatment of muscle related diseases. More specifically, treatment of weak or dystrophic
20 muscle with the protein encoded by this gene could restore muscle mass or function.

Panel 2D Summary: Ag2796 Highest expression of this gene is detected in two liver cancer samples (CTs=32.3). In addition, low levels of expression of this gene is also seen in a lung cancer sample. Expression of this gene is higher in lung and liver cancer as compared to corresponding adjacent normal tissue (CTs=40). Thus, expression of this gene
25 may be used to distinguish between normal and cancer samples and as diagnostic marker to detect lung and liver cancer. In addition, therapeutic modulation of this gene through the use of antibodies may be useful in the treatment of these cancers.

Panel 4D Summary: Ag2796 Low but significant expression of this gene is detected exclusively in colon (CT=34.8). Therefore, expression of this gene may be used to
30 distinguish colon from the other tissues on this panel. Furthermore, expression of this gene is decreased in colon samples from patients with inflammatory bowel disease, colitis and Crohn's disease relative to normal colon. Therefore, therapeutic modulation of the activity

of the SEZ-6 protein encoded by this gene may be useful in the treatment of inflammatory bowel disease.

AI. CG55698-02: Colipase precursor protein-like protein.

Expression of gene CG55698-02 was assessed using the primer-probe set Ag7086,
5 described in Table AIA. Results of the RTQ-PCR runs are shown in Table AIB. Note that CG55698-02 represents a full-length physical clone.

Table AIA. Probe Name Ag7086

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - cattatcaacctgacgctctatg-3'	23	88	408
Probe	TET-5' - ccacgctcacaggacactttagta -3' - TAMRA	26	116	409
Reverse	5' -atggtcttgtctccctcaca-3'	20	149	410

Table AIB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7086, Run 296433065	Tissue Name	Rel. Exp.(%) Ag7086, Run 296433065
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	12.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0

Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB- 75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0

Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.4	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	100.0

CNS_neurodegeneration_v1.0 Summary: Ag7086 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag7086 Highest expression of this gene is seen in pancreas (CT=22.7). Therefore, expression of this gene may be used to distinguish pancreas from other samples in this panel. This gene codes for a deletion variant of colipase. Pancreatic colipase is a 12-kD polypeptide cofactor for pancreatic lipase, an enzyme essential for the absorption of dietary long-chain triglyceride fatty acids. Colipase is thought to anchor lipase noncovalently to the surface of lipid micelles, counteracting the destabilizing influence of intestinal bile salts (OMIM 120105). Therefore, therapeutic modulation of expression of this gene or colipase encoded by this gene may be useful in the treatment of dietary fat related disorders including pancreatic insufficiency and fat malabsorption.

AJ. CG55832-02 and CG55832-03: Tenascin-C Precursor

Protein-like Protein.

Expression of gene CG55832-02 and CG55832-03 was assessed using the primer-probe set Ag4681, described in Table AJA. Results of the RTQ-PCR runs are shown in Tables AJB, AJC and AJD.

Table AJA. Probe Name Ag4681

Primers	Sequences	Length	Start Position	SEQ ID No
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Forward	5'-tggtccaaagagccaacaag-3'	20	2868	411
Probe	TET-5'- ccaaaaccacactcacaggtctgagg -3'-TAMRA	26	2894	412
Reverse	5'-agcagaaactccaatcccatat- 3'	22	2931	413

Table AJB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4681, Run 222811927	Tissue Name	Rel. Exp.(%) Ag4681, Run 222811927
Adipose	0.9	Renal ca. TK-10	0.4
Melanoma* Hs688(A).T	18.2	Bladder	1.3
Melanoma* Hs688(B).T	7.3	Gastric ca. (liver met.) NCI-N87	1.3
Melanoma* M14	10.8	Gastric ca. KATO III	0.3
Melanoma* LOXIMVI	7.7	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	3.8	Colon ca. SW480	0.2
Squamous cell carcinoma SCC-4	1.2	Colon ca.* (SW480 met) SW620	6.7
Testis Pool	1.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	7.7	Colon ca. HCT-116	0.0
Prostate Pool	1.7	Colon ca. CaCo-2	0.3
Placenta	0.1	Colon cancer tissue	3.7
Uterus Pool	2.5	Colon ca. SW1116	0.1
Ovarian ca. OVCAR-3	3.2	Colon ca. Colo-205	0.3
Ovarian ca. SK-OV-3	0.2	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.5	Colon Pool	5.9
Ovarian ca. OVCAR-5	0.2	Small Intestine Pool	3.4
Ovarian ca. IGROV-1	13.9	Stomach Pool	2.9
Ovarian ca. OVCAR-8	4.6	Bone Marrow Pool	2.9
Ovary	0.2	Fetal Heart	0.1
Breast ca. MCF-7	0.0	Heart Pool	3.7
Breast ca. MDA-MB-231	2.6	Lymph Node Pool	7.9

Breast ca. BT 549	2.4	Fetal Skeletal Muscle	0.4
Breast ca. T47D	0.4	Skeletal Muscle Pool	1.0
Breast ca. MDA-N	3.7	Spleen Pool	2.0
Breast Pool	4.5	Thymus Pool	2.5
Trachea	3.1	CNS cancer (glio/astro) U87-MG	29.1
Lung	0.1	CNS cancer (glio/astro) U-118-MG	100.0
Fetal Lung	8.7	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.2	CNS cancer (astro) SF- 539	3.6
Lung ca. LX-1	3.6	CNS cancer (astro) SNB- 75	37.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB- 19	13.1
Lung ca. SHP-77	1.0	CNS cancer (glio) SF-295	8.2
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.4
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.3
Lung ca. NCI-H23	0.1	Brain (fetal)	3.4
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.4
Lung ca. HOP-62	11.8	Cerebral Cortex Pool	0.4
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.5
Liver	0.1	Brain (Thalamus) Pool	0.7
Fetal Liver	0.2	Brain (whole)	0.9
Liver ca. HepG2	0.0	Spinal Cord Pool	1.0
Kidney Pool	11.3	Adrenal Gland	0.4
Fetal Kidney	7.1	Pituitary gland Pool	0.2
Renal ca. 786-0	2.2	Salivary Gland	0.3
Renal ca. A498	0.3	Thyroid (female)	0.1
Renal ca. ACHN	0.5	Pancreatic ca. CAPAN2	0.4
Renal ca. UO-31	1.3	Pancreas Pool	3.5

Table A1C. Oncology_cell_line_screening_panel_v3.1

Tissue Name	Rel. Exp.(%) Ag4681, Run 224056814	Tissue Name	Rel. Exp.(%) Ag4681, Run 224056814
Daoy Medulloblastoma/Cerebellum	8.6	Ca Ski_Cervical epidermoid carcinoma (metastasis)	18.7
TE671 Medulloblastom/Cerebellum	9.2	ES-2_Ovarian clear cell carcinoma	6.0
D283 Med Medulloblastoma/Cerebellum	0.1	Ramos/6h stim_ Stimulated with PMA/ionomycin 6h	0.0
PFSK-1 Primitive Neuroectodermal/Cerebellum	4.4	Ramos/14h stim_ Stimulated with PMA/ionomycin 14h	0.0
XF-498_CNS	100.0	MEG-01_Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78_CNS/glioma	66.4	Raji_Burkitt's lymphoma	0.0
SF-268_CNS/glioblastoma	2.0	Daudi_Burkitt's lymphoma	0.0
T98G_Glioblastoma	5.0	U266_B-cell plasmacytoma/myeloma	0.0
SK-N-SH_Neuroblastoma (metastasis)	78.5	CA46_Burkitt's lymphoma	0.0
SF-295_CNS/glioblastoma	6.4	RL_non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.2	JM1_pre-B-cell lymphoma/leukemia	0.0
Cerebellum	0.4	Jurkat_T cell leukemia	0.0
NCI-H292_Mucoepidermoid lung ca.	1.6	TF-1_Erythroleukemia	0.0
DMS-114_Small cell lung cancer	0.4	HUT 78_T-cell lymphoma	0.0
DMS-79_Small cell lung cancer/neuroendocrine	0.2	U937_Histiocytic lymphoma	0.0
NCI-H146_Small cell lung cancer/neuroendocrine	0.0	KU-812_Myelogenous leukemia	0.0
NCI-H526_Small cell lung cancer/neuroendocrine	0.1	769-P_Clear cell renal ca.	0.0
NCI-N417_Small cell lung cancer/neuroendocrine	1.8	Caki-2_Clear cell renal ca.	0.7
NCI-H82_Small cell lung cancer/neuroendocrine	0.0	SW 839_Clear cell renal ca.	4.1

NCI-H157_Squamous cell lung cancer (metastasis)	5.6	G401_Wilms' tumor	0.0
NCI-H1155_Large cell lung cancer/neuroendocrine	0.0	Hs766T_Pancreatic ca. (LN metastasis)	0.0
NCI-H1299_Large cell lung cancer/neuroendocrine	0.3	CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)	0.1
NCI-H727_Lung carcinoid	0.2	SU86.86_Pancreatic carcinoma (liver metastasis)	4.3
NCI-UMC-11_Lung carcinoid	0.0	BxPC-3_Pancreatic adenocarcinoma	0.0
LX-1_Small cell lung cancer	9.0	HPAC_Pancreatic adenocarcinoma	0.5
Colo-205_Colon cancer	1.3	MIA PaCa-2_Pancreatic ca.	0.1
KM12_Colon cancer	3.3	CFPAC-1_Pancreatic ductal adenocarcinoma	10.3
KM20L2_Colon cancer	0.2	PANC-1_Pancreatic epithelioid ductal ca.	0.9
NCI-H716_Colon cancer	0.0	T24_Bladder ca. (transitional cell)	0.1
SW-48_Colon adenocarcinoma	0.0	5637_Bladder ca.	13.8
SW1116_Colon adenocarcinoma	0.4	HT-1197_Bladder ca.	0.1
LS 174T_Colon adenocarcinoma	2.4	UM-UC-3_Bladder ca. (transitional cell)	2.9
SW-948_Colon adenocarcinoma	0.1	A204_Rhabdomyosarcoma	61.1
SW-480_Colon adenocarcinoma	0.1	HT-1080_Fibrosarcoma	1.3
NCI-SNU-5_Gastric ca.	0.2	MG-63_Osteosarcoma (bone)	2.2
KATO III_Stomach	0.2	SK-LMS-1_Leiomyosarcoma (vulva)	28.1
NCI-SNU-16_Gastric ca.	25.7	SJRH30_Rhabdomyosarcoma (met to bone marrow)	23.0
NCI-SNU-1_Gastric ca.	0.0	A431_Epidermoid ca.	0.1
RF-1_Gastric adenocarcinoma	0.0	WM266-4_Melanoma	51.1
RF-48_Gastric adenocarcinoma	0.0	DU 145_Prostate	4.5
MKN-45_Gastric ca.	0.3	MDA-MB-468_Breast adenocarcinoma	0.0
NCI-N87_Gastric ca.	0.2	SSC-4_Tongue	3.3
OVCAR-5_Ovarian ca.	0.3	SSC-9_Tongue	15.5
RL95-2_Uterine carcinoma	0.0	SSC-15_Tongue	9.9

HeLaS3_Cervical adenocarcinoma	0.0	CAL 27_Squamous cell ca. of tongue	31.9
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Table AJD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4681, Run 268722514	Tissue Name	Rel. Exp.(%) Ag4681, Run 268722514
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	8.5
Primary Th2 rest	0.0	Small airway epithelium none	3.1
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	10.2
CD45RA CD4 lymphocyte act	14.4	Coronary artery SMC rest	1.4
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	3.5
CD8 lymphocyte act	0.0	Astrocytes rest	9.6
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL- 1beta	7.7
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	15.1

LAK cells rest	0.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	22.4
LAK cells IL-2	0.0	Liver cirrhosis	0.6
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.1
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	1.1
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.1
LAK cells PMA/ionomycin	0.4	NCI-H292 IL-13	2.2
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.1
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	46.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	19.8
PBMC PWM	0.0	Lung fibroblast IL-4	74.7
PBMC PHA-L	0.0	Lung fibroblast IL-9	75.3
Ramos (B cell) none	0.0	Lung fibroblast IL-13	44.4
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	53.2
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	27.7
B lymphocytes CD40L and IL-4	0.1	Dermal fibroblast CCD1070 TNF alpha	26.4
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	31.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	12.8
Dendritic cells none	0.6	Dermal fibroblast IL-4	100.0
Dendritic cells LPS	0.6	Dermal Fibroblasts rest	4.6
Dendritic cells anti-CD40	0.2	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.1	Colon	0.5
Macrophages rest	0.1	Lung	0.4
Macrophages LPS	0.2	Thymus	0.2

HUVEC none	0.0	Kidney	1.2
HUVEC starved	0.0		

General_screening_panel_v1.4 Summary: Ag4681 Highest expression of this gene is seen in a brain cancer cell line (CT=20.3). Prominent expression of this gene is also seen in a cluster of samples derived from brain cancer cell lines. High levels of expression are also seen in cell lines from colon, renal, ovarian, lung, breast, prostate, and melanoma cancers. This gene encodes a homolog of tenascin-C, an extracellular matrix protein that appears at active sites of tissue remodelling during cancer invasion. Tenascin has been shown to be highly expressed around tumours, including invasive breast carcinomas and may be expressed by these invasive carcinomas (Adams M. Cancer Res 2002 Jun 1;62(11):3289-97). Zagzag et. al has suggested a potential role for tenascin-C in pathological angiogenesis (Cancer Res 2002 May 1;62(9):2660-8). Thus, expression of this gene could be used to differentiate between these cell lines and other samples on this panel, and as a marker of brain cancer. Based on the homology of this gene to tenascin-C and the expression in brain cancer cell lines, therapeutic modulation of the expression or function of this protein may be useful in the treatment of colon, brain, renal, ovarian, lung, breast, prostate, and melanoma cancers.

Oncology_cell_line_screening_panel_v3.1 Summary: Ag4681 Highest expression of this gene is seen in a brain cancer cell line (CT=23.7), consistent with expression in panel 1.4. In addition, high levels of expression are seen in other cell lines on this panel, including samples from gastric and lung cancers. See Panel 1.4 for discussion of this gene in cancer.

Panel 4.1D Summary: Ag4681 Highest expression of this gene is seen in IL-4 treated dermal fibroblasts (CT=22.72). High levels of expression of this gene are seen in treated and untreated lung and dermal fibroblasts, keratinocytes, astrocytes, and bronchial and small airway epithelium. Moderate to low levels of expression of this gene is also seen in naive T cells, resting and activated dendritic cells and activated B lymphocytes. Expression of this gene in dendritic cells suggests a role for this gene in antigen presentation. This gene has homology to tenascin-C, an extracellular matrix glycoprotein that is expressed during inflammatory and fibrotic disorders, and specifically, is deposited in increased amounts in the asthmatic airway (Johnson PR. Clin Exp Pharmacol Physiol 2001 Mar;28(3):233-6). The preferential expression of this gene in cells derived from the

lung and skin suggests that this gene product may be involved in normal conditions as well as pathological and inflammatory lung and skin disorders that include chronic obstructive pulmonary disease, asthma, allergy, psoriasis and emphysema.

5 **AK. CG56054-02: Integrin alpha 7-like protein.**

Expression of gene CG56054-02 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6428, Ag6429, Ag6430, Ag6431, Ag6439, Ag6413 and Ag6964, described in Tables AKA, AKB, AKC, AKD, AKE, AKF, AKG, AKH, AKI and AKJ. Results of the RTQ-PCR runs are shown in Tables AKK, AKL, AKM, AKN, AKO and

10 AKP.

Table AKA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - ccaggtcaccttctacctcatc-3'	22	2435	414
Probe	TET-5' - cttagcacctccgggacagcatt- 3' - TAMRA	24	2457	415
Reverse	5' - aacagcagctctacctccagtt-3'	22	2491	416

Table AKB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - gatgtggacagtagggatagga-3'	22	2874	417
Probe	TET-5' - ccacctgagcagcaggagcct-3' - TAMRA	21	2913	418
Reverse	5' -gcgcagtcagggtg-3'	15	2999	419

Table AKC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' -ctgggttctgccagca-3'	16	742	420

Probe	TET-5'- cacagctgccgccttctccc-3'- TAMRA	20	761	421
Reverse	5'-aaaagcaaccccttccaa-3'	18	824	422

Table AKD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcattctaccatgggagca- 3'	20	1394	423
Probe	TET-5'- ccttcacaggtgctggagggc- 3'-TAMRA	21	1434	424
Reverse	5'-agggagtagccgaagctct- 3'	19	1471	425

Table AKE. Probe Name Ag6429

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgtgccccagtaccat-3'	17	3382	426
Probe	TET-5'- cgggcaccatcctgaggaacaac- 3'-TAMRA	23	3448	427
Reverse	5'-gggcccagccaggat-3'	15	3484	428

Table AKF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga- 3'	23	843	429
Probe	TET-5'- ccccgaccagctggtgtataaaactttg -3'-TAMRA	28	866	430
Reverse	5'-gggagccggtcagca-3'	15	899	431

5

Table AKG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcacccctggactgc-3'	19	2993	432
Probe	TET-5'- tggtgttcagctgcccactctacag- 3'-TAMRA	25	3034	433

Reverse	5'-ccgcgcggtcaaa-3'	13	3060	434
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Table AKH. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtgggtggcagaaggagt-3'	19	3250	435
Probe	TET-5'- ccctgggtgggtcatcctctg-3'-TAMRA	21	3270	436
Reverse	5'- gaagaatcccatcttccacag-3'	21	3336	437

Table AKI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'- ggtgaagacaagatctgccag-3'	21	2073	438
Probe	TET-5'- tgtaccgggtcagcgacacg-3'-TAMRA	21	2124	439
Reverse	5'-gctgttggttccatccacatc-3'	20	2166	440

Table AKJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	3079	441
Probe	TET-5'- actctacagctttgaccgcgcgg-3'-TAMRA	23	3050	442
Reverse	5'-gccaaactgtgtggtgttca-3'	19	3024	443

5 Table AKK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	21.6	19.2
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	28.9	49.7
AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	6.1	20.4

AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	17.6	5.6
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	42.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	90.1
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	32.5	28.5
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	37.9	86.5
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	6.4	0.0
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	24.5	16.8
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	27.5	21.6
AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	9.0	5.7
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	30.4	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	38.7	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	47.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	50.3	59.9
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	24.0	46.7
Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	14.9	50.0

Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	16.5	9.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	23.8	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	39.8	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	24.8	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	11.9	31.0
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	21.6	39.5
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	16.0	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	10.2	4.9
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	18.6	11.1
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	22.7	42.3
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	22.1	14.8
Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	7.2	8.8
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	29.3	82.4
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	19.2	8.8

Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	13.6	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	39.5	100.0
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	7.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	5.9	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.4	32.8
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	15.7	9.2
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	37.1	28.1
Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	10.8	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	37.9	69.3
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	18.7	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	12.0	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	27.9	27.5

Table AKL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0

Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF- 539	0.2

Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AKM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1

Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF- 539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB- 75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB- 19	63.7

Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AKN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	20.0	8.2	17.4	13.8	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.5	0.8	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.0	4.1	0.6	2.5	2.2	2.9	2.4
Melanoma* M14	0.3	0.0	0.7	0.7	0.4	0.4	0.4	0.7

Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	0.0	30.4	22.5	18.2	14.6	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.1
Testis Pool	5.2	0.0	8.8	4.2	10.4	9.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	2.5	1.0	1.9	1.8	1.3	4.3
Prostate Pool	8.1	0.0	11.5	8.5	11.3	12.1	28.5	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.1	0.5	0.4
Uterus Pool	2.2	0.0	4.5	2.6	4.6	4.5	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	1.1	0.8	0.7	1.1	1.6	4.0
Ovarian ca. SK-OV-3	0.8	0.0	1.7	1.5	0.8	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.5	0.4	0.8	0.9	0.5
Ovarian ca. OVCAR-5	1.6	0.0	2.9	1.5	1.3	1.7	1.4	7.9
Ovarian ca. IGROV-1	100.0	100.0	77.9	90.8	84.7	97.9	69.3	75.8
Ovarian ca. OVCAR-8	13.6	5.6	14.0	11.9	15.6	14.6	17.3	16.7
Ovary	2.7	0.0	5.2	2.1	3.1	2.3	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.4	0.1	0.2	0.5	0.5
Breast ca. MDA-MB- 231	0.1	0.0	0.4	0.4	0.2	0.2	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.3	0.1	0.5	0.6	0.4
Breast ca. T47D	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.5

Breast ca. MDA-N	0.6	0.0	0.7	0.7	0.6	0.6	0.6	0.8
Breast Pool	15.0	0.0	21.8	19.5	14.6	10.7	12.2	16.7
Trachea	4.5	0.0	8.4	2.9	4.8	4.2	4.7	5.6
Lung	2.8	0.0	2.3	1.3	4.2	3.2	3.9	5.1
Fetal Lung	3.9	0.0	9.1	4.0	5.0	4.8	5.3	6.1
Lung ca. NCI-N417	2.0	2.0	3.5	2.7	3.3	2.6	4.0	2.3
Lung ca. LX- 1	3.5	3.1	6.5	7.0	5.0	3.5	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.5	0.1	0.2	0.1	0.1
Lung ca. SHP-77	4.0	2.3	6.8	6.3	5.3	4.5	4.5	3.8
Lung ca. A549	0.3	0.0	0.9	0.3	0.0	0.4	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.7	0.6	0.3	0.4	0.5
Lung ca. NCI-H23	2.9	0.0	4.6	4.5	4.8	3.2	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.5	0.6	1.0	0.6	0.5	0.7
Lung ca. NCI-H522	1.7	0.0	2.3	2.4	1.7	1.3	3.3	8.9
Liver	0.1	0.0	0.0	0.1	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.0	1.1	0.6	0.6	0.5	0.8	8.2
Liver ca. HepG2	0.1	0.0	0.2	0.1	0.0	0.2	0.1	2.4
Kidney Pool	27.9	6.5	47.0	34.9	33.9	28.1	43.2	32.8
Fetal Kidney	1.4	0.0	4.9	5.1	4.1	4.0	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.2	0.3	0.1	0.3	0.9

Renal ca. A498	0.0	0.0	0.2	0.1	0.0	0.3	0.5	8.5
Renal ca. ACHN	1.5	0.0	2.5	0.7	1.7	1.5	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.3	0.2	0.2	0.6	0.3
Renal ca. TK-10	1.9	0.0	3.1	2.5	2.0	1.9	2.1	4.6
Bladder	4.2	0.0	5.9	3.0	5.5	5.1	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	1.7	0.9	1.2	1.1	6.7
Gastric ca. KATO III	0.4	0.0	0.8	0.4	0.2	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.0	0.2	0.0	0.2	0.2	0.3	1.2
Colon ca. SW480	20.9	9.5	41.8	39.0	27.0	23.3	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	16.4	15.5	12.8	10.3	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.2	0.2	0.0	0.3
Colon ca. HCT-116	2.1	1.6	3.2	3.8	2.5	2.0	2.1	4.3
Colon ca. CaCo-2	15.0	10.4	27.0	22.2	19.1	16.7	18.3	38.2
Colon cancer tissue	9.0	0.0	11.0	6.5	11.9	7.6	7.7	20.4
Colon ca. SW1116	1.3	0.0	2.5	1.7	2.0	1.5	1.8	6.0
Colon ca. Colo-205	0.1	0.0	0.3	0.2	0.2	0.0	0.2	0.8
Colon ca. SW-48	0.8	0.0	1.4	1.3	1.5	1.5	1.4	2.6
Colon Pool	20.3	0.0	28.1	28.7	23.2	18.7	25.5	20.6

Small Intestine Pool	14.0	0.0	17.1	10.5	11.2	13.0	12.8	10.4
Stomach Pool	8.1	0.0	14.3	6.2	9.5	9.3	8.5	10.7
Bone Marrow Pool	6.8	0.0	14.3	11.3	10.2	8.7	18.7	12.5
Fetal Heart	10.1	0.0	25.5	24.3	24.5	21.8	33.7	20.7
Heart Pool	28.7	5.2	29.7	23.0	25.9	17.2	33.7	26.1
Lymph Node Pool	17.6	0.0	33.7	30.4	22.1	23.7	19.9	24.7
Fetal Skeletal Muscle	31.9	36.9	54.3	46.7	48.6	46.3	19.1	50.7
Skeletal Muscle Pool	17.4	12.3	29.3	21.5	29.5	25.9	22.1	32.3
Spleen Pool	0.9	0.0	1.9	2.0	2.0	1.7	2.7	3.1
Thymus Pool	4.4	0.0	10.4	7.5	8.1	9.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	14.9	6.1	10.7	10.0	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	4.7	2.9	3.8	3.1	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	1.7	2.1	1.0	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.2	0.1	0.2	0.1	0.1
CNS cancer (astro) SNB-75	8.1	1.9	14.9	5.9	6.5	10.0	11.7	9.7
CNS cancer (glio) SNB-19	79.6	84.1	100.0	100.0	100.0	100.0	100.0	100.0
CNS cancer (glio) SF-295	8.2	1.8	11.3	9.0	8.0	7.8	8.2	14.8

Brain (Amygdala) Pool	3.7	2.3	7.7	6.9	6.2	4.8	8.0	5.3
Brain (cerebellum)	12.0	6.6	19.8	11.1	10.7	9.7	8.8	9.7
Brain (fetal)	4.2	3.0	12.7	11.5	6.6	5.6	6.8	6.4
Brain (Hippocamp us) Pool	7.5	3.1	11.7	11.0	8.6	6.9	11.0	10.2
Cerebral Cortex Pool	9.7	1.7	11.0	7.5	7.5	0.7	11.6	8.7
Brain (Substantia nigra) Pool	7.4	1.8	11.7	8.5	10.4	4.7	10.0	9.3
Brain (Thalamus) Pool	7.6	0.0	13.2	10.0	9.3	0.2	9.7	8.7
Brain (whole)	6.1	0.0	10.6	8.0	5.8	0.3	5.6	8.7
Spinal Cord Pool	10.1	3.2	14.7	12.8	11.0	7.6	12.2	9.0
Adrenal Gland	3.5	0.0	9.9	6.1	3.9	3.7	4.8	4.1
Pituitary gland Pool	0.9	0.0	1.1	0.8	1.2	1.1	1.4	0.5
Salivary Gland	0.9	0.0	1.8	1.1	1.3	0.9	1.1	1.0
Thyroid (female)	2.0	0.0	3.1	0.8	2.5	2.5	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.8	0.8	0.7	0.6	0.7	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.1	1.6	3.2	2.3

Table AKO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	1.3	0.0	0.7	0.0
Secondary Th2 act	0.5	0.3	1.2	0.0	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.4	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.3	0.0	0.4	0.0
Primary Tr1 act	0.1	0.0	0.7	0.0	0.7	0.0
Primary Th1 rest	0.0	0.0	0.1	0.0	0.3	1.2
Primary Th2 rest	0.0	0.0	0.4	0.0	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	5.4	0.0	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	1.5	0.0	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.7	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	8.8	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.4	0.0	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.5	0.0	0.4	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2
LAK cells rest	5.6	5.0	11.8	0.1	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+IL- 12	0.2	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.1	0.1	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	3.4	0.0	2.5	1.4
Two Way MLR 3 day	1.4	1.1	2.2	0.0	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.8	0.0	0.9	0.0
Two Way MLR 7 day	2.3	0.7	1.1	0.0	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	1.3	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.6	0.0	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.7	0.0	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.9	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	29.1	0.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	4.1	0.0	5.3	0.0
Dendritic cells LPS	1.6	0.3	1.0	0.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	0.5	0.0	0.2	0.0
Monocytes rest	0.2	0.0	0.4	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	5.7	0.0	1.8	2.6
Macrophages rest	0.9	1.8	0.6	0.0	0.6	0.0
Macrophages LPS	7.5	4.0	5.4	0.1	6.3	9.2
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0

HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.4	0.0	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.4	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronary artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronary artery SMC TNFalpha + IL-1beta	0.4	0.9	0.3	0.0	1.5	0.0
Astrocytes rest	67.8	97.3	100.0	12.0	100.0	100.0
Astrocytes TNFalpha + IL-1beta	100.0	100.0	97.3	100.0	74.7	95.9
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL- 1beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	2.6	0.0	6.7	8.5
NCI-H292 none	0.3	0.3	1.7	0.0	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.7	0.0	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.9	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.5	0.0	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	95.9	0.2	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	48.6	0.1	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	27.4	0.1	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	24.0	0.1	26.8	96.6
Lung fibroblast IL- 13	31.6	14.6	11.9	0.0	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	55.9	0.2	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	6.0	0.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	2.7	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	5.6	0.0	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	30.6	0.1	20.2	26.6
Dermal fibroblast IL-4	10.7	14.6	30.8	0.1	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	54.3	0.1	46.7	47.3

Neutrophils TNFa+LPS	0.7	0.0	0.9	0.0	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.6	0.0	9.5	8.4
Lung	2.2	1.2	2.8	0.0	4.6	2.1
Thymus	3.1	0.8	0.0	0.0	0.4	2.4
Kidney	4.2	4.4	7.8	0.1	9.7	5.2

Table AKP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	100.0	100.0	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2

Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus,

cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

- 5 **General_screening_panel_v1.5 Summary:** Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

- 10 In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

- 15 **Summary:** Ag6413/Ag6424/Ag6428/Ag6430/Ag6431/Ag6439/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous
20 system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6429 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D

- 25 **Summary:** Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

- 30 In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AL. CG56054-03: Integrin alpha 7-like protein.

Expression of gene CG56054-03 was assessed using the primer-probe sets Ag6424, Ag6425, Ag6428, Ag6430 and Ag6432, described in Tables ALA, ALB, ALC, ALD and ALE. Results of the RTQ-PCR runs are shown in Tables ALF, ALG and ALH.

Table ALA. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	444

Probe	TET-5' - cacagctgccgccttctccc-3' - TAMRA	20	761	445
Reverse	5' -aaaagcaaccccttccaa-3'	18	824	446

Table ALB. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' -cggatgcacaccccat-3'	16	1981	447
Probe	TET-5' - catcccgagctgggcccc-3' - TAMRA	18	2013	448
Reverse	5' -gccttggatgcccat-3'	15	2032	449

Table ALC. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' -cttcacatcaccatgggagca- 3'	20	1394	450
Probe	TET-5' - ccttcacaggtgctggagggc- 3' -TAMRA	21	1434	451
Reverse	5' -agggagtagccgaagctct- 3'	19	1471	452

Table ALD. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' -gtgaccaacattgatagctcaga- 3'	23	843	453
Probe	TET-5' - ccccgaccagctggtgtataaaactttg- 3' -TAMRA	28	866	454
Reverse	5' -gggagccggtcagca-3'	15	899	455

5

Table ALE. Probe Name Ag6432

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5' - gacctgtcctacagtctccagac- 3'	24	1934	456

Probe	TET-5' - tgacacccccatcctggctgct- 3' -TAMRA	22	1985	457
Reverse	5' -gctcgggatgcccg-3'	15	2008	458

Table ALF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085
AD 1 Hippo	18.0	20.0
AD 2 Hippo	32.3	48.0
AD 3 Hippo	3.7	11.6
AD 4 Hippo	10.7	17.1
AD 5 hippo	53.2	39.2
AD 6 Hippo	100.0	100.0
Control 2 Hippo	18.7	17.9
Control 4 Hippo	27.0	38.4
Control (Path) 3 Hippo	4.6	10.2
AD 1 Temporal Ctx	12.9	12.1
AD 2 Temporal Ctx	31.0	36.6
AD 3 Temporal Ctx	6.0	11.7
AD 4 Temporal Ctx	20.2	15.6
AD 5 Inf Temporal Ctx	39.2	43.8
AD 5 Sup Temporal Ctx	42.0	56.6
AD 6 Inf Temporal Ctx	49.3	40.9
AD 6 Sup Temporal Ctx	48.3	44.1
Control 1 Temporal Ctx	12.9	11.9
Control 2 Temporal Ctx	18.2	16.7
Control 3 Temporal Ctx	9.6	13.0
Control 4 Temporal Ctx	15.2	18.9
Control (Path) 1 Temporal Ctx	27.0	32.5
Control (Path) 2 Temporal Ctx	16.0	19.5

Control (Path) 3 Temporal Ctx	7.5	12.9
Control (Path) 4 Temporal Ctx	17.1	19.8
AD 1 Occipital Ctx	10.2	16.2
AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 3 Occipital Ctx	6.4	11.7
AD 4 Occipital Ctx	13.0	12.6
AD 5 Occipital Ctx	25.3	16.7
AD 6 Occipital Ctx	20.2	17.8
Control 1 Occipital Ctx	6.0	11.3
Control 2 Occipital Ctx	26.4	24.8
Control 3 Occipital Ctx	10.7	16.4
Control 4 Occipital Ctx	12.0	12.1
Control (Path) 1 Occipital Ctx	35.6	32.8
Control (Path) 2 Occipital Ctx	6.7	9.6
Control (Path) 3 Occipital Ctx	5.4	8.4
Control (Path) 4 Occipital Ctx	13.2	15.9
Control 1 Parietal Ctx	8.8	15.2
Control 2 Parietal Ctx	34.4	39.5
Control 3 Parietal Ctx	11.5	14.5
Control (Path) 1 Parietal Ctx	34.2	33.4
Control (Path) 2 Parietal Ctx	19.6	20.0
Control (Path) 3 Parietal Ctx	3.9	15.0
Control (Path) 4 Parietal Ctx	24.8	28.3

Table ALG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443
Adipose	0.0	2.6	20.0	8.2

Melanoma* Hs688(A).T	0.0	0.0	2.0	0.5
Melanoma* Hs688(B).T	0.0	0.2	4.1	0.6
Melanoma* M14	0.0	0.0	0.7	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0
Melanoma* SK-MEL-5	0.0	2.2	30.4	22.5
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3
Testis Pool	0.0	3.5	8.8	4.2
Prostate ca.* (bone met) PC-3	0.0	0.5	2.5	1.0
Prostate Pool	0.0	1.0	11.5	8.5
Placenta	0.0	0.0	0.7	0.1
Uterus Pool	0.0	1.5	4.5	2.6
Ovarian ca. OVCAR-3	0.0	0.3	1.1	0.8
Ovarian ca. SK-OV-3	0.0	0.2	1.7	1.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.5
Ovarian ca. OVCAR-5	0.0	1.3	2.9	1.5
Ovarian ca. IGROV-1	100.0	100.0	77.9	90.8
Ovarian ca. OVCAR-8	5.6	21.9	14.0	11.9
Ovary	0.0	0.3	5.2	2.1
Breast ca. MCF-7	0.0	0.0	0.3	0.4
Breast ca. MDA-MB- 231	0.0	0.0	0.4	0.4
Breast ca. BT 549	0.0	0.0	0.5	0.3
Breast ca. T47D	0.0	0.0	0.5	0.3
Breast ca. MDA-N	0.0	0.0	0.7	0.7
Breast Pool	0.0	4.1	21.8	19.5
Trachea	0.0	0.7	8.4	2.9
Lung	0.0	0.7	2.3	1.3
Fetal Lung	0.0	0.3	9.1	4.0
Lung ca. NCI-N417	2.0	0.9	3.5	2.7

Lung ca. LX-1	3.1	2.7	6.5	7.0
Lung ca. NCI-H146	0.0	0.0	0.3	0.5
Lung ca. SHP-77	2.3	0.4	6.8	6.3
Lung ca. A549	0.0	2.6	0.9	0.3
Lung ca. NCI-H526	0.0	0.0	0.9	0.7
Lung ca. NCI-H23	0.0	1.0	4.6	4.5
Lung ca. NCI-H460	0.0	0.0	0.2	0.2
Lung ca. HOP-62	0.0	0.0	0.5	0.6
Lung ca. NCI-H522	0.0	0.6	2.3	2.4
Liver	0.0	0.0	0.0	0.1
Fetal Liver	0.0	0.3	1.1	0.6
Liver ca. HepG2	0.0	0.3	0.2	0.1
Kidney Pool	6.5	0.0	47.0	34.9
Fetal Kidney	0.0	0.0	4.9	5.1
Renal ca. 786-0	0.0	0.0	0.2	0.2
Renal ca. A498	0.0	1.8	0.2	0.1
Renal ca. ACHN	0.0	0.5	2.5	0.7
Renal ca. UO-31	0.0	0.0	0.5	0.3
Renal ca. TK-10	0.0	0.4	3.1	2.5
Bladder	0.0	0.0	5.9	3.0
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.7
Gastric ca. KATO III	0.0	0.5	0.8	0.4
Colon ca. SW-948	0.0	1.5	0.2	0.0
Colon ca. SW480	9.5	5.2	41.8	39.0
Colon ca.* (SW480 met) SW620	7.7	4.8	16.4	15.5
Colon ca. HT29	0.0	0.0	0.0	0.0
Colon ca. HCT-116	1.6	0.2	3.2	3.8
Colon ca. CaCo-2	10.4	3.6	27.0	22.2
Colon cancer tissue	0.0	3.3	11.0	6.5
Colon ca. SW1116	0.0	3.0	2.5	1.7

Colon ca. Colo-205	0.0	0.4	0.3	0.2
Colon ca. SW-48	0.0	3.6	1.4	1.3
Colon Pool	0.0	5.0	28.1	28.7
Small Intestine Pool	0.0	1.7	17.1	10.5
Stomach Pool	0.0	2.3	14.3	6.2
Bone Marrow Pool	0.0	1.6	14.3	11.3
Fetal Heart	0.0	2.3	25.5	24.3
Heart Pool	5.2	7.0	29.7	23.0
Lymph Node Pool	0.0	6.1	33.7	30.4
Fetal Skeletal Muscle	36.9	5.2	54.3	46.7
Skeletal Muscle Pool	12.3	9.2	29.3	21.5
Spleen Pool	0.0	0.0	1.9	2.0
Thymus Pool	0.0	2.0	10.4	7.5
CNS cancer (glio/astro) U87-MG	1.6	1.5	14.9	6.1
CNS cancer (glio/astro) U-118-MG	0.0	0.3	4.7	2.9
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	2.6	1.7
CNS cancer (astro) SF- 539	0.0	0.0	0.0	0.2
CNS cancer (astro) SNB-75	1.9	1.1	14.9	5.9
CNS cancer (glio) SNB-19	84.1	79.0	100.0	100.0
CNS cancer (glio) SF- 295	1.8	0.0	11.3	9.0
Brain (Amygdala) Pool	2.3	0.8	7.7	6.9
Brain (cerebellum)	6.6	0.4	19.8	11.1
Brain (fetal)	3.0	0.7	12.7	11.5
Brain (Hippocampus) Pool	3.1	3.2	11.7	11.0
Cerebral Cortex Pool	1.7	0.6	11.0	7.5
Brain (Substantia nigra) Pool	1.8	2.2	11.7	8.5

Brain (Thalamus) Pool	0.0	2.7	13.2	10.0
Brain (whole)	0.0	0.4	10.6	8.0
Spinal Cord Pool	3.2	2.3	14.7	12.8
Adrenal Gland	0.0	0.3	9.9	6.1
Pituitary gland Pool	0.0	0.0	1.1	0.8
Salivary Gland	0.0	0.0	1.8	1.1
Thyroid (female)	0.0	0.3	3.1	0.8
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.8
Pancreas Pool	0.0	0.0	2.0	1.1

Table ALH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563
Secondary Th1 act	0.0	1.3	0.0
Secondary Th2 act	0.0	1.2	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.4	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.0
Primary Tr1 act	0.0	0.7	0.0
Primary Th1 rest	0.0	0.1	0.0
Primary Th2 rest	0.0	0.4	0.0
Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	0.0
CD8 lymphocyte act	0.0	0.7	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0

CD4 lymphocyte none	0.0	0.5	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0
LAK cells rest	2.7	11.8	0.1
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	0.1
NK Cells IL-2 rest	0.0	3.4	0.0
Two Way MLR 3 day	0.0	2.2	0.0
Two Way MLR 5 day	0.0	0.8	0.0
Two Way MLR 7 day	13.2	1.1	0.0
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0
PBMC PHA-L	0.0	0.6	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL- 4	0.0	0.9	0.0
EOL-1 dbcAMP	9.1	29.1	0.1
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0
Dendritic cells none	13.8	4.1	0.0
Dendritic cells LPS	0.0	1.0	0.0
Dendritic cells anti-CD40	3.3	0.5	0.0
Monocytes rest	0.0	0.4	0.0
Monocytes LPS	0.0	5.7	0.0
Macrophages rest	0.0	0.6	0.0
Macrophages LPS	0.0	5.4	0.1
HUVEC none	0.0	0.0	0.0

HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0
Lung Microvascular EC none	0.0	0.4	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microvascular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronary artery SMC rest	0.0	0.0	0.0
Coronary artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0
Astrocytes rest	100.0	100.0	12.0
Astrocytes TNFalpha + IL-1beta	74.2	97.3	100.0
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	0.0
NCI-H292 none	0.0	1.7	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0

NCI-H292 IL-13	0.0	0.9	0.0
NCI-H292 IFN gamma	0.0	0.5	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	0.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	0.1
Lung fibroblast IL-4	19.1	27.4	0.1
Lung fibroblast IL-9	23.5	24.0	0.1
Lung fibroblast IL-13	4.5	11.9	0.0
Lung fibroblast IFN gamma	15.7	55.9	0.2
Dermal fibroblast CCD1070 rest	0.0	6.0	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.0
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.0
Dermal fibroblast IFN gamma	8.5	30.6	0.1
Dermal fibroblast IL-4	4.1	30.8	0.1
Dermal Fibroblasts rest	8.0	54.3	0.1
Neutrophils TNFa+LPS	0.0	0.9	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	4.6	0.0
Lung	0.0	2.8	0.0
Thymus	0.0	0.0	0.0
Kidney	4.9	7.8	0.1

CNS_neurodegeneration_v1.0 Summary: Ag6428/Ag6430 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6424/Ag6425/Ag6428/Ag6430

Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-31). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary Ag6425/Ag6428/Ag6430 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6424/Ag6432 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AM. CG56054-04: Integrin alpha 7-like protein.

Expression of gene CG56054-04 was assessed using the primer-probe sets Ag6424, Ag6427, Ag6430 and Ag6434, described in Tables AMA, AMB, AMC and AMD. Results of the RTQ-PCR runs are shown in Tables AME, AMF and AMG.

Table AMA. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	459
Probe	TET-5'- cacagctgccgccttctctccc-3'- TAMRA	20	761	460
Reverse	5'-aaaagcaacccttccaa-3'	18	824	461